

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 14:30:56 ; Search time 6 Seconds
(without alignments)
3.134 Million cell updates/sec

Title: us-10-006-191-19
Perfect score: 1049
Sequence: 1 ttgaactgattcacatctca.....gtgtatatatttttttataaaa 1049

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 501 seqs, 8964 residues

Total number of hits satisfying chosen parameters: 1002

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 545 summaries

Database : rng.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34.4	3.3	40	1	AAQ34094
2	33.6	3.2	41	1	AAH77495
3	32	3.1	32	1	ABK66312
4	30.2	2.9	37	1	AAQ33710
5	25.2	2.4	30	1	AAZ298502
6	25	2.4	25	1	AAAI5467
7	23.4	2.2	25	1	AAAI5468
8	23.4	2.2	27	1	AAI61970
9	23	2.2	24	1	AAI30425
10	23	2.2	24	1	AAH39074
11	22.2	2.1	27	1	AAQ34044
12	22.2	2.1	27	1	AAQ33678
13	22.2	2.1	27	1	AAQ33804
14	22.2	2.1	27	1	AAQ34181
15	22.2	2.1	27	1	AAQ34012
16	22.2	2.1	27	1	AAQ34143
17	22.2	2.1	27	1	AAI65733
18	22.2	2.1	27	1	AAH46005
19	22	2.1	22	1	AAI30426
20	21.8	2.1	25	1	AAQ33918
21	21.8	2.1	25	1	AAQ33642
22	21.8	2.1	25	1	AAQ33962
23	21.8	2.1	25	1	AAI65734
24	21.8	2.1	26	1	AAQ34083
25	21.8	2.1	26	1	AAQ33684
26	21.8	2.1	26	1	AAQ33704
27	21.8	2.1	26	1	AAQ33831
28	21.8	2.1	26	1	AAQ33837
29	21.8	2.1	27	1	AAQ33740
30	21.8	2.1	27	1	AAQ33951
31	21.8	2.1	27	1	AAH24300
32	21.8	2.1	27	1	AAH46017
33	21.8	2.1	27	1	AAH46001

C	34	21.8	2.1	27	1	AAI60473	Oligonucleotide cl
	35	21.4	2.0	23	1	AAQ33563	Microsatellite seq
	36	21.4	2.0	23	1	AAQ33773	Microsatellite seq
C	37	21.4	2.0	23	1	AAQ33885	Microsatellite seq
	38	21.4	2.0	23	1	AAI66105	Repeat sequence fo
	39	21.4	2.0	23	1	AAI39005	SNP specific upper
	40	21.4	2.0	23	1	AAQ33986	Microsatellite seq
	41	21.4	2.0	24	1	AAQ34158	Sequence of a micr
	42	21.4	2.0	24	1	AAQ33909	Microsatellite seq
	43	21.4	2.0	24	1	AAQ34065	Microsatellite seq
	44	21.4	2.0	24	1	AAQ34024	Microsatellite seq
C	45	21.4	2.0	24	1	AAQ33707	Microsatellite seq
	46	21.4	2.0	24	1	AAI66096	Repeat sequence fo
	47	21.4	2.0	24	1	AAH46015	Synthetic oligonuc
	48	21.4	2.0	24	1	AAH46016	Synthetic oligonuc
	49	21.4	2.0	24	1	AAI99862	Immunostimulatory
	50	21.4	2.0	24	1	AB578584	Angiogenesis inhib
	51	21.4	2.0	24	1	ACH03377	Immunostimulatory
	52	21.4	2.0	24	1	ADB37364	Immunostimulatory
	53	21.4	2.0	25	1	AAQ33861	Microsatellite seq
C	54	21.4	2.0	25	1	AAH40163	SNP specific SNPE
	55	21.4	2.0	25	1	AAH38303	SNP specific SNPE
	56	21.4	2.0	26	1	AAQ47179	MHC DR A intron bi
	57	21.2	2.0	26	1	AAQ44016	Target sequence #8
	58	21	2.0	21	1	AAQ33891	Microsatellite seq
	59	21	2.0	21	1	AAQ33879	Microsatellite seq
C	60	21	2.0	21	1	AAI65738	Repeat sequence fr
	61	21	2.0	21	1	AAH46013	Synthetic oligonuc
	62	21	2.0	21	1	AAI99702	Immunostimulatory
	63	21	2.0	21	1	AB578423	Angiogenesis inhib
C	64	21	2.0	21	1	ABX87131	Human connective t
	65	21	2.0	21	1	ACH03241	Immunostimulatory
	66	21	2.0	21	1	ADB37204	Microsatellite seq
	67	21	2.0	22	1	AAQ33810	Microsatellite seq
	68	21	2.0	22	1	AAQ33675	Microsatellite seq
	69	21	2.0	22	1	AAQ34038	Microsatellite seq
	70	21	2.0	22	1	AAQ34080	Microsatellite seq
	71	21	2.0	22	1	AAQ33891	Microsatellite seq
C	72	21	2.0	22	1	AAQ83952	Oligonucleotide cl
	73	21	2.0	22	1	AAI65727	Repeat sequence fr
C	74	21	2.0	22	1	AAI64448	SSR motif #8. Uni
	75	21	2.0	23	1	AAI60472	Oligonucleotide cl
C	76	21	2.0	25	1	AAH40155	SNP specific SNPE
	77	21	2.0	25	1	AAH40159	SNP specific SNPE
C	78	20.6	2.0	23	1	ADB69512	5' anchored (ISSR)
	79	20	1.9	20	1	AAQ34170	Sequence of a micr
	80	20	1.9	20	1	AAQ33816	Microsatellite seq
	81	20	1.9	20	1	AAQ33672	Microsatellite seq
C	82	20	1.9	20	1	AAI30427	Compound simple se
	83	20	1.9	20	1	AAI93829	Antitumoural phosph
	84	20	1.9	20	1	AAV06824	Oligonucleotide wh
	85	20	1.9	20	1	AAI39091	20-mer oligonucleo
	86	20	1.9	20	1	AAI33762	Simple sequence re
C	87	20	1.9	20	1	AAI33705	Simple sequence re
	88	20	1.9	20	1	AAI75569	Mrell related prob
C	89	20	1.9	20	1	AAI62932	Human PEPCK-cytoso
	90	20	1.9	20	1	AAI28355	DNA oligomer #5.
C	91	20	1.9	20	1	AAH48201	Antibody binding o
	92	20	1.9	20	1	AAI64445	SSR motif #5. Uni
C	93	20	1.9	20	1	AAI64449	SSR motif #9. Uni
	94	20	1.9	20	1	ABX87132	Human connective t
	95	20	1.9	20	1	AAI45125	Oligonucleotide sy
C	96	20	1.9	20	1	AAI96307	Oligonucleotide SE
	97	20	1.9	20	1	ABX96306	Oligonucleotide (C
C	98	20	1.9	20	1	AB224438	Oligonucleotide (T
	99	20	1.9	20	1	AB224439	Human connective t
C	100	20	1.9	20	1	ADB25647	Human connective t
	101	20	1.9	20	1	ADB25669	Human connective t
C	102	20	1.9	20	1	ADB25654	Human connective t
	103	20	1.9	20	1	ADB25649	Human connective t
C	104	20	1.9	20	1	ADB25648	Human connective t
	105	20	1.9	20	1	ADB25653	Human connective t
C	106	20	1.9	20	1	ADB25656	Human connective t

C 107	20	1.9	20	1	ADB25671	Human connective t	C 180	17.4	1.7	20	1	AA521755	Mouse Survivin ant
C 108	20	1.9	20	1	ADB25666	Human connective t	C 181	17.4	1.7	20	1	AB597835	Human NADPH quinon
C 109	20	1.9	20	1	ADB25702	Human connective t	C 182	17	1.6	17	1	AAQ34164	Sequence of a micr
C 110	20	1.9	20	1	ADB25652	Human connective t	C 183	17	1.6	17	1	AAQ33783	Microsatellite seq
C 111	20	1.9	20	1	ADB25703	Human connective t	C 184	17	1.6	17	1	AA568655	WO9513834 Oligonuc
C 112	20	1.9	20	1	ADB25655	Human connective t	C 185	17	1.6	17	1	AA766099	Repeat sequence fo
C 113	20	1.9	20	1	ADB25650	Human connective t	C 186	17	1.6	17	1	AA761062	Methylphosphonate
C 114	20	1.9	20	1	ADB25651	Human connective t	C 187	17	1.6	17	1	AA761062	5', variation gener
C 115	20	1.9	20	1	ADB25700	Human connective t	C 188	17	1.6	17	1	AA761062	5', variation gener
C 116	20	1.9	20	1	ADB25704	Human connective t	C 189	17	1.6	17	1	AA761062	5', variation gener
C 117	20	1.9	20	1	ADB25667	Human connective t	C 190	17	1.6	17	1	AA761062	5', variation gener
C 118	20	1.9	20	1	ADB25672	Human connective t	C 191	17	1.6	17	1	AA761062	5', variation gener
C 119	20	1.9	20	1	ADB25699	Human connective t	C 192	17	1.6	17	1	AA761062	5', variation gener
C 120	20	1.9	20	1	ADB25701	Human connective t	C 193	17	1.6	17	1	AA761062	5', variation gener
C 121	20	1.9	20	1	ADB25646	Human connective t	C 194	17	1.6	17	1	AA761062	5', variation gener
C 122	20	1.9	20	1	ADB25668	Human connective t	C 195	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 123	20	1.9	20	1	ADB25668	Human connective t	C 196	16.8	1.6	20	1	AAQ75581	Human MCL1 gene re
C 124	20	1.9	20	1	ADB25670	Human connective t	C 197	16.8	1.6	20	1	AAQ75581	Human MCL1 gene re
C 125	20	1.9	20	1	ADB26665	Polynucleotide (ds	C 198	16.8	1.6	20	1	AAQ75581	Human uridine diph
C 126	20	1.9	20	1	AA902096	Microsatellite seq	C 199	16.8	1.6	20	1	AAQ75581	Human uridine diph
C 127	20	1.9	20	1	AA902096	Oligonucleotide RT	C 200	16.8	1.6	20	1	AAQ75581	Human oligonucleot
C 128	20	1.9	20	1	AAH46014	Synthetic oligonuc	C 201	16.8	1.6	20	1	AAQ75581	EST polymorphic DN
C 129	20	1.9	20	1	ABN88973	Phosphorothioate 2	C 202	16.8	1.6	20	1	AAQ75581	Mouse connective t
C 130	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 203	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 131	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 204	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 132	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 205	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 133	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 206	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 134	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 207	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 135	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 208	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 136	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 209	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 137	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 210	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 138	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 211	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 139	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 212	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 140	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 213	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 141	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 214	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 142	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 215	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 143	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 216	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 144	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 217	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 145	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 218	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 146	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 219	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 147	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 220	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 148	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 221	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 149	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 222	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 150	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 223	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 151	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 224	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 152	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 225	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 153	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 226	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 154	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 227	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 155	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 228	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 156	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 229	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 157	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 230	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 158	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 231	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 159	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 232	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 160	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 233	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 161	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 234	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 162	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 235	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 163	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 236	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 164	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 237	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 165	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 238	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 166	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 239	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 167	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 240	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 168	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 241	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 169	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 242	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 170	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 243	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 171	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 244	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 172	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 245	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 173	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 246	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 174	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 247	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 175	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 248	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 176	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 249	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 177	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 250	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 178	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 251	16.8	1.6	20	1	AAQ75581	Reverse transcript
C 179	20	1.9	20	1	ABN88972	Phosphorothioate 2	C 252	16.8	1.6	20	1	AAQ75581	Reverse transcript

476	1	ABC683666	Oligonucleotide	SE
477	1,2	ABC683667	Oligonucleotide	SE
478	1,2	ABC1216	Oligonucleotide	SE
479	1,2	ABC14215	Oligonucleotide	SE
480	1,2	ABC96635	Oligonucleotide	SE
481	1,2	ABC87882	Oligonucleotide	SE
482	1,2	ABC89602	Oligonucleotide	SE
483	1,2	ASH25451	Oligonucleotide	SE
484	1,2	ASF87883	Oligonucleotide	SE
485	1,2	ASF64975	Oligonucleotide	SE
486	1,2	ASF83714	Oligonucleotide	SE
487	1,2	ABC23106	Oligonucleotide	SE
488	1,2	ABC23106	Oligonucleotide	SE
489	1,2	ABC23106	Oligonucleotide	SE

Oligonucleotide SE

AAH77495;
20-NOV-2001 (first entry)
Human zinc finger protein 14 coding sequence probe #1.
Human; zinc finger protein 14; cancer; haemopathy; HIV infection; immunological disease; inflammation; gene therapy; probe; ss.
Homo sapiens.
WO20016583-A1.
13-SEP-2001.
26-FEB-2001; 2001WO-CN000187.
10-MAR-2000; 2000CN-00111978.
(SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.
Mao Y, Xie Y;
WPI; 2001-555570/63.
New human zinc finger protein 14 for diagnosing and treating malignant neoplasm, hemopathy, human immunodeficiency virus infection, immunological diseases and various inflammations.
Example 6; Page 20; 37pp; Chinese.
The present invention provides the protein and coding sequences of human zinc finger protein 14. The sequences can be used in the treatment of human cancer, haemopathy, HIV infection, immunological diseases and inflammation. The present sequence is a probe for the coding sequence of the invention
Sequence 41 BP; 9 A; 0 C; 11 G; 21 T; 0 U; 0 Other;
Query Match 3.2%; Score 33.6; DB 1; Length 41;
Best Local Similarity 90.0%; Pred. No. 2.5;
Matches 36; Conservative 0; Mismatches 4; Indels 0; Gaps
QY 1793 TGCTGTGCTGTGTGTGTATATATATATATATATATATAC 1832
Dd 1 TGTGTGTGTGTGTGTGTGTATATATATATAAATTATA 40
RESULT 3
ABK66312/c
ID ID ABK66312 standard; DNA; 32 BP.
XX AC ABK66312;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #400.
XX KW Primer; ss; DNA microarray; differential expression analysis; human.
OS Homo sapiens.
XX US6352829-B1.
PD 05-MAR-2002.

Query Match 3.3%; Score 34.4; DB 1; Length 40;
Best Local Similarity 97.2%; Pred. No. 2;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTATATATATATATG 1828

sequences which can be used as DNA markers. The new method markedly improves the efficiency of isolation of satellite sequences in comparison to prior art methods which are reliant on base sequences. Sequences AA29483-514 represent sequences from Haliotis discus, used in the method of the invention

Query Match 2.4%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 20;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1793 TGTGTGTGTGTGTGTGTGTGTATATATA 1822
30 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 6
AAAL15467/c
ID AAAL15467 standard; DNA; 25 BP.
XX
AC AAAL15467;
XX
DT 21-SEP-2000 (first entry)
XX
DE Antisense primer for a rat connective tissue growth factor DNA.
XX
KW Rat; connective tissue growth factor; CTGF; cell proliferative disorder;
KW connective tissue cell; scleroderma; arthritis; cirrhosis;
KW hepatic fibrosis; renal fibrosis; atherosclerosis; cardiac fibrosis;
KW adhesion; surgical scarring; antisense primer; DNA-RNA hybrid; ss.
XX
OS Rattus sp.

Key Location/Qualifiers
misc_RNA 13..25 /*tag= a
WO200027868-A2.
18-MAY-2000.
05-NOV-1999; 99WO-US026189.
06-NOV-1998; 98US-00187478.
14-APR-1999; 99US-00292036.
(FIBR-) FIBROGEN INC.
Schmidt BF, Allen ML, Sverdrup F, Carmichael DF;
WPI; 2000-376484/32.
New rat connective tissue growth factor, its related gene and antisense sequences useful for modulating CTGF and treatment of cell proliferative disorders.
Claim 24; Page 44; 55pp; English.

The present sequence represents an antisense primer which is used to inhibit expression of the rat connective tissue growth factor (CTGF) gene. The polypeptide may play a significant role in the normal development, growth and repair of mammalian tissue. Antisense sequences can be used to inhibit the expression of CTGF in a cell. In particular, the antisense sequences are useful for ameliorating cell proliferative disorders associated with CTGF, e.g. overgrowth of cells, e.g. connective tissue cells. The regulation of CTGF activity comprises down-regulation. The disorders, which can be treated, are chosen from scleroderma, arthritis, cirrhosis, hepatic fibrosis, renal fibrosis, atherosclerosis, cardiac fibrosis, adhesions and surgical scarring. The antisense sequences can also be used to detect expression of CTGF in a sample

Sequence 25 BP; 6 A; 8 C; 4 G; 2 T; 5 U; 0 Other;

Query Match 2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1718 ATTAGACTGCACAGCTTGTGGCAAG 1742
25 ATTAGACTGCACAGCTTGTGGCAAG 1

RESULT 7
AAAL15468/c
ID AAAL15468 standard; DNA; 25 BP.
XX
AC AAAL15468;
XX
DT 21-SEP-2000 (first entry)
XX
DE Antisense primer for a rat connective tissue growth factor DNA.

Rat; connective tissue growth factor; CTGF; cell proliferative disorder;
connective tissue cell; scleroderma; arthritis; cirrhosis;
hepatic fibrosis; renal fibrosis; atherosclerosis; cardiac fibrosis;
adhesion; surgical scarring; antisense primer; DNA-RNA hybrid; ss.
Rattus sp.

Key Location/Qualifiers
misc_RNA 10..22 /*tag= a
WO200027868-A2.
18-MAY-2000.
05-NOV-1999; 99WO-US026189.
06-NOV-1998; 98US-00187478.
14-APR-1999; 99US-00292036.
(FIBR-) FIBROGEN INC.
Schmidt BF, Allen ML, Sverdrup F, Carmichael DF;
WPI; 2000-376484/32.
New rat connective tissue growth factor, its related gene and antisense sequences useful for modulating CTGF and treatment of cell proliferative disorders.
Claim 24; Page 44; 55pp; English.

The present sequence represents an antisense primer which is used to inhibit expression of the rat connective tissue growth factor (CTGF) gene. The polypeptide may play a significant role in the normal development, growth and repair of mammalian tissue. Antisense sequences can be used to inhibit the expression of CTGF in a cell. In particular, the antisense sequences are useful for ameliorating cell proliferative disorders associated with CTGF, e.g. overgrowth of cells, e.g. connective tissue cells. The regulation of CTGF activity comprises down-regulation. The disorders, which can be treated, are chosen from scleroderma, arthritis, cirrhosis, hepatic fibrosis, renal fibrosis, atherosclerosis, cardiac fibrosis, adhesions and surgical scarring. The antisense sequences can also be used to detect expression of CTGF in a sample

Sequence 25 BP; 5 A; 7 C; 5 G; 4 T; 4 U; 0 Other;

Query Match 2.2%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 28;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1742 GTGAATTTCCTGTAAACAGCCAGA 1766

Db 25 GTGAATTTCGGTAAACAAGCCAGA 1

RESULT 8

AA161970/c
ID AA161970 standard; DNA; 27 BP.

XX
AC AA161970;

XX 16-OCT-2001 (first entry)

XX Soybean 240017 region G3 DNA forward primer, SEQ ID NO: 601.

XX Soybean; antihelminthic; gene therapy; soybean cyst nematode; SCN;
KW SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;
KW 240017 region G3; 318013 region A3; 515002 region G2; PCR primer; ss.

XX Glycine max.

XX WO200151627-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001WO-US000552.

XX 07-JAN-2000; 2000US-0174880P.

XX (MONS) MONSANTO CO.

XX Hauge BM, Wang ML, Parsons JD, Parnell LD;

XX WPI; 2001-425872/45.

XX New purified nucleic acid for producing a soybean plant having soybean
PT cyst nematode resistance and for use in plant breeding programs.

XX Claim 25; Page 1178; 1353pp; English.

XX The invention relates to nucleic acid molecules from regions of the
CC soybean genome which are associated with soybean cyst nematode (SCN)
CC resistance. The nucleic acids are used to transform plants, and can
CC produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.
CC The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes
CC of soybean plants and for introgressing SCN resistance or partial SCN
CC resistance into soybean plants. They can also be used in plant breeding
CC programmes. The invention also relates to proteins encoded by such
CC nucleic acid molecules, as well as antibodies capable of recognising
CC these proteins. The present sequence is a primer used to amplify a region
CC of the soybean genome

SQ Sequence 27 BP; 12 A; 11 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 2.2%; Score 23.4; DB 1; Length 27;
Best Local Similarity 96.0%; Pred. No. 30;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1795 TGTGTGTGTGTGTGTGTATAT 1819

Db 27 TGTGTGTGTGTGTGTATAAAT 3

RESULT 9

AA130425/c

ID AAT30425 standard; DNA; 24 BP.

XX
AC AAT30425;

XX 28-JAN-1997 (first entry)

XX Compound simple sequence repeat primer (CA)4.5(TA)7.5.

XX Detection; polymorphism; perfect compound simple sequence repeat;
KW adaptor directed primer; genome; genetic; fingerprinting;

KW amplified fragment length polymorphism assay; microsatellite region;
KW genetic trait marking; germplasm comparisons; compound; ss.

OS Synthetic.

XX WO9617082-A2.

XX .06-JUN-1996.

XX 21-NOV-1995; 95WO-US015150.

XX 28-NOV-1994; 94US-00346456.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Morgante M, Vogel JM;

XX WPI; 1996-277795/28.

XX Modified amplified fragment length polymorphism assay - for detection of
PT polymorphism esp. in microsatellite regions.

XX Disclosure; Fig 1c; 173pp; English.

XX Detecting polymorphisms between 2 nucleic acid samples, esp. in
CC microsatellite regions, comprises digesting the nucleic acid to generate
CC fragments, ligating adaptor segments to their ends, amplifying them using
CC primer directed amplification and comparing the prods. to detect
CC differences. The primers used in the amplification comprise a primer
CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor
CC directed primer, comprising a sequence complementary to an adaptor
CC segment. The present sequence is an example of a compound SSR primer. The
CC method represents a modified amplified fragment length polymorphism
CC assay, which is partic. useful for genome fingerprinting, i.e. for
CC genetic trait marking and germplasm comparisons

SQ Sequence 24 BP; 12 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 2.2%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1805 TGTGTGTGTATATATATATATAT 1827

Db 24 TGTGTGTGTATATATATATATAT 2

RESULT 10

AAH39074/c

ID AAH39074 standard; DNA; 24 BP.

XX
AC AAH39074;

XX 14-AUG-2001 (first entry)

XX SNP specific lower PCR primer SEQ ID 1870.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.

XX Homo sapiens.

XX WO200129262-A2.

XX 26-APR-2001.

XX 13-OCT-2000; 2000WO-US028436.

XX 15-OCT-1999; 99US-0160096P.

XX PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX PI Picoult-Newburg L, Pohl M;
 XX DR WPI; 1992-284684/34.
 XX PS New genotyping oligonucleotide, useful for detecting the presence,
 XX PT absence or identity of single polynucleotide polymorphism in a nucleic
 XX PT acid sample.
 XX PS Claim 1; Page 59; 83pp; English.
 XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence
 XX
 XX SQ Sequence 24 BP; 12 A; 11 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 2.2%; Score 23; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1791 ATTGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
 Db 23 ATTGTGTGTGTGTGTGTGTGTGTGTGTGT 1
 RESULT 11
 AAQ34044
 ID AAQ34044 standard; DNA; 27 BP.
 XX AC AAQ34044;
 XX DT 25-MAR-2003 (revised)
 XX DT 02-FEB-1993 (first entry)
 XX DE Microsatellite sequence from clone TGLA435.
 XX KW PCR; selection; primers; OptiPRIM; breeding; cattle; parentage;
 XX KW genetic mapping; traits; amplification; ss.
 XX OS Bos taurus.
 XX PN WO9213102-A1.
 XX PD 06-AUG-1992.
 XX PF 15-JAN-1992; 92WO-US000340.
 XX PR 15-JAN-1991; 91US-00642342.
 XX PA (GENM-) GENMARK.
 XX PI Georges M, Massey JM;
 XX DR WPI; 1992-284684/34.
 XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
 XX PT mapping, and selective breeding.
 XX PS Table 7; Page 201; 517pp; English.

XX Georges M, Massey JM;
 XX WPI; 1992-284684/34.
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 XX mapping, and selective breeding.
 XX Table 7; Page 348; 517pp; English.
 XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (TC)_n > 9 microsatellites
 CC in the bovine genome is estimated at >100,000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
 Query Match 2.1%; Score 22.2; DB 1; Length 27;
 Best Local Similarity 88.9%; Pred. No. 42;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTATAT 1819
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27
 RESULT 12
 AAQ33678
 ID AAQ33678 standard; DNA; 27 BP.
 XX AC AAQ33678;
 XX DT 25-MAR-2003 (revised)
 XX DT 02-FEB-1993 (first entry)
 XX DE Microsatellite sequence from clone TGLA12.
 XX KW PCR; selection; primers; OptiPRIM; breeding; cattle; parentage;
 XX KW genetic mapping; traits; amplification; ss.
 XX OS Bos taurus.
 XX PN WO9213102-A1.
 XX PD 06-AUG-1992.
 XX PF 15-JAN-1992; 92WO-US000340.
 XX PR 15-JAN-1991; 91US-00642342.
 XX PA (GENM-) GENMARK.
 XX PI Georges M, Massey JM;
 XX DR WPI; 1992-284684/34.
 XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
 XX PT mapping, and selective breeding.
 XX PS Table 7; Page 201; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obt'd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;
 SQ
 Query Match 2.1%; Score 22.2; DB 1; Length 27;
 Best Local Similarity 88.9%; Pred. No. 42;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
 |||||
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 13

AAQ33804
 ID AAQ33804 standard; DNA; 27 BP.

XX AAQ33804;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA210.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-Al.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.

XX Table 7; Page 251; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obt'd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

SQ
 Query Match 2.1%; Score 22.2; DB 1; Length 27;
 Best Local Similarity 88.9%; Pred. No. 42;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1819
 |||||
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 14

AAQ34181

ID AAQ34181 standard; DNA; 27 BP.

XX AAQ34181;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA98.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-Al.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.

XX Table 7; Page 403; 517pp; English.

XX The sequence is a bovine microsatellite sequence obt'd. by screening a
 CC library of bovine MboI DNA fragments of between 250 and 500 bp with an
 CC (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-
 CC hybridised. Assuming independent distribution of microsatellites and MboI
 CC sites, the frequency of (T6)n >9 microsatellites in the bovine genome is
 CC estimated at >100, 000. The sequence information for ca. 230 such bovine
 CC microsatellites is summarised in the specification and indexed herein.
 CC (see below). The sequences upstream and downstream of the microsatellite
 CC sequence were used to generate the required PCR primers for in vitro
 CC amplification of the corresp. microsatellite (using the program
 CC OPTIPRIM). The microsatellites may be used to identify individuals, for
 CC parentage testing, and in the genetic mapping of economic trait loci, or
 CC genes involved in the determination of economically important traits esp. in
 CC cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on
 CC 25-MAR-2003 to correct PN field.)

XX Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

SQ
 Query Match 2.1%; Score 22.2; DB 1; Length 27;
 Best Local Similarity 88.9%; Pred. No. 42;

```

Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1793 TGTGTGTGTGTGTGTGTGTGTATAT 1819
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 15
AAQ34012
ID AAQ34012 standard; DNA; 27 BP.
XX
AC AAQ34012;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA417.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A1..
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 335; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 16
AAQ34143
ID AAQ34143 standard; DNA; 27 BP.
XX
AC AAQ34143;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Sequence of a microsatellite from clone TGLA76.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 388; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 17
AAQ34143/c
ID AAQ34143 standard; DNA; 27 BP.
XX
AC AAQ34143;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1997 (first entry)
XX
DE Repeat sequence from polymorphic marker clone Mfd31.
XX
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;

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XX AAQ34143;
AC
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Sequence of a microsatellite from clone TGLA76.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
PS Table 7; Page 388; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100,000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 17
AAQ34143/c
ID AAQ34143 standard; DNA; 27 BP.
XX
AC AAQ34143;
XX
DT 25-MAR-2003 (revised)
DT 17-JUN-1997 (first entry)
XX
DE Repeat sequence from polymorphic marker clone Mfd31.
XX
KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;

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KW linkage analysis; genetic disease; animal; plant; breeding; locus;
 KW hybridisation; chromosome; ds.

XX Homo sapiens.

XX US5582979-A.

XX 10-DEC-1996.

XX 04-APR-1994; 94US-00222177.

XX 21-APR-1989; 89US-00341562.

XX 05-SEP-1991; 91US-00754351.

XX (MARS-) MARSHFIELD CLINIC.

XX Weber JL;

XX WPI; 1997-042299/04.

XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
 PT using novel nucleic acid mols. as primers.

XX Claim 1; Col 9-10; 186pp; English.

XX The invention relates to the isolation of polymorphic repeat sequences
 CC having the sequence (dC-dA)n (dG-dT)n which can be used as genetic
 CC markers. Primers based on these sequences can be used to detect these
 CC repeats, especially for use in e.g. paternity or maternity testing, human
 CC genetic analysis such as linkage analysis of genetic disease, commercial
 CC animal or plant breeding or pedigree analysis. Clones containing the
 CC repeat sequences were isolated by hybridisation of chromosome-specific
 CC phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100
 CC repeat blocks were isolated. The inserts from the clones were amplified
 CC by primers AA65798-T66047. Those clones where the repeat sequence has
 CC been determined are shown in AA65704-797. This repeat sequence is from
 CC the marker clone Mdf31 which contains the repeat sequence having the
 CC formula: (AC)13A. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 27 BP; 14 A; 13 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;

Best Local Similarity 88.9%; Pred. No. 42;

Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1793 TGTGTGTGTGTGTGTGTGTGTGTGTATAT 1819

Db 27 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 18

AAH46005

ID AAH46005 standard; DNA; 27 BP.

XX AC AAH46005;

XX 12-SEP-2001 (first entry)

XX Synthetic oligonucleotide 5.

XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
 KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
 KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
 KW lymphoma; ss.

XX Synthetic.

XX WO200144465-A2.

XX 21-JUN-2001.

XX 12-DEC-2000; 2000WO-CA001467.

XX

PR 13-DEC-1999; 99US-0170325P.

PR 29-AUG-2000; 2000US-0228925P.

XX (BION-) BIONICHE LIFE SCI INC.

XX Phillips NC, Fillion MC;

XX WPI; 2001-398150/42.

XX Composition comprising synthetic oligonucleotides which comprise multiple
 PT repeats of dinucleotides such as GT, TG useful for treating cancer by
 PT inducing cell cycle arrest, inhibiting proliferation, activating
 PT caspases.

XX Example 4; Page 16; 77pp; English.

XX The present sequence is that of a synthetic oligonucleotide useful to the
 CC invention. The invention relates to a composition, comprising a 2 to 20
 CC base 3'-OH synthetic oligonucleotide which comprises multiple
 CC repeats of dinucleotides such as GT, TG, etc., according to specific
 CC formula and having cytostatic activity. The oligonucleotide compositions
 CC are useful for inducing cell cycle arrest, inhibition of proliferation,
 CC activation of caspases and induction of apoptosis or production of
 CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
 CC necrosis factor (TNF)-alpha by immune system cells, in an animal having
 CC cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
 CC and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
 CC colorectal, ovarian or bone cancer. The compositions induce apoptosis
 CC independent of Fas, p53/p21, p21/waf-1/Cip1, p15(ink4B), p16(ink4), drug
 CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
 CC and hormone dependence

XX Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 2.1%; Score 22.2; DB 1; Length 27;

Best Local Similarity 88.9%; Pred. No. 42;

Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1793 TGTGTGTGTGTGTGTGTGTGTGTGTATAT 1819

Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 19

AAAT30426/c

ID AAAT30426 standard; DNA; 22 BP.

XX AC AAAT30426;

XX 28-JAN-1997 (first entry)

XX Compound single sequence repeat primer (CA)6.5(TA)4.5.

XX Detection; polymorphism; perfect compound simple sequence repeat;
 KW adaptor directed primer; genome; genetic; fingerprinting;
 KW amplified fragment length polymorphism assay; microsatellite region;
 KW genetic trait marking; germplasm comparisons; compound; ss.

XX Synthetic.

XX WO9617082-A2.

XX 06-JUN-1996.

XX 21-NOV-1995; 95WO-US015150.

XX 28-NOV-1994; 94US-00346456.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Morgante M, Vogel JM;

XX WPI; 1996-277795/28.

DR

XX Modified amplified fragment length polymorphism assay - for detection of
PT polymorphism esp. in microsatellite regions.
XX
PS Disclosure; Fig 1c; 173pp; English.
XX
CC Detecting polymorphisms between 2 nucleic acid samples, esp. in
CC microsatellite regions, comprises digesting the nucleic acid to generate
CC fragments, ligating adaptor segments to their ends, amplifying them using
CC primer directed amplification and comparing the prods. to detect
CC differences. The primers used in the amplification comprise a primer
CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor
CC directed primer, comprising a sequence complementary to an adaptor
CC segment. The present sequence is an example of a compound SSR primer. The
CC method represents a modified amplified fragment length polymorphism
CC assay, which is partic. useful for genome fingerprinting, i.e. for
CC genetic trait marking and germplasm comparisons
XX
SQ Sequence 22 BP; 11 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 2.1%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1801 TGTGTGTGTGTGTATATATA 1822
DB 22 TGTGTGTGTGTGTATATATA 1
XX
RESULT 20
AAQ33918
ID AAQ33918 standard; DNA; 25 BP.
AC AAQ33918;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA327.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX
XX Table 7; Page 297; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
XX in the bovine genome is estimated at >100, 000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the

CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
Query Match 2.1%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 44;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTATAT 1817
DB 1 TGTGTGTGTGTGTGTGTGTGT 25
XX
RESULT 21
AAQ33642
ID AAQ33642 standard; DNA; 25 BP.
XX
AC AAQ33642;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone MTGT13B.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX
XX Table 7; Page 186; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
XX in the bovine genome is estimated at >100, 000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX
XX required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program OPTIPRIM). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
SQ Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 44;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
DB 1 TGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 22
AAQ33962
ID AAQ33962 standard; DNA; 25 BP.
XX AC AAQ33962;
XX DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA354.
XX KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX WP1; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX PS Table 7; Page 315; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine Mb1 DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and Mb1 sites, the frequency of (16)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX SQ Sequence 25 BP; 0 A; 0 C; 12 G; 13 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 44;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
DB 1 TGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 23

AAAT65734/c
ID AAAT65734 standard; DNA; 25 BP.
XX AC AAAT65734;
XX DT 25-MAR-2003 (revised)
DT 17-JUN-1997 (first entry)
XX DE Repeat sequence from polymorphic marker clone Mfd32.
XX KW Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW linkage analysis; genetic disease; animal; plant; breeding; locus;
KW hybridisation; chromosome; ds.
XX OS Homo sapiens.
XX PN US5582979-A.
XX PD 10-DEC-1996.
XX PF 04-APR-1994; 94US-00222177.
XX PR 21-APR-1989; 89US-00341562.
PR 05-SEP-1991; 91US-00754351.
XX PA (MARS-) MARSHFIELD CLINIC.
XX PI Weber JL;
XX WP1; 1997-042299/04.
XX PT Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
PT using novel nucleic acid mols. as primers.
XX PS Disclosure; Col 9-10; 186pp; English.
XX CC The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic disease, commercial
CC animal or plant breeding or pedigree analysis. Clones containing the
CC repeat sequences were isolated by hybridisation of chromosome-specific
CC phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100
CC repeat blocks were isolated. The inserts from the clones were amplified
CC by primers AAAT65798-T66047. Those clones where the repeat sequence has
CC been determined are shown in AAAT65704-797. This repeat sequence is from
CC the marker clone Maf32 which contains the repeat sequence having the
CC formula: (AC)12A. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 25 BP; 13 A; 12 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 44;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
DB 25 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 24
AAQ34083
ID AAQ34083 standard; DNA; 26 BP.
XX AC AAQ34083;
XX DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA49.
XX

KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX Bos taurus.

XX WO9213102-A1.
 XX 06-AUG-1992.
 XX 15-JAN-1992; 92WO-US000340.
 XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.

XX Table 7; Page 364; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 92.0%; Pred. No. 45;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
 DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 25
 AAQ33684
 ID AAQ33684 standard; DNA; 26 BP.

XX AAQ33684;

XX 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA123.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.
 PR (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.

XX Table 7; Page 203; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 92.0%; Pred. No. 45;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
 DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 26
 AAQ33704
 ID AAQ33704 standard; DNA; 26 BP.

XX AAQ33704;

XX 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA130.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene

PT mapping, and selective breeding.
XX Table 7; Page 211; 517pp; English.
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 2.1%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 45;
Matches .23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26
RESULT 27
AAQ33831
ID AAQ33831 standard; DNA; 26 BP.
AC AAQ33831;
XX
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX
DE Microsatellite sequence from clone TGLA231.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
KM
XX
XX Bos taurus.
OS
XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX Table 7; Page 262; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 2.1%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 45;
Matches .23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGT 25
RESULT 28
AAQ33837
ID AAQ33837 standard; DNA; 26 BP.
AC AAQ33837;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX Microsatellite sequence from clone TGLA25.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
KM
XX
XX Bos taurus.
OS
XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX Table 7; Page 264; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX SQ Sequence 26 BP; 0 A; 0 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 2.1%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 45;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTGTAT 1817
DB 1 TGTGTGTGTGTGTGTGTGTGT 25

RESULT 29
AAQ33740
ID AAQ33740 standard; DNA; 27 BP.
XX
XX AAQ33740;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
DE
DE Microsatellite sequence from clone TGLA154.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW Genetic mapping; traits; amplification; ss.
KW
XX Bos taurus.
OS
XX
XX WO9213102-A1.
PN
XX
XX
XX 06-AUG-1992.
PD
XX
XX 15-JAN-1992; 92WO-US000340.
PF
XX
XX 15-JAN-1991; 91US-00642342.
PR
XX
XX (GENM-) GENMARK.
PA
XX
XX Georges M, Massey JM;
PI
XX
XX WPI; 1992-284684/34.
DR
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
PT
XX
XX Table 7; Page 226; 517pp; English.
PS
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)_n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 27 BP; 2 A; 0 C; 12 G; 13 T; 0 U; 0 Other;
SQ

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1797 TGTGTGTGTGTGTGTGTATAT 1821
DB 1 TGTGTGTGTGTGTGTATATGTGT 25

KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
KW lymphoma; ss.

OS Synthetic.

PN WO200144465-A2.

XX 21-JUN-2001.

XX 12-DEC-2000; 2000WO-CA001467.

XX 13-DEC-1999; 99US-0170325P.

PR 29-AUG-2000; 2000US-0228925P.

XX (BION-) BIONICHE LIFE SCI INC.

XX Phillips NC, Fillion MC;

XX WPI; 2001-398150/42.

XX Composition comprising synthetic oligonucleotides which comprise multiple
PT repeats of dinucleotides such as GT, TG useful for treating cancer by
PT inducing cell cycle arrest, inhibiting proliferation, activating
PT caspases.

XX Example 4; Page 16; 77pp; English.

XX The present sequence is that of a synthetic oligonucleotide useful to the
CC invention. The invention relates to a composition, comprising a 2 to 20
CC base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
CC repeats of dinucleotides such as GT, TG, etc., according to specific
CC formula and having cytostatic activity. The oligonucleotide compositions
CC are useful for inducing cell cycle arrest, inhibition of proliferation,
CC activation of caspases and induction of apoptosis or production of
CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
CC necrosis factor (TNF)-alpha by immune system cells, in an animal having
CC cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
CC and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
CC colorectal, ovarian or bone cancer. The compositions induce apoptosis
CC independent of Fas, p53/p21, p21/waf-1/Cip, p15(ink4B), p16(ink4), drug
CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
CC and hormone dependence

XX Sequence 27 BP; 0 A; 0 C; 14 G; 13 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1793 TGTGTGTGTGTGTGTGTGTGTAT 1817

Db 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 34

AAF60473/C

ID AAF60473 standard; DNA; 27 BP.

AC AAF60473;

XX 27-APR-2001 (first entry)

XX Oligonucleotide clamp #19.

XX Oligonucleotide clamp; ds.

XX Unidentified.

XX US6180777-B1.

XX 30-JAN-2001.

XX 03-JAN-1997; 97US-00787321.

XX 12-JAN-1996; 96US-0009918P.

XX (FARB) BAYER CORP.

XX Horn T;

XX WPI; 2001-201911/20.

XX Synthesizing branched nucleic acids useful as diagnostic and molecular
PT probes, involves combining first units having haloalkylamino groups and
PT second units having thiol or phosphorothioate groups.

XX Disclosure; Col 29-30; 20pp; English.

XX The present invention relates to a method for synthesising a branched or
CC multiply connected macromolecular structure, comprising oligonucleotide
CC clamps (OC). The macromolecular structure is capable of specifically
CC binding to a target molecule, and can therefore be used as probes. At
CC least one OC comprises a target binding sequence that binds specifically
CC and stably with the target molecule, and at least two OCs comprise signal
CC generation moieties capable of generating a detectable signal in the
CC presence of the target molecule. In addition the OCs are connected to one
CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC present sequence is an OC used in the present invention

XX Sequence 27 BP; 13 A; 14 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 47;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1793 TGTGTGTGTGTGTGTGTGTAT 1817

Db 26 TGTGTGTGTGTGTGTGTGTGTGTGT 2

RESULT 35

AAQ33663

ID AAQ33663 standard; DNA; 23 BP.

XX AAQ33663;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA110.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENN-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.

XX Table 7; Page 195; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obt'd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (76)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX
 SQ Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;
 Query Match 2.0%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 46;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
 |||||
 DB 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 36

AAQ33773
 ID AAQ33773 standard; DNA; 23 BP.

XX
 AC AAQ33773;

XX 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)

DE Microsatellite sequence from clone TGLA176.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.

XX Table 7; Page 239; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (76)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX SQ Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 46;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
 |||||
 DB 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 37

AAQ33885

ID AAQ33885 standard; DNA; 23 BP.

XX AAQ33885;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

DE Microsatellite sequence from clone TGLA304.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.

XX Table 7; Page 283; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (76)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX SQ Sequence 23 BP; 0 A; 0 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 46;

DT	14-AUG-2001	(first entry)
DE	XX	
DE	XX	SNP specific upper PCR primer SEQ ID 1801.
DE	XX	
KW	XX	Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW	XX	SNPs; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW	XX	Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW	XX	polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW	XX	acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW	XX	inflammation; forensic investigation; paternity analysis; PCR primer; ss.
OS	XX	Homo sapiens.
OS	XX	
PN	XX	WO200129252-A2.
PN	XX	
PD	XX	26-APR-2001.
PD	XX	
XX	XX	13-OCT-2000; 200WO-US028436.
XX	XX	
XX	XX	15-OCT-1999; 99US-0150096P.
XX	XX	(ORCH-) ORCHID BIOSCIENCES INC.
XX	XX	Picoult-Newburg L, Pohl M;
PI	XX	
DR	XX	WPI; 2001-290930/30.
DR	XX	
PT	XX	New genotyping oligonucleotide, useful for detecting the presence,
PT	XX	absence or identity of single polynucleotide polymorphism in a nucleic
PT	XX	acid sample.
PT	XX	
XX	XX	Claim 1; Page 59; 83pp; English.
XX	XX	
CC	XX	Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC	XX	primer extension (SNPE) primers, and the sequences of regions flanking
CC	XX	sites of single nucleotide polymorphisms SNPs. The present invention
CC	XX	includes kits for determining the presence or absence of a SNP, using the
CC	XX	oligonucleotides of the invention. The PCR primers are used to amplify a
CC	XX	SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC	XX	The oligonucleotides are useful for genotyping a nucleic acid sample by
CC	XX	performing a single-nucleotide primer extension reaction. The
CC	XX	oligonucleotides are useful for determining the presence, absence or
CC	XX	identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC	XX	assess by association analysis the genotype of an individual or group of
CC	XX	individuals, having a pathological phenotypic trait suspected of being
CC	XX	caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC	XX	agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC	XX	dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC	XX	osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC	XX	traits also include symptoms of or susceptibility to multifactorial
CC	XX	disease of which a component is or may be genetic such as autoimmune
CC	XX	disease, including, rheumatoid arthritis, multiple sclerosis,
CC	XX	inflammation, cancer, nervous system diseases and infection by pathogenic
CC	XX	microorganism. The method is also useful in forensic investigations and
CC	XX	paternity analysis. The present sequence represents a PCR primer specific
CC	XX	for a human SNP containing DNA sequence
XX	XX	
XX	XX	Sequence 23 BP; 0 A; 0 C; 10 G; 13 T; 0 U; 0 Other;
XX	XX	
Query Match	2.0%;	Score 21.4; DB 1; Length 23;.
Best Local Similarity	95.7%;	Pred. No. 46;
Matches	22; Conservative	0; Mismatches 1; Indels 0; Gaps
QY	1790	TATTGTGTGTGTGTGTGTGTG 1812
DB	1	TTTGTGTGTGTGTGTGTGTG 23
RESULT 40		
AAQ33986		
ID	AAQ33986	standard; DNA; 24 BP.
XX	XX	
AC	AAQ33986;	

[illegible]

XX Georges M, Massey JM;
PI WPI; 1992-284684/34.
DR Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX Table 7; Page 293; 517pp; English.
XX The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
SQ Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 24
RESULT 43
AAQ34065
ID AAQ34065 standard; DNA; 24 BP.
XX AAQ34065;
XX Bos taurus.
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX Microsatellite sequence from clone TGLA444.
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX Bos taurus.
XX WO9213102-A1.
XX 06-AUG-1992.
XX 15-JAN-1992; 92WO-US000340.
XX 15-JAN-1991; 91US-00642342.
XX (GENM-) GENMARK.
XX Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX Table 7; Page 357; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
SQ Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGT 24
RESULT 44
AAQ34024
ID AAQ34024 standard; DNA; 24 BP.
XX AAQ34024;
XX Bos taurus.
XX WO9213102-A1.
XX 06-AUG-1992.
XX 15-JAN-1992; 92WO-US000340.
XX 15-JAN-1991; 91US-00642342.
XX (GENM-) GENMARK.
XX Georges M, Massey JM;
XX WPI; 1992-284684/34.
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX Table 7; Page 340; 517pp; English.
XX The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 45
AAQ33707
ID AAQ33707 standard; DNA; 24 BP.
AC AAQ33707;
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA131.
XX
KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX WO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US000340.
XX
PR 15-JAN-1991; 91US-00642342.
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX
XX WPI; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX
XX Table 7; Page 213; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (TC)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 24;

Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 46
AAT66096/c
ID AAT66096 standard; DNA; 24 BP.
AC AAT66096;
DT 25-MAR-2003 (revised)
DT 18-JUN-1997 (first entry)
XX
DE Repeat sequence found in the human chromosomal clone JW42.

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
KW linkage analysis; genetic disease; animal; plant; breeding; locus;
KW hybridisation; chromosome; ds.
XX Homo sapiens.
XX US5582979-A.
XX
PD 10-DEC-1996.
XX
PF 04-APR-1994; 94US-00222177.
XX
PR 21-APR-1989; 89US-00341562.
PR 05-SEP-1991; 91US-00754351.
XX (MARS-) MARSHFIELD CLINIC.
XX
XX Weber JL;
XX
XX WPI; 1997-042299/04.
XX
XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
XX using novel nucleic acid mols. as primers.
XX
XX Example 9; Col 61-62; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g. paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic diseases, commercial
CC animal or plant breeding or pedigree analysis. The sequences AAT66084-
CC T66107 represent repeat sequences of low informativeness found in
CC specific human genes. This repeat sequence is found in the human
CC chromosomal clone JW42. The sequence is amplified by primers AAT66097-8.
CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 24 BP; 12 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 24 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 47
AAH46015
ID AAH46015 standard; DNA; 24 BP.
XX
XX AAH46015;

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XX 12-SEP-2001 (first entry)
XX Synthetic oligonucleotide 15.
XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
XX lymphoma; ss.
XX Synthetic.
XX WO200144465-A2.
XX 21-JUN-2001.
XX 12-DEC-2000; 2000WO-CA001467.
XX 13-DEC-1999; 99US-0170325P.
XX 29-AUG-2000; 2000US-0228925P.
XX (BION-) BIONICHE LIFE SCI INC.
XX Phillips NC, Fillion MC;
XX WPI; 2001-398150/42.
XX Composition comprising synthetic oligonucleotides which comprise multiple
XX repeats of dinucleotides such as GT, TG useful for treating cancer by
XX inducing cell cycle arrest, inhibiting proliferation, activating
XX caspases.
XX Example 4; Page 17; 77pp; English.
XX The present sequence is that of a synthetic oligonucleotide useful to the
XX invention. The invention relates to a composition, comprising a 2 to 20
XX base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
XX repeats of dinucleotides such as GT, TG, etc., according to specific
XX formula and having cytostatic activity. The oligonucleotide compositions
XX are useful for inducing cell cycle arrest, inhibition of proliferation,
XX activation of caspases and induction of apoptosis or production of
XX cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
XX necrosis factor (TNF)-alpha by immune system cells, in an animal having
XX cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
XX and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
XX colorectal, ovarian or bone cancer. The compositions induce apoptosis
XX independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug
XX resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
XX and hormone dependence
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
XX Query Match 2.0%; Score 21.4; DB 1; Length 24;
XX Best Local Similarity 95.7%; Pred. No. 47;
XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1793 TGTGTGTGTGTGTGTGTGTGTAT 1815
XX 1 TGTGTGTGTGTGTGTGTGTGTGT 23
XX
XX RESULT 48
XX AAH46016
XX ID AAH46016 standard; DNA; 24 BP.
XX AC AAH46016;
XX 12-SEP-2001 (first entry)
XX Synthetic oligonucleotide 16.
XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;

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KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
KW lymphoma; ss.
XX Synthetic.
XX WO200144465-A2.
XX 21-JUN-2001.
XX 12-DEC-2000; 2000WO-CA001467.
XX 13-DEC-1999; 99US-0170325P.
XX 29-AUG-2000; 2000US-0228925P.
XX (BION-) BIONICHE LIFE SCI INC.
XX Phillips NC, Fillion MC;
XX WPI; 2001-398150/42.
XX Composition comprising synthetic oligonucleotides which comprise multiple
XX repeats of dinucleotides such as GT, TG useful for treating cancer by
XX inducing cell cycle arrest, inhibiting proliferation, activating
XX caspases.
XX Claim 6; Page 17; 77pp; English.
XX The present sequence is that of a synthetic oligonucleotide useful to the
XX invention. The invention relates to a composition, comprising a 2 to 20
XX base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
XX repeats of dinucleotides such as GT, TG, etc., according to specific
XX formula and having cytostatic activity. The oligonucleotide compositions
XX are useful for inducing cell cycle arrest, inhibition of proliferation,
XX activation of caspases and induction of apoptosis or production of
XX cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
XX necrosis factor (TNF)-alpha by immune system cells, in an animal having
XX cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
XX and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
XX colorectal, ovarian or bone cancer. The compositions induce apoptosis
XX independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug
XX resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
XX and hormone dependence
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
XX Query Match 2.0%; Score 21.4; DB 1; Length 24;
XX Best Local Similarity 95.7%; Pred. No. 47;
XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1793 TGTGTGTGTGTGTGTGTGTGTAT 1815
XX 2 TGTGTGTGTGTGTGTGTGTGTGT 24
XX
XX RESULT 49
XX AAF99862
XX ID AAF99862 standard; DNA; 24 BP.
XX AC AAF99862;
XX 12-JUN-2001 (first entry)
XX Immunostimulatory nucleic acid #978.
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX Synthetic.
XX WO200122972-A2.

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PD XX 05-APR-2001.
PF XX
PR XX 25-SEP-2000; 2000WO-US026383.
PR XX
PR XX 25-SEP-1999; 99US-0156113P.
PR XX
PR XX 27-SEP-1999; 99US-0156135P.
PR XX
PR XX 23-AUG-2000; 2000US-0227436P.
PR XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
PA
PI Krieg AM, Schetter C, Vollmer J;
XX
XX WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
XX using immunostimulatory Py-rich and TG nucleic acids.
XX
XX Claim 101; Page 59; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
XX response. The method comprises administering an immunostimulatory nucleic
XX acid to a non-rodent subject in sufficient quantity to stimulate an
XX immune response. The present sequence is one such immunostimulatory
XX nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX also useful for preventing cancer, asthma, infectious disease, allergy or
XX immune deficiency. The present sequence can also be used to redirect a
XX Th2 to a Th1 immune response and to activate immune cells. Note: the
XX present sequence may have a phosphorothioate backbone
XX
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 50
ABST6584
ID ABS78584 standard; DNA; 24 BP.
XX
XX ABS78584;
XX
XX 13-DEC-2002 (first entry)
XX
XX Angiogenesis inhibitory oligonucleotide #1068.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;
XX plaque neovascularisation; telangiectasia; haemophilic joint;
XX angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
XX scleroderma; hypertrophic scar.
XX
XX Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US049458.
XX
XX

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PR 14-DEC-2000; 2000US-0255534P.
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
XX antiangiogenic nucleic acid molecule to the subject.
XX
XX Claim 2; Page 38; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule. Also
XX included is a kit comprising a first container housing the antiangiogenic
XX nucleic acids, and instructions for administering them to a subject
XX having a condition characterised by unwanted angiogenesis. The method is
XX useful for inhibiting angiogenesis associated with solid tumour growth,
XX tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
XX diabetic retinopathy, retinopathy of prematurity, macular degeneration,
XX corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
XX rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
XX neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
XX wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
XX hypertrophic scars. The present sequence is an antiangiogenic nucleic
XX acid of the invention
XX
XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 51
ACH03377
ID ACH03377 standard; DNA; 24 BP.
XX
XX ACH03377;
XX
XX 25-SEP-2003 (first entry)
XX
XX Immunostimulatory nucleic acid #1012.
XX
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
XX antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
XX Synthetic.
XX
XX US2003050268-A1.
XX
XX 13-MAR-2003.
XX
XX 29-MAR-2002; 2002US-00112653.
XX
XX 29-MAR-2001; 2001US-0279642P.
XX
XX (KRIE/) KRIEG A M.
XX (BERG/) BERG D J.
XX
XX Krieg AM, Berg DJ;
XX
XX WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
XX allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT

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PT disease by administering an immunostimulatory nucleic acid.
 XX
 PS Disclosure; Page 36; 229pp; English.
 XX

CC The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid
 XX
 XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 24;
 Best Local Similarity 95.7%; Pred. No. 47;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
 DB 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 52
 ADB37364
 ID ADB37364 standard; DNA; 24 BP.
 XX
 AC ADB37364;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #978.

XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX Synthetic.
 OS
 XX US2003087848-A1.
 PN
 XX 08-MAY-2003.
 PD
 XX 02-FEB-2001; 2001US-00776479.
 PF
 XX 03-FEB-2000; 2000US-0179991P.
 PR
 XX (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 XX Bratzler RL, Petersen DM, Fouron Y;
 PI
 XX WPI; 2003-657977/62.
 DR
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 XX Disclosure; Page 20; 221pp; English.

XX The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 24;
 Best Local Similarity 95.7%; Pred. No. 47;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
 DB 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 53
 AAQ33861
 ID AAQ33861 standard; DNA; 25 BP.
 XX
 AC AAQ33861;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA264.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX WO92113102-A1.
 PN
 XX 06-AUG-1992.
 PD
 XX 15-JAN-1992; 92WO-US000340.
 PF
 XX 15-JAN-1991; 91US-00642342.
 PR
 XX (GENM-) GENMARK.
 PA
 XX Georges M. Massey JM;
 PI
 XX WPI; 1992-284684/34.
 DR
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX
 XX Table 7; Page 274; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
 CC in the bovine genome is estimated at >100,000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 25 BP; 0 A; 0 C; 13 G; 12 T; 0 U; 0 Other;

Query Match 2.0%; Score 21.4; DB 1; Length 25;
 Best Local Similarity 95.7%; Pred. No. 49;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
 DB 2 TGTGTGTGTGTGTGTGTGT 24

RESULT 54
 AAH40163/c
 ID AAH40163 standard; DNA; 25 BP.
 XX
 AC AAH40163;

```

XX 14-AUG-2001 (first entry)
XX SNP specific SNPE primer SEQ ID 2959.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia, diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX Homo sapiens.
XX OS
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
XX
XX Claim 1; Page 65; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a single nucleotide
XX primer extension (SNPE) primer specific for a human SNP containing DNA
XX sequence
XX
XX Sequence 25 BP; 12 A; 12 C; 1 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 21.4; DB 1; Length 25;
XX Best Local Similarity 95.7%; Pred. No. 49;
XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1793 TGTGTGTGTGTGTGTGTGTAT 1815
XX
XX 23 TGTGTGTGTGTGTGTGTGTGT 1
XX
XX RESULT 55
XX AAH38303
XX ID AAH38303 standard; DNA; 25 BP.

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XX AC AAH38303;
XX
XX 14-AUG-2001 (first entry)
XX
XX SNP specific SNPE primer SEQ ID 1099.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia, diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX Homo sapiens.
XX OS
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
XX
XX Claim 1; Page 55; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNPE) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a single nucleotide
XX primer extension (SNPE) primer specific for a human SNP containing DNA
XX sequence
XX
XX Sequence 25 BP; 0 A; 0 C; 13 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 21.4; DB 1; Length 25;
XX Best Local Similarity 95.7%; Pred. No. 49;
XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1793 TGTGTGTGTGTGTGTGTGTAT 1815
XX
XX 2 TGTGTGTGTGTGTGTGTGTGT 24
XX
XX RESULT 56

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AAQ47179
 ID AAQ47179 standard; DNA; 26 BP.
 XX
 AC AAQ47179;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-JAN-1994 (first entry)
 XX
 DE MHC DR A intron binding oligomer GTCO.
 XX
 KW MHC; major histocompatibility complex; class II; control oligomers; DR A;
 KW transplantation; antigen; autoimmune disease; ss.
 XX
 OS Synthetic.
 OS
 PN WO9314769-A1.
 XX
 PN 05-AUG-1993.
 XX
 PD 29-JAN-1993; 93WO-US000797.
 XX
 PF 31-JAN-1992; 92US-00830427.
 XX
 PR 14-SEP-1992; 92US-00944868.
 XX
 PR (REGC) UNIV CALIFORNIA.
 PA
 PI Weiss TL, Garovoy MR, Hunt A, Huey B, Tam S;
 XX
 XX WPI; 1993-258367/32.
 XX
 DR Depletion of transplantation antigens in donor cells - using anti-sense
 XX or triplex-forming oligonucleotide(s), used for treating auto-immune
 PT disease and in transplants.
 PT
 PT Example; Page 22; 71pp; English.
 XX
 XX The sequences given in AAQ47176-77 represent triplex forming oligo-
 CC nucleotides which bind to the mRNA sequence of the MHC class II locus DR
 CC A structural gene at positions 851-876. The sequences given in AAQ47178-
 CC 80 represent control oligomers which contain base compositions similar to
 CC that around this DR A region but not containing the correct sequences. DR
 CC A is a transplacation antigen. Binding of this sequence to the DR A gene
 CC inhibits antigen production. This method may be used for treating
 CC individuals with autoimmune disease, characterised by dysfunctional
 CC expression of a transplacation antigen. It may also be used to produce
 CC cells which are more easily transplanted into a recipient. (Updated on 25
 CC -MAR-2003 to correct PN field.)
 XX
 SQ Sequence 26 BP; 0 A; 0 C; 14 G; 12 T; 0 U; 0 Other;
 Query Match 2.0%; Score 21.4; DB 1; Length 26;
 Best Local Similarity 95.7%; Pred. No. 50;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
 DB 3 TGTGTGTGTGTGTGTGTGTGT 25
 RESULT 57
 AAQ44016
 ID AAQ44016 standard; DNA; 26 BP.
 XX
 AC AAQ44016;
 XX
 DT 25-MAR-2003 (revised)
 DT 28-OCT-1993 (first entry)
 XX
 DE Target sequence #8.
 XX
 KW Purine; pyrimidine; tracts; therapeutic; diagnostic; control;
 KW Gene expression; mRNA synthesis suppression; ds.
 XX

OS Synthetic.
 XX
 PN WO9312230-A1.
 XX
 PD 24-JUN-1993.
 XX
 PF 11-DEC-1992; 92WO-US010792.
 XX
 PR 13-DEC-1991; 91US-00808452.
 PR 21-JAN-1992; 92US-00826934.
 XX
 PA (STRI) SRI INT.
 XX
 PI Jayasena SD, Johnston BH;
 XX
 XX WPI; 1993-214172/26.
 DR
 XX
 PT New oligo:nucleotide(s) forming triple helix with target nucleic acid -
 PT contain purine and pyrimidine tracts in specific orientations, useful
 PT therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
 XX
 PS Example; Fig 14a; 101pp; English.
 XX
 CC The sequence is that of the target sequence #8 which was used in an
 CC experiment to determine the in vitro cleavage of target duplexes to
 CC evaluate the lengths of purine and pyrimidine tracts which are useful in
 CC obtaining oligonucleotides capable of triple helix formation with target
 CC nucleic acids. The complementary strand overhangs the 3' end by the
 CC sequence CTAG and the sense strand overhangs the complementary strand by
 CC the sequence AATT. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 26 BP; 2 A; 1 C; 11 G; 12 T; 0 U; 0 Other;
 Query Match 2.0%; Score 21.2; DB 1; Length 26;
 Best Local Similarity 88.5%; Pred. No. 53;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1787 AAATATTGTGTGTGTGTGTGTGTGTG 1812
 DB 1 AATTCGTGTGTGTGTGTGTGTGTGTG 26
 RESULT 58
 AAQ33891
 ID AAQ33891 standard; DNA; 21 BP.
 XX
 AC AAQ33891;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA307.
 XX
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 OS
 PN WO9213102-A1.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US000340.
 XX
 PR 15-JAN-1991; 91US-00642342.
 XX
 PA (GENM-) GENMARK.
 XX
 PI Georges M, Massey JM;
 XX
 XX WPI; 1992-284684/34.
 XX
 XX Polymorphic bovine DNA markers - used in genetic identification, gene

PT mapping, and selective breeding.
Table 7; Page 286; 517pp; English.
The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mb01 DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mb01 sites, the frequency of (76)n > 9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved in the determination of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN field.)
Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 1 TGTGTGTGTGTGTGTGTGTGT 21
RESULT 59
AAQ33879
ID AAQ33879 standard; DNA; 21 BP.
XX
XX AAQ33879;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA301.
XX
XX PCR, selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
XX
XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM;
XX
XX WPT; 1992-284684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
PS
PS Table 7; Page 281; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine Mb01 DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and Mb01 sites, the frequency of (76)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 1 TGTGTGTGTGTGTGTGTGTGT 21
RESULT 60
AAQ65738/C
ID AAQ65738 standard; DNA; 21 BP.
XX
XX AAQ65738;
XX
XX 25-MAR-2003 (revised)
DT 17-JUN-1997 (first entry)
XX
DE Repeat sequence from polymorphic marker clone Mfd37.
XX
XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
XX linkage analysis; genetic disease; animal; plant; breeding; locus;
XX hybridisation; chromosome; ds.
XX
XX Homo sapiens.
XX
XX US5582979-A.
XX
XX 10-DEC-1996.
XX
XX 04-APR-1994; 94US-00222177.
XX
XX 21-APR-1989; 89US-00341562.
XX
XX 05-SEP-1991; 91US-00754351.
XX
XX (MARS-) MARSHFIELD CLINIC.
XX
XX Weber JL;
XX
XX WPI; 1997-042299/04.
XX
XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -
PT using novel nucleic acid mols. as primers.
XX
XX Disclosure; Col 9-10; 186pp; English.
XX
XX The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g. paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic disease, commercial
CC animal or plant breeding or pedigree analysis. Clones containing the
CC repeat sequences were isolated by hybridisation of chromosome-specific
CC phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100
CC repeat blocks were isolated. The inserts from the clones were amplified
CC by primers AAQ65798-T66047. Those clones where the repeat sequence has
CC been determined are shown in AAQ65704-797. This repeat sequence is from
CC the marker clone Mfd37 which contains the repeat sequence having the
CC formula: (AC)10A. (Updated on 25-MAR-2003 to correct PF field.)
CC

XX SQ Sequence 21 BP; 11 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 2.0%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
 DB 21 TGTGTGTGTGTGTGTGTGT 1

RESULT 61
 AAH46013
 ID AAH46013 standard; DNA; 21 BP.
 XX
 AC AAH46013;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synthetic oligonucleotide 13.
 XX
 KW Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
 KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
 KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
 KW lymphoma; ss.
 XX
 OS Synthetic.
 XX
 PN WO200144465-A2.
 XX
 PD 21-JUN-2001.
 XX
 PF 12-DEC-2000; 2000WO-COA001467.
 XX
 PR 13-DEC-1999; 99US-0170325P.
 PR 29-AUG-2000; 2000US-0228925P.
 XX
 PA (BION-) BIONICHE LIFE SCI INC.
 PI Phillips NC, Fillion MC;
 XX
 DR WPI; 2001-398150/42.
 XX
 CC Composition comprising synthetic oligonucleotides which comprise multiple
 PT repeats of dinucleotides such as GT, TG useful for treating cancer by
 PT inducing cell cycle arrest, inhibiting proliferation, activating
 PT caspases.
 XX
 PS Example 4; Page 17; 77pp; English.
 XX
 CC The present sequence is that of a synthetic oligonucleotide useful to the
 CC invention. The invention relates to a composition, comprising a 2 to 20
 CC base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
 CC repeats of dinucleotides such as GT, TG, etc., according to specific
 CC formula and having cytostatic activity. The oligonucleotide compositions
 CC are useful for inducing cell cycle arrest, inhibition of proliferation,
 CC activation of caspases and induction of apoptosis or production of
 CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
 CC necrosis factor (TNF)-alpha by immune system cells, in an animal having
 CC cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
 CC and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
 CC colorectal, ovarian or bone cancer. The compositions induce apoptosis
 CC independent of Fas, p53/p21, p21/waf-1/CIP, p15(Ink4B), p16(Ink4), drug
 CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
 CC and hormone dependence
 XX
 SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 2.0%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
 DB 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 62
 AAF99702
 ID AAF99702 standard; DNA; 21 BP.
 XX
 AC AAF99702;
 XX
 DT 12-JUN-2001 (first entry)
 XX
 DE Immunostimulatory nucleic acid #818.
 XX
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 OS Synthetic.
 OS
 PN WO200122972-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 25-SEP-2000; 2000WO-US026383.
 XX
 PR 25-SEP-1999; 99US-0156113P.
 PR 27-SEP-1999; 99US-0156135P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PI Krieg AM, Schetter C, Vollmer J;
 XX
 DR WPI; 2001-273485/28.
 XX
 PT Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 XX
 PS Claim 101; Page 56; 339pp; English.
 XX
 CC The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX
 SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 2.0%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
 DB 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 63
 ABS78423
 ID ABS78423 standard; DNA; 21 BP.

XX OS Synthetic.
XX PN US2003050268-A1.
XX PD 13-MAR-2003.
XX PF 29-MAR-2002; 2002US-00112653.
XX PR 29-MAR-2001; 2001US-0279642P.
XX PA (KRIE/) KRIEG A M.
XX PA (BERG/) BERG D J.
XX PI Krieg AM, Berg DJ;
XX PN WPI; 2003-521815/49.
XX DR Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
XX PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
XX PT disease by administering an immunostimulatory nucleic acid.
XX PS Disclosure; Page 32; 229pp; English.
XX CC The invention describes a method of treating non-allergic inflammatory
XX CC disease comprising administering to a subject having or at risk of
XX CC developing a non-allergic inflammatory disease an immunostimulatory
XX CC nucleic acid for prevention or treatment of the disease. The method is
XX CC useful for treating non-allergic inflammatory diseases, such as
XX CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
XX CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
XX CC This sequence represents an immunostimulatory nucleic acid
XX SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. NO. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 66
ADB37204
ID ADB37204 standard; DNA; 21 BP.
XX AC ADB37204;
XX DT 04-DEC-2003 (first entry)
XX DE Immunostimulatory nucleic acid #818.
XX KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX KW hypo-responsive subject; immunostimulatory.
XX OS Synthetic.
XX PN US2003087848-A1.
XX PD 08-MAY-2003.
XX PF 02-FEB-2001; 2001US-00776479.
XX PR 03-FEB-2000; 2000US-0179991P.
XX PA (BRAT/) BRATZLER R L.
XX PA (PETER/) PETERSEN D M.
XX PA (FOUR/) FOURON Y.
XX PI Bratzler RL, Petersen DM, Fouron Y;
XX

DR WPI; 2003-657977/62.
XX Treating and/or preventing allergy or asthma using an immunostimulatory
XX PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX PS Disclosure; Page 17; 221pp; English.
XX CC The invention relates to a method of treating or preventing allergy or
XX CC asthma which comprises administering to a subject a poly-G nucleic acid
XX CC in an aerosol formulation. The methods and compositions of the present
XX CC invention are useful for diagnosing and/or treating asthma and allergy
XX CC especially in a hypo-responsive subject. The present sequence represents
XX CC an immunostimulatory nucleic acid of the invention.
XX SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;

Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. NO. 47;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 67
AAQ33810
ID AAQ33810 standard; DNA; 22 BP.
XX AC AAQ33810;
XX DT 25-MAR-2003 (revised)
XX DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA214.
XX KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
XX KW Genetic mapping; traits; amplification; ss.
XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENW-) GENMARK.
XX PI Georges M, Massey JM;
XX PN WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX PT mapping, and selective breeding.
XX PS Table 7; Page 253; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obtd. by
XX CC screening a library of bovine MboI DNA fragments of between 250 and 500
XX CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX CC clones cross-hybridised. Assuming independent distribution of
XX CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX CC in the bovine genome is estimated at >100,000. The sequence information
XX CC for ca. 230 such bovine microsatellites is summarised in the
XX CC specification and indexed herein (see below). The sequences upstream and
XX CC downstream of the microsatellite sequence were used to generate the
XX CC required PCR primers for in vitro amplification of the corresp.
XX CC microsatellite (using the program OPTIPRIM). The microsatellites may be
XX CC used to identify individuals, for parentage testing, and in the genetic
XX CC mapping of economic trait loci, or genes involved in the determination of

CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;

Query Match 2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 2 TGTGTGTGTGTGTGTGTGTGT 22

RESULT 68
AAQ33675
ID AAQ33675 standard; DNA; 22 BP.
XX
AC AAQ33675;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA117.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
KW
XX Bos taurus.
OS
XX WO9213102-A1.
FN
XX 06-AUG-1992.
PD
XX 15-JAN-1992; 92WO-US000340.
PF
XX 15-JAN-1991; 91US-00642342.
PR
XX (GENM-) GENMARK.
PA
XX Georges M, Massey JM;
PI
XX WPI; 1992-284684/34.
DR
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
PT
XX Table 7; Page 199; 517pp; English.
PS
XX The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (TC)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;

Query Match 2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 69
AAQ34038
ID AAQ34038 standard; DNA; 22 BP.
XX
AC AAQ34038;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA432.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
KW
XX Bos taurus.
OS
XX WO9213102-A1.
FN
XX 06-AUG-1992.
PD
XX 15-JAN-1992; 92WO-US000340.
PF
XX 15-JAN-1991; 91US-00642342.
PR
XX (GENM-) GENMARK.
PA
XX Georges M, Massey JM;
PI
XX WPI; 1992-284684/34.
DR
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
PT
XX Table 7; Page 346; 517pp; English.
PS
XX The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (TC)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;

Query Match 2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 70
AAQ34080
ID AAQ34080 standard; DNA; 22 BP.
XX
AC AAQ34080;

XX 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA48.
 XX
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 FN W09213102-A1.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US000340.
 XX
 PR 15-JAN-1991; 91US-00642342.
 XX
 XX (GENM-) GENMARK.
 XX
 XX Georges M, Massey JM;
 XX
 DR WPI; 1992-284684/34.
 XX
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX
 PS Table 7; Page 363; 517pp; English.
 XX
 CC The sequence is that of a bovine microsatellite sequence obt'd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (TC)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
 Query Match 2.0%; Score 21; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
 DB 1 TGTGTGTGTGTGTGTGTGTGT 21
 RESULT 71
 AAQ33991
 ID AAQ33991 standard; DNA; 22 BP.
 XX
 AC AAQ33991;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA39.
 XX
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.

XX W09213102-A1.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US000340.
 XX
 PR 15-JAN-1991; 91US-00642342.
 XX
 XX (GENM-) GENMARK.
 XX
 XX Georges M, Massey JM;
 XX
 DR WPI; 1992-284684/34.
 XX
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX
 PS Table 7; Page 327; 517pp; English.
 XX
 CC The sequence is that of a bovine microsatellite sequence obt'd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (TC)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
 Query Match 2.0%; Score 21; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
 DB 1 TGTGTGTGTGTGTGTGTGTGT 21
 RESULT 72
 AAQ83952/c
 ID AAQ83952 standard; DNA; 22 BP.
 XX
 AC AAQ83952;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-OCT-1995 (first entry)
 XX
 DE Oligonucleotide clamp n, for producing comb-type brached polymer.
 XX
 KW HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /note= "Modified with BrCH2(=O)CNH-"
 FT modified_base 8..9
 FT /*tag= b
 FT /note= "C(pnp)A, pnp = a linkage or monomer containing a
 FT bromoacetyl amino functionality, and p = phosphodiester
 FT linkage"
 FT modified_base 14..15

OS	Homo sapiens.
XX	
PN	U95582979-A.
XX	
PD	10-DEC-1996.
XX	
PF	04-APR-1994; 94US-00222177.
XX	
PR	21-APR-1989; 89US-00341562.
PR	05-SEP-1991; 91US-00754351.
XX	
PA	(MARS-) MARSHFIELD CLINIC.
XX	
PI	Weber JL;
XX	
DR	WEI; 1997-042239/04.
XX	
PT	Detection of polymorphic genetic markers of the form (dc-da)n(dg-dt)n -
PT	using novel nucleic acid mols. as primers.
XX	
PS	Disclosure; Col 9-10; 186pp; English.
XX	
CC	The invention relates to the isolation of polymorphic repeat sequences
CC	having the sequence (dc-da)n.(dg-dr)n which can be used as genetic
CC	markers. Primers based on these sequences can be used to detect these
CC	repeats, especially for use in e.g paternity or maternity testing, human
CC	genetic analysis such as linkage analysis of genetic disease, commercial
CC	animal or plant breeding or pedigree analysis. Clones containing the
CC	repeat sequences were isolated by hybridisation of chromosome-specific
CC	phage libraries with a synthetic poly(dc-da).(dg-dr) probe. Over 100
CC	repeat blocks were isolated. The inserts from the clones were amplified
CC	by primers AAT65798-T66047. Those clones where the repeat sequence has
CC	been determined are shown in AAT65704-797. This repeat sequence is from
CC	the marker clone Mdf25 which contains the repeat sequence having the
CC	formula: (AC)11. (Updated on 25-MAR-2003 to correct PF field.)
XX	
SQ	Sequence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
	Query Match 2.0%; Score 21; DB 1; Length 22;
	Best Local Similarity 100.0%; Pred. No. 49;
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1793 TGGTGTTGGTGTGTGTGTGTGT 1813
Db	21 TGTTGTGTGTGTGTGTGTGTGT 1
RESULT 74	
AAI64448	
ID	AAI64448 standard; DNA; 22 BP.
XX	
AC	AAI64448;
XX	
DT	23-NOV-2001 (first entry)
XX	
DE	SSR motif #8.
XX	
KW	Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
KW	trait mapping; marker-assisted selection; gene selection; legume;
KW	DNA profiling; breeding; ds.
XX	
OS	Unidentified.
XX	
PN	NZ509194-A.
XX	
FD	25-MAY-2001.
XX	
PF	03-JAN-2001; 2001NZ-00509194.
XX	
PR	24-DEC-1999; 99AU-00004907.
PR	28-MAR-2000; 2000AU-00006520.
XX	
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.


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XX
PI Koelliker R, Forster JW;
XX
DR WPI; 2001-431058/46.
XX
PT Novel simple sequence repeats in clover species useful for selection of
PT Genes in legume breeding, for profiling legume species varieties and for
PT testing the purity of legume seed batches.
XX
PS Claim 6; Page 35; 52pp; English.
XX
CC The present invention relates to Simple Sequence Repeats (SSRs) from
CC clover species. SSRs, also called microsatellites, are based on a 1-7
CC nucleotide core element which is tandemly repeated. The SSR array is
CC embedded in complex flanking DNA. SSRs are ideal markers for genome
CC mapping, trait mapping and marker-assisted selection. The SSRs may be
CC used in methods for selecting genes in clover/ legume breeding. The SSRs
CC are also useful for DNA profiling of clover varieties and for testing the
CC purity of legume seed batches. The present sequence is a SSR motif, which
CC was used in the present invention
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
Query Match 2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 75
AAF60472/c
ID AAF60472 standard; DNA; 23 BP.
XX
AC AAF60472;
XX
DT 27-APR-2001 (first entry)
XX
DE Oligonucleotide clamp #17.
XX
XX Oligonucleotide clamp; ds.
XX
XX Unidentified.
XX
XX US6180777-B1.
XX
XX 30-JAN-2001.
XX
XX 03-JAN-1997; 97US-00787321.
XX
XX 12-JAN-1996; 96US-0009918P.
XX
XX (FARB ) BAYER CORP.
XX
XX Horn T;
XX
XX WPI; 2001-201911/20.
XX
PT Synthesizing branched nucleic acids useful as diagnostic and molecular
PT probes, involves combining first units having haloalkylamino groups and
PT second units having thiol or phosphorothioate groups.
XX
XX Example 7; Col 19; 20pp; English.
XX
CC The present invention relates to a method for synthesising a branched or
CC multiply connected macromolecular structure, comprising oligonucleotide
CC clamps (OC). The macromolecular structure is capable of specifically
CC binding to a target molecule, and can therefore be used as probes. At
CC least one OC comprises a target binding sequence that binds specifically
CC and stably with the target molecule, and at least two OCs comprise signal
CC generation moieties capable of generating a detectable signal in the

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CC presence of the target molecule. In addition the OCs are connected to one
CC another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC present sequence is an OC used in the present invention
XX
SQ Sequence 23 BP; 11 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 2.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 22 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 76
AAH40155/c
ID AAH40155 standard; DNA; 25 BP.
XX
AC AAH40155;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 2951.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 65; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,

```

CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence

XX
SQ Sequence 25 BP; 11 A; 11 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 2.0%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 54;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
|||
Db 21 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 77
AAH40159/C
ID AAH40159 standard; DNA; 25 BP.

XX
XX AAH40159;
XX
XX 14-AUG-2001 (first entry)
XX
XX SNP specific SNPE primer SEQ ID 2955.

XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.

XX
OS Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Picoult-Newburg L, Pohl M;
XX
XX WFI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
XX Claim 1; Page 65; 83pp; English.

XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial

disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a single nucleotide primer extension (SNPE) primer specific for a human SNP containing DNA sequence

Sequence 25 BP; 11 A; 12 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 2.0%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGCTGTGCTGTGTGTGTGTGT 1813
Db 22 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 78
ADD59512
ID ADD69512 standard; DNA; 23 BP.
XX AC ADD69512;
XX DT
XX XX
XX DE 15-JAN-2004 (first entry)
XX 5' anchored (ISSR)-PCR primer - SEQ ID 5 alternative.
XX inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
KW animal; Basmati rice; ss.
XX Synthetic.
OS
XX WO2003085133-A2.
FN PD 16-OCT-2003.
XX PF 09-JAN-2003; 2003WO-IBO00041.
XX PR 08-APR-2002; 2002IN-CHO00260.
XX PA (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
XX Nagaraju JG;
PI WPT; 2003-804317/75.
DR
XX New set of inter-simple sequence repeats (ISSR)-PCR primers for
PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
PT animal systems.
XX Claim 1; Page 17; 60pp; English.

The invention relates to a novel set of inter-simple sequence repeats (ISSR)-PCR primers for genotyping eukaryotes. The primers of the invention may be useful for genotyping diverse genomes of plant and animal systems, in particular for distinguishing Basmati rice varieties from non-Basmati rice varieties and traditional Basmati rice varieties from evolved Basmati rice varieties. The current sequence is that of the 5' anchored (ISSR)-PCR primer of the invention.

Sequence 23 BP; 0 A; 1 C; 9 G; 11 T; 0 U; 2 Other;

Query Match 2.0%; Score 20.6; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 57;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGCTGTGCTGTGTGTGTGTGT 1813
Db 3 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 79
 AAQ34170
 ID AAQ34170 standard; DNA; 20 BP.
 XX
 AC AAQ34170;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Sequence of a microsatellite from clone TGLA86.
 XX
 DE PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 PN WO9213102-A1.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US000340.
 XX
 PR 15-JAN-1991; 91US-00642342.
 XX
 PA (GENM-) GENMARK.
 XX
 OS Georges M, Massey JM;
 PN WPI; 1992-284684/34.
 XX
 PD Polymorphic bovine DNA markers - used in genetic identification, gene
 PF mapping, and selective breeding.
 XX
 PR Table 7; Page 397; 517pp; English.
 XX
 PA The sequence is that of a bovine microsatellite sequence obt'd. by
 XX screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T₆)_n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
 XX
 Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTG 1812
 DB 1 TGTGTGTGTGTGTGTGTG 20
 XX
 RESULT 80
 AAQ33816
 ID AAQ33816 standard; DNA; 20 BP.
 XX
 AC AAQ33816;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA22.
 XX

XX
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 PN WO9213102-A1.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US000340.
 XX
 PR 15-JAN-1991; 91US-00642342.
 XX
 PA (GENM-) GENMARK.
 XX
 OS Georges M, Massey JM;
 PN WPI; 1992-284684/34.
 XX
 PD Polymorphic bovine DNA markers - used in genetic identification, gene
 PF mapping, and selective breeding.
 XX
 PR Table 7; Page 256; 517pp; English.
 XX
 PA The sequence is that of a bovine microsatellite sequence obt'd. by
 XX screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T₆)_n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
 XX
 Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTG 1812
 DB 1 TGTGTGTGTGTGTGTGTG 20
 XX
 RESULT 81
 AAQ33672
 ID AAQ33672 standard; DNA; 20 BP.
 XX
 AC AAQ33672;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA116.
 XX
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 PN WO9213102-A1.
 XX
 PD 06-AUG-1992.
 XX

PF 15-JAN-1992; 92WO-US000340.
 XX
 PR 15-JAN-1991; 91US-00642342.
 XX
 PA (GENM-) GENMARK.

XX Georges M, Massey JM;
 XX
 PI WPI; 1992-284684/34.
 XX

DR WPI; 1992-284684/34.
 XX

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 XX mapping, and selective breeding.
 PT
 PT

XX Table 7; Page 198; 517pp; English.
 PS

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (16)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved the determinism of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding, for example this microsatellite is a marker for the Weaver
 CC condition and the QTL trait of enhanced milk prodn. in Brown Swiss
 CC cattle. See also AAQ33501-34442. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX

XX Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
 SQ

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGTGT 1813
 Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 82

AAAT30427/C
 ID AAT30427 standard; DNA; 20 BP.

XX AAT30427;
 XX

XX 28-JAN-1997 (first entry)
 XX

XX Compound simple sequence repeat primer (CA)4.5(TA)7.5.
 XX

XX Detection; polymorphism; perfect compound simple sequence repeat;
 KW adaptor directed primer; genome; genetic; fingerprinting;
 KW amplified fragment length polymorphism assay; microsatellite region;
 KW genetic trait marking; germplasm comparisons; compound; ss.

XX Synthetic.
 XX

XX WO9617082-A2.
 XX

XX 06-JUN-1996.
 XX

XX 21-NOV-1995; 95WO-US015150.
 XX

XX 28-NOV-1994; 94US-00346456.
 XX

XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX

XX Morgante M, Vogel JM;
 PI

XX WPI; 1996-277795/28.
 DR

XX Modified amplified fragment length polymorphism assay - for detection of
 XX polymorphism esp. in micro:satellite regions.
 PT

XX Disclosure; Fig 1c; 173pp; English.
 PS

XX Detecting polymorphisms between 2 nucleic acid samples, esp. in
 CC microsatellite regions, comprises digesting the nucleic acid to generate
 CC fragments, ligating adaptor segments to their ends, amplifying them using
 CC primer directed amplification and comparing the prods. to detect
 CC differences. The primers used in the amplification comprise a primer
 CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor
 CC directed primer, comprising a sequence complementary to an adaptor
 CC segment. The present sequence is an example of a compound SSR primer. The
 CC method represents a modified amplified fragment length polymorphism
 CC assay, which is partic. useful for genome fingerprinting, i.e. for
 CC genetic trait marking and germplasm comparisons

XX Sequence 20 BP; 10 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1799 TGCTGTGTGTGTGTATATA 1818

Db 20 TGCTGTGTGTGTGTATATA 1

RESULT 83

AAT93829
 ID AAT93829 standard; DNA; 20 BP.

XX AAT93829;
 XX

XX 25-MAR-2003 (revised)
 DT

DT 24-FEB-1998 (first entry)
 DT

XX Antitumoural phosphodiester oligonucleotide 19 with cytotoxic activity.
 XX Phosphodiester; selective binding; cell viability; growth;
 KW tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
 KW lymphoblastic tumour; ss.

XX Synthetic.
 XX

XX Key Location/Qualifiers
 FH modified_base 1..20

FT /*tag= a
 FT /note= "phosphodiester oligonucleotide"

XX WO9720924-A1.
 XX

XX 12-JUN-1997.
 XX

XX 04-DEC-1996; 96WO-EP005388.
 XX

XX 04-DEC-1995; 95IT-MI002539.
 XX

XX (SAIC-) SAICOM SRL.
 XX

XX Scaggiante B, Quadrifoglio F;
 XX

XX WPI; 1997-319771/29.
 XX

XX New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
 PT selective cytotoxic effect on tumour cells, for treating both solid and
 PT liquid tumours.
 XX

XX Claim 11; Page 4; 38pp; English.
 PS

XX

CC The present phosphodiesteric oligonucleotide is based on the generic
CC formula, in the 3'-5' or 5'-3' direction: (GaTa'a')a'-(GbTb')b'-'
CC (GcTc')c'-(GdTd')d'-(GeTe')e'-(GfTf')f'-(G-gTg')g'-N', where: N and
CC N' = T or G, equal or different from each other; x = 0-8, equal or
CC different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC 16, equal or different from each other; Oligonucleotides of this generic
CC sequence (see also AA793811-27) are believed to selectively bind and
CC sequester some proteins which are essential to the viability and growth
CC of tumoural cell line. They have specific and selective cytotoxic
CC activity against tumour cells, and can be used for treating tumours of
CC the liquid type, in particular of lymphoblastic origin, and of solid
CC type, in particular lymphomas. The present oligonucleotide is known, but
CC no biological activity has been reported until the reported cytotoxic
CC antitumour activity. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 84
AAV06824
ID AAV06824 standard; DNA; 20 BP.
AC AAV06824;
XX
DT 01-JUL-1998 (first entry)
XX
DE Oligonucleotide which binds retroviral nucleocapsid protein.
XX
KW Retroviral nucleocapsid protein; NC; high affinity; viral replication;
KW gene therapy; retroviral infection; HIV; transduced cell; ss.
XX
OS Synthetic.
XX
PN WO9744064-A2.
XX
PD 27-NOV-1997.
XX
PF 19-MAY-1997; 97WO-US0008936.
XX
PR 20-MAY-1996; 96US-0017128P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rein A, Casas-Finet J, Fisher R, Fivash M, Henderson LE;
XX
DR WPI; 1998-018230/02.
XX
PT Oligonucleotide which binds to retroviral nucleocapsid protein with high
PT affinity - used in targeted molecules, transduced cells and gene therapy
PT vectors for treatment of retroviral infections such as those caused by
PT HIV.
XX
PS Claim 7; Page 56; 70pp; English.
XX
CC This sequence represents an oligonucleotide which binds to a retroviral
CC nucleocapsid (NC) protein with high affinity. The invention relates to a
CC targeted molecule which binds to a retroviral nucleocapsid protein with
CC high affinity and comprises the oligonucleotide and a fusion partner.
CC Retroviral nucleocapsid proteins, such as NC and the Gag precursors, bind
CC to specific nucleic acid sequences with high affinity. This binding is
CC dependent upon the zinc fingers of the NC protein and has a strong
CC hydrophobic component. The specific nucleic acid sequences which bind NC
CC are useful as molecular decoys for retroviral NC proteins, for making

CC fusion proteins which inactivate retroviral NC proteins, in screening
CC assays for detecting molecules which inactivate retroviral NC proteins.
CC nucleic acid binding, and for purification of retroviral NC proteins. In
CC particular, the targeted molecules, the transduced cells and gene therapy
CC vectors based on the oligonucleotides can be used for treatment and
CC prevention of retroviral infections such as those caused by HIV
XX
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1812
Db 1 TGTGTGTGTGTGTGTGTGTGT 20

RESULT 85
AAA39091
ID AAA39091 standard; DNA; 20 BP.
XX
AC AAA39091;
XX
DT 30-AUG-2000 (first entry)
XX
DE 20-mer-oligonucleotide sequence.
XX
KW Displacement chromatography; purification; separation; ss.
XX
OS Unidentified.
XX
PN WO200023798-A1.
XX
PD 27-APR-2000.
XX
PF 20-OCT-1999; 99WO-GB003463.
XX
PR 20-OCT-1998; 98GB-00022963.
XX
PA (MARS/) MARSDEN J C.
PA (AGNE/) AGNER E.
XX
PI Agner E;
XX
DR WPI; 2000-339759/29.
XX
PT Displacement chromatography for purification of peptide samples by non-
PT homogeneous application of sample components to chromatography bed.
XX
PS Example 2; Page 22; 37pp; English.
XX
CC The present invention describes a method (I) for sample displacement
CC chromatography separation. The method comprises applying a multicomponent
CC sample to one end of a chromatography bed, distributing the sample along
CC the bed by passing non-eluting mobile solvent phase over the bed, and
CC recovering a desired component of the sample from at least portion of the
CC bed. The sample components are applied in a non-homogeneous manner to
CC enhance concentration of at least one component with relatively low
CC and/or high affinity for the stationary phase material, respectively,
CC during an earlier and later part of the sample application. The method is
CC useful for chromatographic separation of samples. The method permits
CC recovery of sample components at significantly higher concentrations and
CC generally makes more efficient use of the stationary phase material. The
CC method allows ten-fold greater loading than comparable gradient elution
CC separation, it involves minimal use of costly HPLC solvents and fraction
CC analysis, avoids the use of displacer solution during actual separation
CC and operating costs are lower. The present sequence represents a 20-mer
CC oligonucleotide which is used in an example from the present invention
CC for the purification of an oligonucleotide by sample displacement
CC chromatography
XX
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTG 1812
|||||
Db 1 TGTGTGTGTGTGTGTGTG 20

RESULT 86
AAS13762
ID AAS13762 standard; DNA; 20 BP.
XX AC AAS13762;
XX DT 08-MAY-2002 (first entry)
XX DE Simple sequence repeat, SSR, #34.
XX KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
KW cereal profiling; grass profiling; seed batch purity testing.
XX OS Lolium perenne.
XX PN NZ509193-A.
XX PD 25-MAY-2001.
XX PF 03-JAN-2001; 2001NZ-00509193.
XX PR 24-DEC-1999; 99AU-00004906.
XX PR 04-MAY-2000; 2000AU-00007310.
XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
PA (UYSC-) UNIV SOUTHERN CROSS.
PA (VIC-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
PA (UYAD-) UNIV ADELAIDE.
PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX Forster JW, Jones ES;
XX WPI; 2001-512563/56.

New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.

Example 1; Fig 6; 72pp; English.

The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR

Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
|||||
Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 87
AAS13705/C
ID AAS13705 standard; DNA; 20 BP.
XX AC AAS13705;
XX DT 08-MAY-2002 (first entry)
XX DE Simple sequence repeat, SSR, #2.
XX KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
KW cereal profiling; grass profiling; seed batch purity testing.
XX OS Poa.
XX PN NZ509193-A.
XX PD 25-MAY-2001.
XX PF 03-JAN-2001; 2001NZ-00509193.
XX PR 24-DEC-1999; 99AU-00004906.
XX PR 04-MAY-2000; 2000AU-00007310.
XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
PA (UYSC-) UNIV SOUTHERN CROSS.
PA (VIC-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
PA (UYAD-) UNIV ADELAIDE.
PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX Forster JW, Jones ES;
XX WPI; 2001-512563/56.

New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.

Claim 6; Page 51; 72pp; English.

The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR

Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;

XX

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XX

[illegible]

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02-JUL-1998; 98US-0091481P.
11-DEC-1998; 98US-0111800P.
02-JUL-1999; 99US-00347443.
(REGC ) UNIV CALIFORNIA.
Dev AP, Bruice TC;
WPI; 2001-122276/13.
Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in
antisense therapy, by synthesizing oligonucleotides comprising backbone
of alkyl or alkoxy thiourea linkages in solution or on solid phase.
Example 7; Fig 16; 48pp; English.
The present sequence was used to demonstrate the ability of deoxynucleic
S-Methylthiourea (DMt) compounds to form triplexes with DNA oligomers. An
increase in the C content of the oligos resulted in a large decrease in
binding. This experiment was performed as an example of a method for
preparing oligonucleotides comprising a backbone of alkyl or alkoxy
thiourea linkages. The method is useful for preparing oligonucleotides
for use in antisense or antigen therapy, to inhibit production of
proteins associated with genetic diseases, cardiovascular, inflammatory
and neurocellular diseases, and for antiviral therapy, e.g. to treat
human immunodeficiency virus, human-cytomegalovirus, influenza and herpes
infections. The compounds are also useful as diagnostic reagents to
detect the presence or absence of the target DNA or RNA sequences to
which they specifically bind and by antagonising the normal biological
activity of a target protein, they can be used in the manipulation of
tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
cultures. The method provides an efficient and rapid solid-phase method
for the synthesis of thiourea and S-methylthiourea
Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1793 TGTGTGTGTGTGTGTGTGTG 1812
|||||
DB 20 TGTGTGTGTGTGTGTGTG 1
|||||
RESULT 91
AAH48201
ID AAH48201 standard; DNA; 20 BP.
XX AAH48201;
XX
DT 20-SEP-2001 (first entry)
XX
DE Antibody binding oligonucleotide.
XX
DE Antibody affinity; DNA epitope; anti-DNA antibody; lupus nephritis;
XX systemic lupus erythematosus; immunotolerance; ds.
XX Synthetic.
XX
XX WO200141813-A2.
XX
XX 14-JUN-2001.
XX
XX 28-NOV-2000; 2000WO-US042307.
XX
XX 28-NOV-1999; 99US-0167716P.
XX (LJOL-) LA JOLLA PHARM CO.
XX
XX Linnik MD, Mcnealy PA;
XX WPI; 2001-451501/48.
XX

```

Treating systemic lupus erythematosus in individual comprises e.g. administering conjugate comprising non-immunogenic valency platform molecule and double stranded DNA epitopes which specifically bind to antibody from individual.
 Claim 4; Page 57; 87pp; English.
 The present invention describes a method of treating systemic lupus erythematosus and lupus nephritis, involving administering a conjugate comprising a non-immunogenic valency platform molecule and 2 double stranded DNA epitopes which specifically bind to dsDNA-binding antibodies. Affinity of the epitopes for the antibody is used as a basis for selecting individuals to receive treatment. The present sequence is an antibody binding dsDNA sequence described in the exemplification of the invention
 Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
 Query March 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
 DB 1 GTGTGTGTGTGTGTGTGTGT 20
 RESULT 92
 AAI64445/C
 ID AAI64445 standard; DNA; 20 BP.
 XX AC AAI64445;
 XX AC
 DT DT
 XX AC
 DE DE
 XX AC
 KW KW
 KW KW
 XX OS
 XX OS
 PN PN
 XX PN
 PD PD
 XX XX
 PF PF
 XX XX
 PR PR
 PR PR
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX PA
 XX PA
 PI PI
 XX PI
 XX WPI; 2001-431058/46.
 DR DR
 XX DR
 PT PT
 PT PT
 PT PT
 XX PT
 XX PS
 XX PS
 XX PS
 The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 nucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNA. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/ legume breeding. The SSRs are also useful for DNA profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which

CC was used in the present invention
 XX Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
 SQ Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
 Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 93
 AAI64449
 ID AAI64449 standard; DNA; 20 BP.
 XX AAI64449;
 AC
 XX
 XX
 DT 23-NOV-2001 (first entry)
 XX
 DE SSR motif #9.
 XX
 XX Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
 KW trait mapping; marker-assisted selection; gene selection; legume;
 KW DNA profiling; breeding; ds.
 XX
 XX Unidentified.
 OS
 XX NZ509194-A.
 PN
 XX
 XX 25-MAY-2001.
 PD
 XX
 XX 03-JAN-2001; 2001NZ-00509194.
 PF
 XX
 XX 24-DEC-1999; 99AU-00004907.
 PR
 XX 28-MAR-2000; 2000AU-00006520.
 PX
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA
 XX
 XX Koelliker R, Forster JW;
 PI
 XX WPI; 2001-431058/46.
 DR
 XX Novel simple sequence repeats in clover species useful for selection of
 PT genes in legume breeding, for profiling legume species varieties and for
 PT testing the purity of legume seed batches.
 XX
 XX Claim 6; Page 35; 52pp; English.
 PS
 XX The present invention relates to Simple Sequence Repeats (SSRs) from
 CC clover species. SSRs, also called microsatellites, are based on a 1-7
 CC nucleotide core element which is tandemly repeated. The SSR array is
 CC embedded in complex flanking DNA. SSRs are ideal markers for genome
 CC mapping, trait mapping and marker-assisted selection. The SSRs may be
 CC used in methods for selecting genes in clover/ legume breeding. The SSRs
 CC are also useful for DNA profiling of clover varieties and for testing the
 CC purity of legume seed batches. The present sequence is a SSR motif, which
 CC was used in the present invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
 Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 94
 ABK87132

ID
 XX ABK87132 standard; DNA; 20 BP.
 AC
 XX ABK87132;
 DT 07-OCT-2002 (first entry)
 XX
 DE Human connective tissue growth factor, RT-PCR primer #2.
 XX
 XX Human, endothelial cell-specific molecule 4; ECSM4; neovasculature;
 KW imaging vascular endothelium; proliferative disease; cancer; psoriasis;
 KW diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage;
 KW tumour neovasculature; cardiac disease; endometriosis; hypoxic condition;
 KW angiogenesis; cytostatic; RT-PCR; connective tissue growth factor;
 KW reverse transcription-PCR; primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX W0200236771-A2.
 PN
 XX
 PD 10-MAY-2002.
 XX
 XX 06-NOV-2001; 2001WO-GB004906.
 PF
 XX
 XX 06-NOV-2000; 2000US-0245566P.
 PR
 XX 07-MAR-2001; 2001US-0273662P.
 PX
 XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 PA
 XX Bicknell R, Huminlecki L;
 PI
 XX WPI; 2002-508120/54.
 DR
 XX Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
 PT imaging, diagnosing and treating a condition involving vascular
 PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.
 XX
 XX Example 1; Page 165; 248pp; English.
 PS
 XX The present invention relates to endothelial cell-specific molecule 4
 CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins
 CC are useful for imaging vascular endothelium in the body of an individual,
 CC and for diagnosing and treating a proliferative disease or condition
 CC involving the vascular endothelium (preferably, neovasculature) such as
 CC cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia.
 CC The ECSM4 proteins are also useful in the manufacture of diagnostic or
 CC prognostic agent for such conditions. The proteins are also useful for
 CC detecting endothelial damage or activation, detecting a tumour or tumour
 CC neovasculature, cardiac disease, or endometriosis by detecting the amount
 CC of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4
 CC are useful in gene therapy for treating a hypoxic condition such as
 CC cancer, cardiac disease, endometriosis or atherosclerosis and in the
 CC manufacture of medicaments for treating the above disease. The sequences
 CC are useful for modulating angiogenesis in an individual. The present
 CC sequence represents a RT-PCR primer for RNA encoding human connective
 CC tissue growth factor
 XX
 SQ Sequence 20 BP; 8 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1951 CGTTCAAAGCATGAATGGA 1970
 Db 1 CGTTCAAAGCATGAATGGA 20

RESULT 95
 AAL45125
 ID AAL45125 standard; DNA; 20 BP.
 XX
 XX AAL45125;
 AC
 XX

DT 24-MAY-2002 (first entry)
XX Oligonucleotide synthesis method related DNA #4.
DE
XX
KW Oligonucleotide synthesis; polynucleotide array; protecting group;
KW oxidation; ss.
XX
OS Synthetic.
XX
PN EP1176151-A1.
XX
PD 30-JAN-2002.
XX
PF 27-JUL-2001; 2001EP-00118360.
XX
PR 28-JUL-2000; 2000US-00627249.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Dellinger DJ, Perbost MCM, Betley JR, Caruthers M;
XX WPI; 2002-156732/21.
XX
XX Synthesis of polynucleotide useful during fabrication of an array
PT involves coupling nucleoside phosphoramidite and a solid-supported
PT nucleoside and treating the product with an oxidation/deprotection
PT composition.
XX
PS Example 1; Page 15; 36pp; English.
XX
XX The present invention relates to a method for the synthesis of a
CC polynucleotide which involves coupling a second nucleoside to a first
CC nucleoside through a phosphite linkage, where the second nucleoside has a
CC non-carbonate protecting group protecting a hydroxyl, and exposing the
CC product to a composition which concurrently oxidizes the phosphite formed
CC to a phosphate and deprotects the protected hydroxyl of the second
CC nucleoside. The method is useful for synthesizing the polynucleotides,
CC for carrying cut either 3' to 5' or 5' to 3' synthesis and for
CC fabricating an addressable array of polynucleotides on a substrate. The
CC present sequence is an oligonucleotide produced to demonstrate the method
CC of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1793 TGTGTGTGTGTGTGTGTGTG 1812
Db 1 TGTGTGTGTGTGTGTGTGTG 20
RESULT 96
ID ABA96307/c
AC ABA96307;
XX
XX 18-MAR-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 2.
DE
XX Immobilisation; Diels-Alder reaction; ss.
KW
XX Synthetic.
OS
XX Key Location/Qualifiers
FH modified_base 1
FT /*tag= a
FT /mod base= OTHER
FT /note= "5' fluorescein label"
XX

PN WO200184234-A1.
XX
PD 08-NOV-2001.
XX
PF 01-MAY-2001; 2001WO-US013956.
XX
PR 01-MAY-2000; 2000US-0201561P.
PR 30-JAN-2001; 2001US-0265020P.
XX
PA (PROL-) PROLIGO LLC.
XX
PI Picken W, Wolter A, Sebesta DP, Leuck M, Latham-Timmons HA;
PI Pilon J, Husar GM;
XX
DR WPI; 2002-114155/15.
XX
PT New method for immobilizing a molecule on a support comprises reacting a
PT derivatized molecule with a derivatized support via a cycloaddition
PT reaction, shows high selectivity and efficiency.
XX
PS Example 6; Page 31; 86pp; English.
XX
XX The invention relates to a method for immobilising a molecule on a
CC support comparing reacting a derivatised molecule with a derivatised
CC support capable of reacting with the molecule via a cycloaddition
CC reaction. The method is used for immobilising molecules on a support
CC using cycloaddition reactions such as the Diels-Alder reaction. The
CC method shows better chemoselectivity, functional groups do not need to be
CC protected and it is highly efficient for immobilising molecules compared
CC to other methods. The present sequence is that of an oligonucleotide,
CC useful to the invention
XX
SQ Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1793 TGTGTGTGTGTGTGTGTGTG 1812
Db 20 TGTGTGTGTGTGTGTGTGTG 1
RESULT 97
ID ABA96306
AC ABA96306;
XX
XX 18-MAR-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 1.
DE
XX Immobilisation; Diels-Alder reaction; ss.
KW
XX Synthetic.
OS
XX WO200184234-A1.
PN
XX 08-NOV-2001.
PD
XX 01-MAY-2001; 2001WO-US013956.
PF
XX 01-MAY-2000; 2000US-0201561P.
PR
XX 30-JAN-2001; 2001US-0265020P.
PR
XX (PROL-) PROLIGO LLC.
PA
XX Picken W, Wolter A, Sebesta DP, Leuck M, Latham-Timmons HA;
PI Pilon J, Husar GM;
XX
XX WPI; 2002-114155/15.
XX

PT New method for immobilizing a molecule on a support comprises reacting a
PT derivatized molecule with a derivatized support via a cycloaddition
PT reaction, shows high selectivity and efficiency.
XX
PS
XX Example 6; Page 31; 86pp; English.
XX
XX The invention relates to a method for immobilising a molecule on a
XX support comprising reacting a derivatised molecule with a derivatised
XX support capable of reacting with the molecule via a cycloaddition
XX reaction. The method is used for immobilising molecules on a support
XX using cycloaddition reactions such as the Diels-Alder reaction. The
XX method shows better chemoselectivity, functional groups do not need to be
XX protected and it is highly efficient for immobilising molecules compared
XX to other methods. The present sequence is that of an oligonucleotide,
XX useful to the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTG 1812
Db 1 TGTGTGTGTGTGTGTGTG 20
RESULT 98
ABZ24438/c
ID ABZ24438 standard; DNA; 20 BP.
XX
XX AC ABZ24438;
XX
XX DT 18-MAR-2003 (first entry)
XX
XX DE Oligonucleotide (CA)10 used in nucleic acid hybridisation.
XX
XX KW Nucleic acid detection; hybridisation; microarray; thermistor;
XX microcalorimetry; ss.
XX
XX OS Synthetic.
XX
XX PN WO200299386-A2.
XX
XX PD 12-DEC-2002.
XX
XX PF 07-JUN-2002; 2002WO-US018200.
XX
XX PR 07-JUN-2001; 2001US-0296685P.
XX
XX PA (PROL-) PROLIGO LLC.
XX
XX PI Roach JS, Wolter A;
XX
XX PS WPI; 2003-148685/14.
XX
XX
XX Detection device useful for detecting binding between members of specific
XX binding pair, and for multiparallel thermal analysis of samples, has an
XX array of addressable thermistors.
XX
XX Example 2; Page 36; 60pp; English.
XX
XX The present sequence is that of a (CA)10 oligonucleotide used to
XX illustrate the method of the invention. The invention provides methods
XX for detecting specific binding interactions through measuring the heat of
XX binding generated when members of specific binding pairs interact with
XX each other. The invention also provides methods to detect analytes in a
XX solution through measurement of the heat of binding or reaction generated
XX from the interaction of the analytes with binding or reaction partners.
XX Detection devices are provided that consist of spatially addressable
XX arrays of thermistors, which are useful in the multiparallel thermal
XX analysis of samples. The methods and devices are particularly in the
XX analysis of nucleic acids, especially DNA/DNA, DNA/RNA, DNA/LNA (linear

CC nucleic acid), DNA/siRNA (short interfering RNA) and DNA/PNA (peptide
CC nucleic acid). The binding between the analyte and its binding partner
CC comprises part of an enzymatic amplification reaction, especially PCR or
CC primer extension reaction. The detection device provides a real time,
CC digital profile of the binding or reaction between the analyte and its
CC binding or reaction partner. An example from the invention, using the
CC present oligonucleotide, showed that the thermal detection technique is
CC able to distinguish between perfectly matched and mismatched DNA
CC sequences
XX
SQ Sequence 20 BP; 10 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTG 1812
Db 20 TGTGTGTGTGTGTGTGTG 1
RESULT 99
ABZ24439
ID ABZ24439 standard; DNA; 20 BP.
XX
XX AC ABZ24439;
XX
XX DT 18-MAR-2003 (first entry)
XX
XX DE Oligonucleotide (TG)10 used in nucleic acid hybridisation.
XX
XX KW Nucleic acid detection; hybridisation; microarray; thermistor;
XX microcalorimetry; ss.
XX
XX OS Synthetic.
XX
XX PN WO200299386-A2.
XX
XX PD 12-DEC-2002.
XX
XX PF 07-JUN-2002; 2002WO-US018200.
XX
XX PR 07-JUN-2001; 2001US-0296685P.
XX
XX PA (PROL-) PROLIGO LLC.
XX
XX PI Roach JS, Wolter A;
XX
XX PS WPI; 2003-148685/14.
XX
XX
XX Detection device useful for detecting binding between members of specific
XX binding pair, and for multiparallel thermal analysis of samples, has an
XX array of addressable thermistors.
XX
XX Example 2; Page 36; 60pp; English.
XX
XX The present sequence is that of a (TG)10 oligonucleotide used to
XX illustrate the method of the invention. The invention provides methods
XX for detecting specific binding interactions through measuring the heat of
XX binding generated when members of specific binding pairs interact with
XX each other. The invention also provides methods to detect analytes in a
XX solution through measurement of the heat of binding or reaction generated
XX from the interaction of the analytes with binding or reaction partners.
XX Detection devices are provided that consist of spatially addressable
XX arrays of thermistors, which are useful in the multiparallel thermal
XX analysis of samples. The methods and devices are particularly in the
XX analysis of nucleic acids, especially DNA/DNA, DNA/RNA, DNA/LNA (linear

CC present oligonucleotide, showed that the thermal detection technique is
 CC able to distinguish between perfectly matched and mismatched DNA
 CC sequences
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;
 Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTG 1812
 Db 1 TGTGTGTGTGTGTGTGTG 20
 RESULT 100
 ADB25647/C
 ID ADB25647 standard; DNA; 20 BP.
 XX AC
 XX ADB25647;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human connective tissue growth factor antisense oligo DNA (SeqID 40).
 XX
 KW antisense; human; ss; connective tissue growth factor; CTGF;
 KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
 KW fisp-12; NOV2;
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cytostatic; dermatological;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 PN WC2003053340-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 09-DEC-2002; 2002WO-US038618.
 XX
 PR 10-DEC-2001; 2001US-00006191.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Gaarde WA, Watt AT;
 XX
 DR WPI; 2003-559091/52.
 XX
 XX New antisense oligonucleotides for modulating connective tissue growth
 PT factor expression, particularly useful for treating cancers (e.g. breast
 PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
 PT atherosclerosis.
 XX
 PS Claim 3; Page 85; 139pp; English.
 XX
 CC This invention relates to novel methods for modulating the expression of
 CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
 CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
 CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in
 CC acute lymphoblastic leukaemia and in tumour or endothelial cells

CC associated with the vasculature. Accordingly, antisense oligonucleotides
 CC that inhibit the expression of CTGF in cells or tissues can be used in
 CC gene therapy to treat various conditions including hyperproliferative
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
 CC such, the present invention describes these antisense oligos as having
 CC cytostatic, dermatological and antiarteriosclerotic activities. This
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 CC human CTGF of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1724 CTGCACAGCTTGCGCAAGT 1743
 Db 20 CTGCACAGCTTGCGCAAGT 1
 RESULT 101
 ADB25669/C
 ID ADB25669 standard; DNA; 20 BP.
 XX AC
 XX ADB25669;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human connective tissue growth factor antisense oligo DNA (SeqID 62).
 XX
 KW antisense; human; ss; connective tissue growth factor; CTGF;
 KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
 KW fisp-12; NOV2;
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cytostatic; dermatological;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 PN WC2003053340-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 09-DEC-2002; 2002WO-US038618.
 XX
 PR 10-DEC-2001; 2001US-00006191.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Gaarde WA, Watt AT;
 XX
 DR WPI; 2003-559091/52.
 XX
 XX New antisense oligonucleotides for modulating connective tissue growth
 PT factor expression, particularly useful for treating cancers (e.g. breast
 PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
 PT atherosclerosis.
 XX
 PS Claim 3; Page 85; 139pp; English.
 XX
 CC This invention relates to novel methods for modulating the expression of

CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC promote chemotaxis of fibroblasts, however, it is also upregulated in
CC acute lymphoblastic leukaemia and in tumour or endothelial cells
CC associated with the vasculature. Accordingly, antisense oligonucleotides
CC that inhibit the expression of CTGF in cells or tissues can be used in
CC gene therapy to treat various conditions including hyperproliferative
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC such, the present invention describes these antisense oligos as having
CC cytostatic, dermatological and antiarteriosclerotic activities. This
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC human CTGF of the invention.
XX
SQ Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2206 TTGTTGAGAGTGTGACCAA 2225
DB 20 TTGTTGAGAGTGTGACCAA 1
|||||
RESULT 102
ADB25654/C
ID ADB25654 standard; DNA; 20 BP.
AC ADB25654;
XX
XX 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 47).
XX
KW antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
XX
XX 10-DEC-2001; 2001US-00006191.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Gaarde WA, Watt AT;
XX
XX WPI; 2003-559091/52.
XX
XX New antisense oligonucleotides for modulating connective tissue growth

PT factor expression, particularly useful for treating cancers (e.g. breast
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT atherosclerosis.
XX
XX Claim 3; Page 85; 139pp; English.
XX
CC This invention relates to novel methods for modulating the expression of
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC promote chemotaxis of fibroblasts, however, it is also upregulated in
CC acute lymphoblastic leukaemia and in tumour or endothelial cells
CC associated with the vasculature. Accordingly, antisense oligonucleotides
CC that inhibit the expression of CTGF in cells or tissues can be used in
CC gene therapy to treat various conditions including hyperproliferative
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC such, the present invention describes these antisense oligos as having
CC cytostatic, dermatological and antiarteriosclerotic activities. This
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC human CTGF of the invention.
XX
SQ Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2213 GAGTGTGACCAAAAGTTACA 2232
DB 20 GAGTGTGACCAAAAGTTACA 1
|||||
RESULT 103
ADB25649/C
ID ADB25649 standard; DNA; 20 BP.
XX
XX ADB25649;
XX
XX 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 42).
XX
KW antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
XX
XX 10-DEC-2001; 2001US-00006191.
XX

PA (ISIS-) ISIS PHARM INC.
XX
XX
PI Gaarde WA, Watt AT;
XX
XX
DR WPI; 2003-559091/52.
XX
XX
PT New antisense oligonucleotides for modulating connective tissue growth
PT factor expression, particularly useful for treating cancers (e.g. breast
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT atherosclerosis.
XX
XX
PS Claim 3; Page 85; 139pp; English.
XX
XX
CC This invention relates to novel methods for modulating the expression of
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC promote chemotaxis of fibroblasts, however, it is also upregulated in
CC acute lymphoblastic leukaemia and in tumour or endothelial cells
CC associated with the vasculature. Accordingly, antisense oligonucleotides
CC that inhibit the expression of CTGF in cells or tissues can be used in
CC gene therapy to treat various conditions including hyperproliferative
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC such, the present invention describes these antisense oligos as having
CC cytostatic, dermatological and antiarteriosclerotic activities. This
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC human CTGF of the invention.
XX
XX
SQ Sequence 20 BP; 9 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1832 AGTTATCTAAGTTAATTAA 1851
Db 20 AGTTATCTAAGTTAATTAA 1
|||||

RESULT 104
ADB25648/c
ID ADB25648 standard; DNA; 20 BP.
XX
XX ADB25648;
XX
XX
DT 20-NOV-2003 (first entry)
XX
XX Human connective tissue growth factor antisense oligo DNA (SeqID 41).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytostatic; dermatological;
XX antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX
XX W02003053340-A2.

XX
XX
XX 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
XX
XX PF
XX
XX 10-DEC-2001; 2001US-00006191.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Gaarde WA, Watt AT;
XX
XX WPI; 2003-559091/52.
XX
XX
PT New antisense oligonucleotides for modulating connective tissue growth
PT factor expression, particularly useful for treating cancers (e.g. breast
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT atherosclerosis.
XX
XX
PS Claim 3; Page 85; 139pp; English.
XX
XX
CC This invention relates to novel methods for modulating the expression of
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC promote chemotaxis of fibroblasts, however, it is also upregulated in
CC acute lymphoblastic leukaemia and in tumour or endothelial cells
CC associated with the vasculature. Accordingly, antisense oligonucleotides
CC that inhibit the expression of CTGF in cells or tissues can be used in
CC gene therapy to treat various conditions including hyperproliferative
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC such, the present invention describes these antisense oligos as having
CC cytostatic, dermatological and antiarteriosclerotic activities. This
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC human CTGF of the invention.
XX
XX
SQ Sequence 20 BP; 8 A; 3 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1827 TGTTACAGTTATCTAAGTTAA 1846
Db 20 TGTTACAGTTATCTAAGTTAA 1
|||||

RESULT 105
ADB25653/c
ID ADB25653 standard; DNA; 20 BP.
XX
XX ADB25653;
XX
XX
DT 20-NOV-2003 (first entry)
XX
XX Human connective tissue growth factor antisense oligo DNA (SeqID 46).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytostatic; dermatological;
XX antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX modified_base 1..20

Qy	2242	CTTCTAGTTGAAAAATAAG	2261
Db	20	CTTCTAGTTGAAAAATAAG	1
RESULT 107			
ADB25671/c			
ID	ADB25671 standard; DNA; 20 BP.		
XX			
AC	ADB25671;		
XX			
DT	20-NOV-2003 (first entry)		
XX			
DE	Human connective tissue growth factor antisense oligo DNA (SeqID 64).		

XX antisense; human; ss; connective tissue growth factor; CTGF;
 KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
 KW fisp-12; NOV2;
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cystostatic; dermatological;
 KW antiarteriosclerotic.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 PN WO2003053340-A2.
 XX
 XX
 PD 03-JUL-2003.
 XX
 XX 09-DEC-2002; 2002WO-US038618.
 PF
 XX 10-DEC-2001; 2001US-00006191.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Gaarde WA, Watt AT;
 PI
 XX WPI; 2003-559091/52.
 DR
 XX
 PS Claim 3; Page 85; 139pp; English.
 XX
 CC This invention relates to novel methods for modulating the expression of
 CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
 CC as ctgofact, fibroblast inducible secreted protein, fisp-12, NOV2,
 CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in
 CC acute lymphoblastic leukaemia and in tumour or endothelial cells
 CC associated with the vasculature. Accordingly, antisense oligonucleotides
 CC that inhibit the expression of CTGF in cells or tissues can be used in
 CC gene therapy to treat various conditions including hyperproliferative
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
 CC such, the present invention describes these antisense oligos as having
 CC cystostatic, dermatological and antiarteriosclerotic activities. This
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 CC human CTGF of the invention.
 XX
 SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
 Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2219 GACCAAAAGTTACATGTTT 2238
 Db 20 GACCAAAAGTTACATGTTT 1
 RESULT 108
 ADB25666/c

ID ADB25666 standard; DNA; 20 BP.
 XX
 AC ADB25666;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human connective tissue growth factor antisense oligo DNA (segid 59).
 XX
 KW antisense; human; ss; connective tissue growth factor; CTGF;
 KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
 KW fisp-12; NOV2;
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cystostatic; dermatological;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 PN WO2003053340-A2.
 XX
 XX 03-JUL-2003.
 PD
 XX 09-DEC-2002; 2002WO-US038618.
 PF
 XX 10-DEC-2001; 2001US-00006191.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Gaarde WA, Watt AT;
 PI
 XX WPI; 2003-559091/52.
 DR
 XX
 PS New antisense oligonucleotides for modulating connective tissue growth
 PT factor expression, particularly useful for treating cancers (e.g. breast
 PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
 PT atherosclerosis.
 XX
 XX Example 15; Page 85; 139pp; English.
 PS
 CC This invention relates to novel methods for modulating the expression of
 CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
 CC as ctgofact, fibroblast inducible secreted protein, fisp-12, NOV2,
 CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in
 CC acute lymphoblastic leukaemia and in tumour or endothelial cells
 CC associated with the vasculature. Accordingly, antisense oligonucleotides
 CC that inhibit the expression of CTGF in cells or tissues can be used in
 CC gene therapy to treat various conditions including hyperproliferative
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
 CC such, the present invention describes these antisense oligos as having
 CC cystostatic, dermatological and antiarteriosclerotic activities. This
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 CC human CTGF of the invention.
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
QY 1723 ACTGCACAGCTTGCGCAAG 1742
DB 20 ACTGCACAGCTTGCGCAAG 1

RESULT 109
ADB25702/c
ID ADB25702 standard; DNA; 20 BP.
XX AC ADB25702;
XX DT 20-NOV-2003 (first entry)
XX DE Human connective tissue growth factor antisense oligo DNA (SeqID 95).
XX KW antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX FT 5-methylcytidines"
XX PN WO2003053340-A2.
XX PD 03-JUL-2003.
XX PF 09-DEC-2002; 2002WO-US038618.
XX PR 10-DEC-2001; 2001US-00006191.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Gaarde WA, Watt AT;
XX PS WPI; 2003-559091/52.
XX CC This invention relates to novel methods for modulating the expression of
XX CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
XX CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
XX CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
XX CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
XX CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
XX CC promote chemotaxis of fibroblasts, however, it is also upregulated in
XX CC acute lymphoblastic leukaemia and in tumour or endothelial cells
XX CC associated with the vasculature. Accordingly, antisense oligonucleotides
XX CC that inhibit the expression of CTGF in cells or tissues can be used in
XX CC gene therapy to treat various conditions including hyperproliferative
XX CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
XX CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
XX CC such, the present invention describes these antisense oligos as having
XX CC cytostatic, dermatological and antiarteriosclerotic activities. This
XX CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX CC human CTGF of the invention.
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XX SQ Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1553 AAATTTAGCGTCTCCTG 1572
DB 20 AAATTTAGCGTCTCCTG 1

RESULT 110
ADB25652/c
ID ADB25652 standard; DNA; 20 BP.
XX AC ADB25652;
XX DT 20-NOV-2003 (first entry)
XX DE Human connective tissue growth factor antisense oligo DNA (SeqID 45).
XX KW antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX FT 5-methylcytidines"
XX PN WO2003053340-A2.
XX PD 03-JUL-2003.
XX PF 09-DEC-2002; 2002WO-US038618.
XX PR 10-DEC-2001; 2001US-00006191.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Gaarde WA, Watt AT;
XX PS WPI; 2003-559091/52.
XX CC New antisense oligonucleotides for modulating connective tissue growth
XX CC factor expression, particularly useful for treating cancers (e.g. breast
XX CC or prostate cancer), pulmonary or renal fibrosis, scleroderma or
XX CC atherosclerosis.
XX CC Claim 3; Page 85; 139pp; English.
XX CC This invention relates to novel methods for modulating the expression of
XX CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
XX CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
XX CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
XX CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
XX CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
XX CC promote chemotaxis of fibroblasts, however, it is also upregulated in
XX CC acute lymphoblastic leukaemia and in tumour or endothelial cells
XX CC associated with the vasculature. Accordingly, antisense oligonucleotides
XX CC that inhibit the expression of CTGF in cells or tissues can be used in
XX CC gene therapy to treat various conditions including hyperproliferative
```

CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
 CC such, the present invention describes these antisense oligos as having
 CC cystostatic, dermatological and antiarteriosclerotic activities. This
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 CC human CTGF of the invention.

XX Sequence 20 BP; 8 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2203 TATTGTTGAGAGTGTGACC 2222

DB 20 TATTGTTGAGAGTGTGACC 1

RESULT 111

ADB25703/c

ID ADB25703 standard; DNA; 20 BP.

XX ADB25703;

XX 20-NOV-2003 (first entry)

DE Human connective tissue growth factor antisense oligo DNA (SeqID 96).

XX antisense; human; ss; connective tissue growth factor; CTGF;

XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;

XX fisp-12; NOV2;

XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;

XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;

XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;

XX scleroderma; atherosclerosis; cytostatic; dermatological;

XX antiarteriosclerotic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 5-methylcytidines"

XX WO2003053340-A2.

XX 03-JUL-2003.

XX 09-DEC-2002; 2002WO-US038618.

XX 10-DEC-2001; 2001US-00006191.

XX (ISIS-) ISIS PHARM INC.

XX Gaarde WA, Watt AT;

XX WPI; 2003-559091/52.

XX New antisense oligonucleotides for modulating connective tissue growth
 PT factor expression, particularly useful for treating cancers (e.g. breast
 PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
 PT atherosclerosis.

XX Example 15; Page 86; 139pp; English.

XX This invention relates to novel methods for modulating the expression of
 CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
 CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,

CC insulin-like growth factor binding protein-related protein 2; IGFBP-rp2,
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in
 CC acute lymphoblastic leukaemia and in tumour or endothelial cells
 CC associated with the vasculature. Accordingly, antisense oligonucleotides
 CC that inhibit the expression of CTGF in cells or tissues can be used in
 CC gene therapy to treat various conditions including hyperproliferative
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
 CC such, the present invention describes these antisense oligos as having
 CC cystostatic, dermatological and antiarteriosclerotic activities. This
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 CC human CTGF of the invention.

XX Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1637 GTTGTTCTTAAGTCAGAAC 1656

DB 20 GTTGTTCTTAAGTCAGAAC 1

RESULT 112

ADB25655/c

ID ADB25655 standard; DNA; 20 BP.

XX ADB25655;

XX 20-NOV-2003 (first entry)

DE Human connective tissue growth factor antisense oligo DNA (SeqID 48).

XX antisense; human; ss; connective tissue growth factor; CTGF;

XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;

XX fisp-12; NOV2;

XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;

XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;

XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;

XX scleroderma; atherosclerosis; cytostatic; dermatological;

XX antiarteriosclerotic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 5-methylcytidines"

XX WO2003053340-A2.

XX 03-JUL-2003.

XX 09-DEC-2002; 2002WO-US038618.

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```

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XX CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2,
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XX CC promote chemotaxis of fibroblasts, however, it is also upregulated in
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XX CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX CC human CTGF of the invention.
XX SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 60;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2218 TGACCAAAAGTTACATGTTT 2237
DB 20 TGACCAAAAGTTACATGTTT 1
XX
XX RESULT 113
XX ID ADB25650/C
XX AC ADB25650 standard; DNA; 20 BP.
XX AC ADB25650;
XX
XX 20-NOV-2003 (first entry)
XX
XX DE Human connective tissue growth factor antisense oligo DNA (SeqID 43).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytosclastic; dermatological;
XX antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT modified_base 1..20 a
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX PN
XX
XX PD 03-JUL-2003.
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XX PF 09-DEC-2002; 2002WO-US038618.
XX
XX PR 10-DEC-2001; 2001US-00006191.
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XX PA (ISIS-) ISIS PHARM INC.
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XX PI Gaarde WA, Watt AT;

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XX WPI; 2003-559091/52.
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XX PT factor expression, particularly useful for treating cancers (e.g. breast
XX PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
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XX CC gene therapy to treat various conditions including hyperproliferative
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XX CC cytosclastic, dermatological and antiarteriosclerotic activities. This
XX CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX CC human CTGF of the invention.
XX SQ Sequence 20 BP; 6 A; 3 C; 3 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 60;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2098 GAACAAATGGCCTTTATTA 2117
DB 20 GAACAAATGGCCTTTATTA 1
XX
XX RESULT 114
XX ADB25651/C
XX ID ADB25651 standard; DNA; 20 BP.
XX AC ADB25651;
XX
XX 20-NOV-2003 (first entry)
XX
XX DE Human connective tissue growth factor antisense oligo DNA (SeqID 44).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgrofact; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytosclastic; dermatological;
XX antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT modified_base 1..20 a
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX PN
XX
XX PD 03-JUL-2003.
XX
XX
XX

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PF 09-DEC-2002; 2002WO-US038618.
XX
PR 10-DEC-2001; 2001US-00006191.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Gaarde WA, Watt AT;
XX
DR WPI; 2003-559091/52.
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XX as ctgfract, fibroblast inducible secreted protein, fisp-12, NOV2,
XX insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
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XX promote chemotaxis of fibroblasts, however, it is also upregulated in
XX acute lymphoblastic leukaemia and in tumour or endothelial cells
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XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX human CTGF of the invention.
XX
SQ Sequence 20 BP; 9 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2198 CAGTTTATTGTTGAGGTG 2217
DB 20 CAGTTTATTGTTGAGGTG 1

RESULT 115
ADB25700/c
ID ADB25700 standard; DNA; 20 BP.
XX
AC ADB25700;
XX
XX 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 93).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgfract; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytostatic; dermatological;
XX antiarteriosclerotic.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /note= "OTHER= phosphorothioate backbone, where 1-5
FT

```

```

FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX W02003053340-A2.
XX
XX 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
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XX 10-DEC-2001; 2001US-00006191.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Gaarde WA, Watt AT;
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XX WPI; 2003-559091/52.
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PT factor expression, particularly useful for treating cancers (e.g. breast
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XX acute lymphoblastic leukaemia and in tumour or endothelial cells
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XX disorders (particularly cancer, e.g. breast, prostate or renal cancer),
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XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX human CTGF of the invention.
XX
SQ Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1274 GTAGCACAGTTTATTTAAAT 1293
DB 20 GTAGCACAGTTTATTTAAAT 1

RESULT 116
ADB25704/c
ID ADB25704 standard; DNA; 20 BP.
XX
AC ADB25704;
XX
XX 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 97).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgfract; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytostatic; dermatological;
XX antiarteriosclerotic.
XX

```

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 XX WO2003053340-A2.
 PN
 XX 03-JUL-2003.
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 XX 09-DEC-2002; 2002WO-US038618.
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 XX (ISIS-) ISIS PHARM INC.
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 XX Gaarde WA, Watt AT;
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 XX WPI; 2003-559091/52.
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 XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
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 XX human CTGF of the invention.
 XX
 XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1713 TGTCGATTAGCTGGACGC 1732
 DB 20 TGTCGATTAGCTGGACGC 1
 RESULT 117
 ADB25667/c
 ID ADB25667 standard; DNA; 20 BP.
 XX
 XX ADB25667;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Human connective tissue growth factor antisense oligo DNA (SeqID 60).
 XX
 XX antisense; human; ss; connective tissue growth factor; CTGF;
 XX chromosome 6q23.1; ctgfract; fibroblast inducible secreted protein;

KW fisp-12; NOV2;
 KW insulin-like growth factor binding protein-2; IGFBP-rp2;
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cytostatic; dermatological;
 KW antiarteriosclerotic.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 FT 5-methylcytidines"
 XX
 XX WO2003053340-A2.
 PN
 XX 03-JUL-2003.
 XX
 XX 09-DEC-2002; 2002WO-US038618.
 XX
 XX 10-DEC-2001; 2001US-00006191.
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 XX Gaarde WA, Watt AT;
 XX
 XX WPI; 2003-559091/52.
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 XX factor expression, particularly useful for treating cancers (e.g. breast
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 XX
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 XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 XX human CTGF of the invention.
 XX
 XX Sequence 20 BP; 7 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1752 CTGTAAACAAGCCAGATTTT 1771
 DB 20 CTGTAAACAAGCCAGATTTT 1
 RESULT 118
 ADB25672/c
 ID ADB25672 standard; DNA; 20 BP.
 XX
 XX ADB25672;
 XX

XX 20-NOV-2003 (first entry)
XX Human connective tissue growth factor antisense oligo DNA (SeqID 65).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytostatic; dermatological;
XX antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
XX 5-methylcytidines"
XX
XX WO2003053340-A2.
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XX 09-DEC-2002; 2002WO-US038618.
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XX human CTGF of the invention.
XX
XX Sequence 20 BP; 8 A; 3 C; 1 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 60;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2243 TTCTAGTTGAAATAAAGT 2262
XX |||||
XX 20 TTCTAGTTGAAATAAAGT 1

RESULT 119
ADB25699/c
ID ADB25699 standard; DNA; 20 BP.
XX
XX ADB25699;
XX
XX 20-NOV-2003 (first entry)
XX Human connective tissue growth factor antisense oligo DNA (SeqID 92).
XX
XX antisense; human; ss; connective tissue growth factor; CTGF;
XX chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
XX fisp-12; NOV2;
XX insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
XX IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
XX hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
XX scleroderma; atherosclerosis; cytostatic; dermatological;
XX antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate backbone, where 1-5 and
XX 16-20 are 2' methoxyethyl nucleotides. All cytidines are
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XX
XX WO2003053340-A2.
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XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX human CTGF of the invention.
XX
XX Sequence 20 BP; 9 A; 1 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX

```
Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
Indels 0;

QY 1242 TCACATCTCATTTTCGTA 1261
    20 TCACATCTCATTTTCGTA 1

Db
RESULT 120
ADB25701/c
ID ADB25701 standard; DNA; 20 BP.
XX
AC ADB25701;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 94).
XX
KW antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003053340-A2.
XX
PD 03-JUL-2003.
XX
PF 09-DEC-2002; 2002WO-US038618.
XX
PR 10-DEC-2001; 2001US-00006191.
XX
PA (ISIS-) ISIS PHARM INC.
PI Gaarde WA, Watt AT;
XX
DR WPI; 2003-559091/52.
XX
PS Example 15; Page 86; 139pp; English.
XX
CC This invention relates to novel methods for modulating the expression of
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC as ctgofact, fibroblast inducible secreted protein, fisp-12, NOV2,
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC promote chemotaxis of fibroblasts, however, it is also upregulated in
CC acute lymphoblastic leukaemia and in tumour or endothelial cells
CC associated with the vasculature. Accordingly, antisense oligonucleotides
CC that inhibit the expression of CTGF in cells or tissues can be used in
CC gene therapy to treat various conditions including hyperproliferative
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC such, the present invention describes these antisense oligos as having
```

```
CC cytostatic, dermatological and antiarteriosclerotic activities. This
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC human CTGF of the invention.
XX
SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Indels 0;

QY 1371 CCAGACACTGCTTTGAAGAA 1390
    20 CCAGACACTGCTTTGAAGAA 1

Db
RESULT 121
ADB25646/c
ID ADB25646 standard; DNA; 20 BP.
XX
AC ADB25646;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human connective tissue growth factor antisense oligo DNA (SeqID 39).
XX
KW antisense; human; ss; connective tissue growth factor; CTGF;
KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
KW fisp-12; NOV2;
KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
KW scleroderma; atherosclerosis; cytostatic; dermatological;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
PN WO2003053340-A2.
XX
PD 03-JUL-2003.
XX
PF 09-DEC-2002; 2002WO-US038618.
XX
PR 10-DEC-2001; 2001US-00006191.
XX
PA (ISIS-) ISIS PHARM INC.
PI Gaarde WA, Watt AT;
XX
DR WPI; 2003-559091/52.
XX
PS New antisense oligonucleotides for modulating connective tissue growth
XX factor expression, particularly useful for treating cancers (e.g. breast
XX or prostate cancer), pulmonary or renal fibrosis, scleroderma or
XX atherosclerosis.
XX
PS Claim 3; Page 85; 139pp; English.
XX
CC This invention relates to novel methods for modulating the expression of
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC as ctgofact, fibroblast inducible secreted protein, fisp-12, NOV2,
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC promote chemotaxis of fibroblasts, however, it is also upregulated in
```


CC acute lymphoblastic leukaemia and in tumour or endothelial cells
 CC associated with the vasculature. Accordingly, antisense oligonucleotides
 CC that inhibit the expression of CTGF in cells or tissues can be used in
 CC gene therapy to treat various conditions including hyperproliferative
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
 CC such, the present invention describes these antisense oligos as having
 CC cytostatic, dermatological and antiarteriosclerotic activities. This
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 CC human CTGF of the invention.

XX Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1719 TTAGACTGGACAGCTGTGG 1738

Db 20 TTAGACTGGACAGCTGTGG 1

RESULT 122

ADB25668/C

ID ADB25668 standard; DNA; 20 BP.

XX ADB25668;

XX 20-NOV-2003 (first entry)

XX Human connective tissue growth factor antisense oligo DNA (SeqID 61).

XX antisense; human; ss; connective tissue growth factor; CTGF;
 KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;
 KW fisp-12; NOV2;
 KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;
 KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;
 KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
 KW scleroderma; atherosclerosis; cytostatic; dermatological;
 KW antiarteriosclerotic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 5-methylcytidines"

XX WO2003053340-A2.

XX 03-JUL-2003.

XX 09-DEC-2002; 2002WO-US038618.

XX 10-DEC-2001; 2001US-00006191.

XX (ISIS-) ISIS PHARM INC.

XX Gaarde WA, Watt AT;

XX WPI; 2003-559091/52.

XX New antisense oligonucleotides for modulating connective tissue growth
 FT factor expression, particularly useful for treating cancers (e.g. breast
 FT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
 FT atherosclerosis.

XX Example 15; Page 85; 139pp; English.

XX

CC This invention relates to novel methods for modulating the expression of
 CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
 CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
 CC as ctgofact, fibroblast inducible secreted protein, fisp-12, NOV2,
 CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
 CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
 CC promote chemotaxis of fibroblasts, however, it is also upregulated in
 CC acute lymphoblastic leukaemia and in tumour or endothelial cells
 CC associated with the vasculature. Accordingly, antisense oligonucleotides
 CC that inhibit the expression of CTGF in cells or tissues can be used in
 CC gene therapy to treat various conditions including hyperproliferative
 CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
 CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
 CC such, the present invention describes these antisense oligos as having
 CC cytostatic, dermatological and antiarteriosclerotic activities. This
 CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
 CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
 CC human CTGF of the invention.

XX Sequence 20 BP; 9 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1834 TTATCTAAGTTAATTAAAG 1853

Db 20 TTATCTAAGTTAATTAAAG 1

RESULT 123

ADB25670/C

ID ADB25670 standard; DNA; 20 BP.

XX ADB25670;

XX 20-NOV-2003 (first entry)

XX Human connective tissue growth factor antisense oligo DNA (SeqID 63).

XX antisense; human; ss; connective tissue growth factor; CTGF;

KW chromosome 6q23.1; ctgofact; fibroblast inducible secreted protein;

KW fisp-12; NOV2;

KW insulin-like growth factor binding protein-related protein 2; IGFBP-rp2;

KW IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy;

KW hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;

KW scleroderma; atherosclerosis; cytostatic; dermatological;

KW antiarteriosclerotic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
 16-20 are 2' methoxyethyl nucleotides. All cytidines are
 5-methylcytidines"

XX WO2003053340-A2.

XX 03-JUL-2003.

XX 09-DEC-2002; 2002WO-US038618.

XX 10-DEC-2001; 2001US-00006191.

XX (ISIS-) ISIS PHARM INC.

XX Gaarde WA, Watt AT;

XX WPI; 2003-559091/52.

XX

PT New antisense oligonucleotides for modulating connective tissue growth
PT factor expression, particularly useful for treating cancers (e.g. breast
PT or prostate cancer), pulmonary or renal fibrosis, scleroderma or
PT atherosclerosis.
XX
XX Claim 3; Page 85; 139pp; English.
XX
XX This invention relates to novel methods for modulating the expression of
CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 6q23.1, and is also known
CC as ctgfract, fibroblast inducible secreted protein, fisp-12, NOV2,
CC insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and
CC promote chemotaxis of fibroblasts, however, it is also upregulated in
CC acute lymphoblastic leukaemia and in tumour or endothelial cells
CC associated with the vasculature. Accordingly, antisense oligonucleotides
CC that inhibit the expression of CTGF in cells or tissues can be used in
CC gene therapy to treat various conditions including hyperproliferative
CC disorders (particularly cancer, e.g. breast, prostate or renal cancer),
CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
CC such, the present invention describes these antisense oligos as having
CC cytostatic, dermatological and antiarteriosclerotic activities. This
CC oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
CC with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
CC human CTGF of the invention.
XX
XX Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
SQ

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2212 AGAGTGTGACCAAAAGTTAC 2231
Db 20 AGAGTGTGACCAAAAGTTAC 1

RESULT 124
ADD26665
ID ADD26665 standard; DNA; 20 BP.
AC ADD26665;
XX

15-JAN-2004 (first entry)

Polynucleotide (dsDNA) used in treatment of SLE.

Systemic lupus erythematosus; SLE; impaired renal function;
LJP 394 conjugate; dermatological; immunosuppressive; antiinflammatory;
ds.

Unidentified.

US2003114405-A1.

19-JUN-2003.

13-AUG-2002; 2002US-00219238.

13-AUG-2001; 2001US-0311858P.

22-AUG-2001; 2001US-0314281P.

(LINN//) LINNIK M D.

(HEPB//) HEPBURN B.

Linnik MD, Hepburn B;

WPI; 2003-810915/76.

Treating systemic lupus erythematosus comprises selecting an individual
PT having significantly impaired renal function and administering conjugate
PT having non-immunogenic valency platform molecule and double stranded DNA
PT epitopes.

XX Claim 3; Page 18; 22pp; English.
XX
XX The present invention relates to a method of treating systemic lupus
CC erythematosus (SLE) in an individual. The method comprises selecting an
CC individual having SLE, significantly impaired renal function, and
CC antibodies with high affinity to a polynucleotide epitope by
CC administering a conjugate comprising non-immunogenic valency platform
CC molecules and two or more double stranded DNA (dsDNA) epitopes that are
CC polynucleotides. Also disclosed is a kit comprising the conjugate, LJP
CC 394. The conjugate is administered in an amount effective to reduce
CC incidence of renal flares in the individual. A medication chosen from
CC corticosteroids and cyclophosphamide is also administered to the
CC individual. The conjugate is administered in an amount effective to
CC reduce the amount of a corticosteroid or cyclophosphamide administered to
CC the individual. The present sequence represents a polynucleotide (dsDNA)
CC used in the treatment of SLE.

SQ Sequence 20 BP; 0 A; 0 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 125
AAQ34015
ID AAQ34015 standard; DNA; 21 BP.
XX
XX AC AAQ34015;

25-MAR-2003 (revised)

02-FEB-1993 (first entry)

Microsatellite sequence from clone TGLA419.

PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.

Bos taurus.

WO9213102-A1.

06-AUG-1992.

15-JAN-1992; 92WO-US000340.

15-JAN-1991; 91US-00642342.

(GENM-) GENMARK.

Georges M, Massey JM;

WPI; 1992-284684/34.

Polymorphic bovine DNA markers - used in genetic identification, gene
mapping, and selective breeding.

Table 7; Page 336; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between 250 and 500
bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MboI sites, the frequency of (T6)_n > 9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence were used to generate the

CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved in the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 21 BP; 0 A; 0 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
|||||
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 126
AAX90296
ID AAX90296 standard; DNA; 21 BP.
AC AAX90296;
XX
DT 24-SEP-1999 (first entry)
XX
DE Oligonucleotide R7C05 used in an Example from US5932556.
XX
KW CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;
KW immune system mediated disease; gamma-interferon; IL-8; ss.
XX
OS Synthetic.

XX
PN US5932556-A.
XX
PD 03-AUG-1999.
XX
PF 18-SEP-1995; 95US-00529878.
XX
PR 09-FEB-1995; 95US-00387041.
XX
PR 18-SEP-1995; 95US-00529878.
XX
PA (TAMR/) TAM R C.
XX
PI Tam RC;
XX
DR WPI; 1996-384228/38.

XX
PT Oligonucleotide which reduces CD28 gene expression in T cells - for
PT treating immune system diseases, e.g. graft vs. host disease, septic
PT shock, psoriasis, etc.
XX
PS Example; Col 13; 45pp; English.
XX
CC The present invention describes a method for inhibiting the expression of
CC CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises
CC subcutaneous administration of an oligonucleotide (OGN). AAX90288 to
CC AAX90291 represent specifically claimed OGNs for use in the method. The
CC OGNs are used for the treatment of immune system-mediated diseases.
CC AAX90292 to AAX90323 represent oligonucleotides used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
|||||
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 127
AAH46014
ID AAH46014 standard; DNA; 21 BP.
XX
AC AAH46014;
XX
DT 12-SEP-2001 (first entry)
XX
DE Synthetic oligonucleotide 14.

XX
KW Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
KW lymphoma; ss.
XX
OS Synthetic.

XX
PN WO200144465-A2.
XX
PD 21-JUN-2001.
XX
PF 12-DEC-2000; 2000WO-CA001467.
XX
PR 13-DEC-1999; 99US-0170325P.
XX
PR 29-AUG-2000; 2000US-0228925P.
XX
PA (BION-) BIONICHE LIFE SCI INC.
XX
PI Phillips NC, Fillion MC;
XX
DR WPI; 2001-398150/42.

XX
PT Composition comprising synthetic oligonucleotides which comprise multiple
PT repeats of dinucleotides such as GT, TG useful for treating cancer by
PT inducing cell cycle arrest, inhibiting proliferation, activating
PT caspases.
XX
PS Example 4; Page 17; 77pp; English.

XX
CC The present sequence is that of a synthetic oligonucleotide useful to the
CC invention. The invention relates to a composition, comprising a 2 to 20
CC base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
CC repeats of dinucleotides such as GT, TG, etc., according to specific
CC formula and having cytostatic activity. The oligonucleotide compositions
CC are useful for inducing cell cycle arrest, inhibition of proliferation,
CC activation of caspases and induction of apoptosis or production of
CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
CC necrosis factor (TNF)-alpha by immune system cells, in an animal having
CC cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
CC and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
CC colorectal, ovarian or bone cancer. The compositions induce apoptosis
CC independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug
CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
CC and hormone dependence
XX
SQ Sequence 21 BP; 0 A; 0 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
|||||
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 128
ABN88973
ID ABN88973 standard; DNA; 21 BP.
XX
AC ABN88973;
XX

```

DT 22-AUG-2002 (first entry)
XX Phosphorothioate 21mer oligonucleotide SEQ ID NO:2.
DE Phosphorothioate; oligonucleotide synthesis; phosphoramidite; ss.
KW Phosphorothioate; oligonucleotide synthesis; phosphoramidite; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..21
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "phosphorothioate linkages"
XX WO200220543-A2.
XX PN 14-MAR-2002.
XX PD
XX PF
XX PP
XX PR 06-SEP-2001; 2001WO-GB003973.
XX PP
XX PR 07-SEP-2000; 2000US-0230685P.
XX PP
XX PA (AVEC-) AVECIA BIOTECHNOLOGY INC.
XX PA (AVEC-) AVECIA LTD.
XX PI Sinha N;
XX PI WPI; 2002-479457/51.
XX DR
XX PP
XX PR Novel phosphoramidite compound, useful for the synthesis of
XX FT oligonucleotides, comprising nucleoside moieties linked by one or more
XX FT internucleoside phosphorus atoms.
XX PS Example 4; Page 28; 67pp; English.
XX CC The present invention describes a phosphoramidite compound (I) comprising
XX CC two or more nucleoside moieties linked by one or more internucleoside
XX CC phosphorus atoms, where the internucleoside phosphorus atoms are
XX CC phosphorus (III) atoms. Also described: (1) preparing a trivalent
XX CC phosphorus multimer or its stereoisomer (I); (2) a trivalent phosphorus
XX CC multimer derivatised solid support (II); and (3) preparing (II). (I) or
XX CC (II) can be used for the synthesis of oligonucleotides. The present
XX CC sequence represents a phosphorothioate 21mer oligonucleotide which is
XX CC synthesised in an example from the present invention
XX SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 20; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 62;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGTGT 20
XX
RESULT 129
ABN88972/C
ID ABN88972 standard; DNA; 21 BP.
XX AC
XX AC ABN88972;
XX XX
XX DT 22-AUG-2002 (first entry)
XX XX
XX DE Phosphorothioate 21mer oligonucleotide SEQ ID NO:1.
XX KW Phosphorothioate; oligonucleotide synthesis; phosphoramidite; ss.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX modified_base 1..21
XX FT /*tag= a

```

```

FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
XX WO200220543-A2.
XX PN 14-MAR-2002.
XX PD
XX PF
XX PP
XX PR 06-SEP-2001; 2001WO-GB003973.
XX PP
XX PR 07-SEP-2000; 2000US-0230685P.
XX PP
XX PA (AVEC-) AVECIA BIOTECHNOLOGY INC.
XX PA (AVEC-) AVECIA LTD.
XX PI Sinha N;
XX PI WPI; 2002-479457/51.
XX DR
XX PP
XX PR Novel phosphoramidite compound, useful for the synthesis of
XX FT oligonucleotides, comprising nucleoside moieties linked by one or more
XX FT internucleoside phosphorus atoms.
XX PS Example 4; Page 28; 67pp; English.
XX CC The present invention describes a phosphoramidite compound (I) comprising
XX CC two or more nucleoside moieties linked by one or more internucleoside
XX CC phosphorus atoms, where the internucleoside phosphorus atoms are
XX CC phosphorus (III) atoms. Also described: (1) preparing a trivalent
XX CC phosphorus multimer or its stereoisomer (I); (2) a trivalent phosphorus
XX CC multimer derivatised solid support (II); and (3) preparing (II). (I) or
XX CC (II) can be used for the synthesis of oligonucleotides. The present
XX CC sequence represents a phosphorothioate 21mer oligonucleotide which is
XX CC synthesised in an example from the present invention
XX SQ Sequence 21 BP; 10 A; 10 C; 0 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.9%; Score 20; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 62;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGTGT 1
XX
RESULT 130
ABZ57678
ID ABZ57678 standard; DNA; 24 BP.
XX AC
XX AC ABZ57678;
XX XX
XX DT 10-APR-2003 (first entry)
XX DE
XX DE Human zinc finger protein 9.46 RT-PCR primer, SEQ ID NO:3.
XX KW Human; zinc finger protein 9.46; recombinant production; gene therapy;
XX KW malignant tumour; cancer; blood disease; human immunodeficiency virus;
XX KW HIV infection; immune disorder; inflammatory condition; cytostatic;
XX KW antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR;
XX KW primer; ss.
XX OS Homo sapiens.
XX XX
XX PN CNL1361165-A.
XX PD 31-JUL-2002.
XX XX
XX PF 26-DEC-2000; 2000CN-00136331.
XX XX
XX PR 26-DEC-2000; 2000CN-00136331.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX

```

PI Mao Y, Xie Y;
 DR WPI; 2003-000239/01.
 XX
 XX New polypeptide human zinc finger protein 9.46 and polynucleotides
 PT encoding this polypeptide.
 XX
 XX Example 2; Page 16 (Disclosure); 31pp; Chinese.
 XX
 XX The invention relates to human zinc finger protein 9.46 (ABP59904) and
 CC nucleic acids encoding it (ABZ57677). The protein has a molecular weight
 CC of 9.46 kD. The invention also relates to a method for the recombinant
 CC production of the protein, an antagonist of the protein, and the use of
 CC the protein, gene and antagonist in therapeutic applications. Zinc finger
 CC protein 9.46 can be used in the treatment of a variety of diseases such
 CC as malignant tumours, blood diseases, HIV (human immunodeficiency virus)
 CC infection, immune disorders and inflammatory conditions. Sequences
 CC ABZ57678-ABZ57679 represent reverse transcription-PCR (RT-PCR) primers
 CC used in an exemplification of the invention to isolate human zinc finger
 CC protein 9.46 cDNA
 XX
 XX Sequence 24 BP; 0 A; 0 C; 13 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 1.9%; Score 19.8; DB 1; Length 24;
 Best Local Similarity 91.3%; Pred. No. 73;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
 DB 2 TGTGTGTGTGTGTGTGTGTGT 24
 RESULT 131
 AAQ33789
 ID AAQ33789 standard; DNA; 21 BP.
 AC
 AC AAQ33789;
 XX
 XX 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA2.
 XX
 XX PCR; selection; primers; OPIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 KW
 XX Bos taurus.
 OS
 XX WO9213102-A1.
 PN
 XX 06-AUG-1992.
 PD
 XX 15-JAN-1992; 92WO-US000340.
 PF
 XX 15-JAN-1991; 91US-00642342.
 PR
 XX (GENM-) GENMARK.
 PA
 XX Georges M, Massey JM;
 PI WPI; 1992-284684/34.
 XX
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX
 XX Table 7; Page 245; 517pp; English.
 PS
 XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)_n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 21 BP; 0 A; 1 C; 10 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 1.8%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 73;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGT 1813
 DB 1 TGTGTGTGTGTGTGTGTGT 21
 RESULT 132
 AAT58080/C
 ID AAT58080 standard; DNA; 21 BP.
 AC
 AC AAT58080;
 XX
 XX 25-MAR-2003 (revised)
 DT 18-MAR-1997 (first entry)
 XX
 DE ICAM-1 antisense oligonucleotide #10.
 XX
 XX Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect;
 KW human intercellular adhesion molecule-1; ICAM-1; inflammation;
 KW adult respiratory distress syndrome; multiple organ failure; GM1594;
 KW septic shock; ss.
 XX
 OS Synthetic.
 OS
 XX USS580969-A.
 PN
 XX 03-DEC-1996.
 PD
 XX 12-OCT-1993; 93US-00136118.
 PF
 XX 24-JUL-1992; 92US-00918259.
 PR
 XX (USNA) US SEC OF NAVY.
 PA
 XX Lee C, Hoke GD, Bradley MO, Williams TU;
 PI WPI; 1997-033603/03.
 XX
 XX Anti-sense oligonucleotide(s) for blocking ICAM-1 mRNA translation - for
 PT treating septic shock, adult respiratory distress syndrome etc.
 PS
 XX Claim 1; Col 21; 16pp; English.
 XX
 XX The sequences given in AAT58071-85 represent oligonucleotides which are
 CC antisense to sequences contained in the pre-mRNA or mature mRNA
 CC transcript of human intercellular adhesion molecule-1 (ICAM-1). These
 CC oligonucleotides may be used for treating septic shock and the
 CC manifestations of septic shock, e.g. inflammation, and vascular and
 CC tissue defects. They are also useful in the treatment of septic shock
 CC associated diseases, e.g. adult respiratory distress syndrome, multiple
 CC organ failure etc. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 1.8%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 73;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1793	TGTGTCGTGTCGTGTCGTGT	1813
DBD	21	TGTGTCGTGTCGTGTCGTGT	1
RESULT 133			
ID	AAV38616	standard; DNA; 21 BP.	
XX	AAV38616;		
XX	13-OCT-1998	(first entry)	
XX	Human ICAM-1,	E-selectin, VCAM-1 antisense oligonucleotide.	
XX	ICAM-1;	intracellular adhesion molecule-; E-selectin; VCAM-1;	
XX	vascular cell adhesion molecule-1;	antisense; inflammatory; disease;	
XX	treatment; septic shock;	psoriasis; wounds; burns; acne; arthritis;	
XX	organ rejection;	inhibition; expression; ss.	
XX	Synthetic.		
OS	Homo sapiens.		
PN	WO9824797-A1.		
XX	11-JUN-1998.		
XX	02-DEC-1996;	96WO-US019194.	
XX	02-DEC-1996;	96WO-US019194.	
PA	(DYAD-) DYAD PHARM CORP.		
PI	Hoke GD, Bradley MO, Williams TJ, Lee C;		
PS	WPI; 1998-333253/29.		
PT	Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 - useful for treating diseases having an inflammatory component, e.g. psoriasis, wounds and septic shock.		
XX	Claim 8; Page 40; 48pp; English.		
XX	The sequence is that of an antisense oligonucleotide which is substantially complementary to at least a portion of the pre- or mature RNA transcript of human intracellular adhesion molecule (ICAM), E-selectin or vascular cell adhesion molecule (VCAM). It can be used to inhibit expression of these proteins. Inhibition of these proteins forms the basis for treatment of conditions and diseases that have an inflammatory component, e.g. acne, psoriasis, arthritis, organ rejection, wounds, burns, septic shock or inflammatory complications of septic shock		
XX	Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;		
QY	Query Match	1.8%; Score 19.4; DB 1; Length 21;	
DB	Best Local Similarity	95.2%; Pred.No.73;	
	Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1793	TGTGTCGTGTCGTGTCGTGT	1813
DB	21	TGTGTCGTGTCGTGTCGTGT	1
RESULT 134			
ID	ABS97829/C		
ID	ABS97829	standard; DNA; 21 BP.	
XX	AC	ABS97829;	
XX	23-DEC-2002	(first entry)	
DE	Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #37.		

CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention
 XX
 SQ Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 1.8%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 73;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
 DB 21 TATGTGTGTGTGTGTGTGTGTGTGTGT 1
 RESULT 135
 ABS97831/C
 ID ABS97831 standard; DNA; 21 BP.
 XX AC ABS97831;
 XX
 XX 23-DEC-2002 (first entry)
 DT
 DE Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #39.
 XX
 KW Human; db; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
 KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
 KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR1I2;
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 KW NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase thermolabile; STM;
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KW multidrug resistance 1; lactoferrin; orphan nuclear receptor;
 KW multidrug resistance associated protein 3; cancer; prostate;
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KW altered drug metabolism; cardiovascular function; colorectal tumour;
 KW central nervous system; pulmonary; immunological; SNP;
 KW single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 XX W0200257410-A2.
 XX
 XX 25-JUL-2002.
 XX
 XX 28-NOV-2001; 2001WO-US044838.
 XX
 XX 28-NOV-2000; 2000US-00724389.
 XX
 XX (DNAS-) DNA SCI LAB INC.
 XX
 XX Guida M, Hall J;
 XX
 XX WPI; 2002-698522/75.
 XX
 XX Isolated nucleic acid molecules having polymorphisms in known human genes
 XX e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
 XX for locating, identifying and characterizing the genes responsible for
 XX disorder-related traits.
 XX
 XX Example 16; Page 131; 714pp; English.
 XX
 XX This invention relates to the sequence of an isolated nucleic acid
 XX molecule comprising at least one base variation from that of a known
 XX human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
 XX cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),

CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxyltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactoferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP45002E1,
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered central
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention
 XX
 SQ Sequence 21 BP; 11 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 1.8%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 73;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
 DB 21 TATGTGTGTGTGTGTGTGTGTGTGTGT 1
 RESULT 136
 AAQ33716
 ID AAQ33716 standard; DNA; 22 BP.
 XX AC AAQ33716;
 XX
 XX 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 XX Microsatellite sequence from clone TGLA135.
 XX
 XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 XX genetic mapping; traits; amplification; ss.
 XX
 XX Bos taurus.
 XX
 XX W09213102-A1.
 XX
 XX 06-AUG-1992.
 XX
 XX 15-JAN-1992; 92WO-US000340.
 XX
 XX 15-JAN-1991; 91US-00642342.
 XX
 XX (GENM-) GENMARK.
 XX
 XX Georges M, Massey JM;
 XX

DR WPI; 1992-284684/34.
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX Table 7; Page 216; 517pp; English.
 XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (Tf)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program Optiprimer). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 1.8%; Score 19.4; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 76;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
 DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 21

RESULT 137
 AA164456/c
 ID AA164456 standard; DNA; 22 BP.
 XX
 XX AA164456;
 XX
 XX 23-NOV-2001 (first entry)
 XX
 XX SSR motif #16.
 XX
 XX Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
 KW trait mapping; marker-assisted selection; gene selection; legume;
 KW DNA profiling; breeding; ds.
 XX
 XX Unidentified.
 OS
 XX NZ509194-A.
 XX
 XX 25-MAY-2001.
 XX
 XX 03-JAN-2001; 2001NZ-00509194.
 XX
 XX 24-DEC-1999; 99AU-00004907.
 PR
 XX 28-MAR-2000; 2000AU-00006520.
 XX
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA
 XX
 XX Koelliker R, Forster JW;
 FI
 XX WPI; 2001-431058/46.
 DR
 XX Novel simple sequence repeats in clover species useful for selection of
 XX genes in legume breeding, for profiling legume species varieties and for
 PT testing the purity of legume seed batches.
 PT
 XX
 XX Claim 6; Page 35; 52pp; English.
 PS
 XX The present invention relates to Simple Sequence Repeats (SSRs) from

CC clover species. SSRs, also called microsatellites, are based on a 1-7
 CC nucleotide core element which is tandemly repeated. The SSR array is
 CC embedded in complex flanking DNA. SSRs are ideal markers for genome
 CC mapping, trait mapping and marker-assisted selection. The SSRs may be
 CC used in methods for selecting genes in clover/ legume breeding. The SSRs
 CC are also useful for DNA profiling of clover varieties and for testing the
 CC purity of legume seed batches. The present sequence is a SSR motif, which
 CC was used in the present invention

XX Sequence 22 BP; 10 A; 12 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 1.8%; Score 19.4; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 76;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
 DB 22 TGTGTGTGTGTGTGTGTGTGTGTGTGT 2

RESULT 138
 ADD69447
 ID ADD69447 standard; DNA; 23 BP.
 XX
 XX AC ADD69447;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX 5' anchored (ISSR)-PCR primer - SEQ ID 5.
 DE
 XX inter-simple sequence repeat; ISSR; PCR; primer; genotyping; plant;
 KW animal; Basmati rice; ss.
 KW
 XX Synthetic.
 OS
 XX WO2003085133-A2.
 PN
 XX 16-OCT-2003.
 PD
 XX 09-JAN-2003; 2003WO-IB000041.
 PF
 XX 08-APR-2002; 2002IN-CH000260.
 PR
 XX (DNAP-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
 PA
 XX Nagaraju JG;
 PI
 XX WPI; 2003-804317/75.
 DR
 XX New set of inter-simple sequence repeats (ISSR)-PCR primers for
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
 PT animal systems.
 PT
 XX Claim 1; SEQ ID NO 5; 60pp; English.
 PS
 XX The invention relates to a novel set of inter-simple sequence repeats
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
 CC invention may be useful for genotyping diverse genomes of plant and
 CC animal systems, in particular for distinguishing Basmati rice varieties
 CC from non-Basmati rice varieties and traditional Basmati rice varieties
 CC from evolved Basmati rice varieties. The current sequence is that of the
 CC 5' anchored (ISSR)-PCR primer of the invention.
 CC
 XX Sequence 23 BP; 1 A; 1 C; 10 G; 11 T; 0 U; 0 Other;
 SQ

Query Match 1.8%; Score 19.4; DB 1; Length 23;
 Best Local Similarity 95.2%; Pred. No. 78;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
 DB 3 TATGTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 140	
ABZ70239/C	
ID	ABZ70239 standard; DNA; 24 BP.
XX	XX
XX	AC
XX	AC
XX	DT
XX	25-APR-2003 (first entry)
DE	Murine tricarboxylic acid carrier 13.53 PCR primer #1.
DE	
XX	Murine, tricarboxylic acid carrier 13.53; tumour; cytostatic; haemopathy;
KW	HIV infection; anti-HIV; immunological disease; inflammation; PCR;
KW	primer; ss.
KX	XX
OS	Mus sp.
XX	XX
PN	CN1361126-A.
XX	XX
PD	31-JUL-2002.
XX	XX
PF	26-DEC-2000; 2000CN-00136313.
XX	XX
PR	26-DEC-2000; 2000CN-00136313.
XX	(BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA	
XX	Mao Y, Xie Y;
FI	XX
XX	WPI; 2002-751545/82.
XX	XX
PT	New polypeptide murine tricarboxylic acid carrier 13.53 and
PT	polynucleotides encoding this polypeptide.
XX	XX
DS	Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX	The present invention relates to murine tricarboxylic acid carrier 13.53
CC	(see ABP59163). The protein is useful for treating various diseases, such
CC	as malignant tumours, haemopathy, HIV infection, immunological diseases
CC	and various inflammations. The present sequence is a PCR primer, which
CC	was used in an example from the invention
XX	XX
SQ	Sequence 24 BP; 10 A; 12 C; 2 G; 0 T; 0 U; 0 Other;
	Query Match 1.8%; Score 19.4; DB 1; Length 24;
	Best Local Similarity 95.2%; Pred. NO. 81;
	Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps
QY	1793 TGCTGTGCTGTGTGTGTGTGT 1813
DB	22 TGCTGTGCTGTGTGTGTGTGT 2
RESULT 141	
AAQ33728	
ID	AAQ33728 standard; DNA; 19 BP.
XX	XX
AC	AAQ33728;
XX	XX
DT	25-MAR-2003 (revised)
DT	02-FEB-1993 (first entry)
XX	Microsatellite sequence from clone TGLA147.
DE	
XX	PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW	genetic mapping; traits; amplification; ss.
XX	XX
OS	Bos taurus.
XX	XX
PN	WO9213102-A1.
PD	06-AUG-1992.

XX 15-JAN-1992; 92WO-U8000340.
 XX 15-JAN-1991; 91US-00642342.
 XX (GENM-) GENMARK.
 XX Georges M, Massey JM;
 XX WPI; 1992-284684/34.
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 mapping, and selective breeding.
 XX Table 7; Page 221; 517pp; English.
 XX The sequence is that of a bovine microsatellite sequence obt'd. by
 screening a library of bovine MboI DNA fragments of between 250 and 500
 bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
 clones cross-hybridised. Assuming independent distribution of
 microsatellites and MboI sites, the frequency of (76)_n > 9 microsatellites
 in the bovine genome is estimated at >100,000. The sequence information
 for ca. 230 such bovine microsatellites is summarised in the
 specification and indexed herein (see below). The sequences upstream and
 downstream of the microsatellite sequence were used to generate the
 required PCR primers for in vitro amplification of the corresp.
 microsatellite (using the program OPRIM). The microsatellites may be
 used to identify individuals, for parentage testing, and in the genetic
 mapping of economic trait loci, or genes involved in the determination of
 economically important traits esp. in cattle, to allow selective
 breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 field.)
 XX Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;
 Query Match 1.8%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGT 1811
 Db 1 TGTGTGTGTGTGTGTGTGT 19
 RESULT 142
 AAT30412
 ID AAT30412 standard; DNA; 19 BP.
 XX AAT30412;
 XX 28-JAN-1997 (first entry)
 XX Compound simple sequence repeat primer (GT)_{7.5}(AT)₂.
 DE Detection; polymorphism; perfect compound simple sequence repeat;
 KW adaptor directed primer; genome; genetic; fingerprinting;
 KW amplified fragment length polymorphism assay; microsatellite region;
 KW genetic trait marking; germplasm comparisons; compound; ss.
 XX Synthetic.
 OS WO9617082-A2.
 XX 06-JUN-1996.
 XX 21-NOV-1995; 95WO-US015150.
 XX 28-NOV-1994; 94US-00346456.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Morgante M, Vogel JM;
 XX

DR WPI; 1996-277795/28.
 XX Modified amplified fragment length polymorphism assay - for detection of
 PT polymorphism esp. in microsatellite regions.
 XX Example 2; Page 84; 173pp; English.
 XX Detecting polymorphisms between 2 nucleic acid samples, esp. in
 CC microsatellite regions, comprises digesting the nucleic acid to generate
 CC fragments, ligating adaptor segments to their ends, amplifying them using
 CC primer directed amplification and comparing the prods. to detect
 CC differences. The primers used in the amplification comprise a primer
 CC consisting of a perfect cpd. simple sequence complementary to an adaptor
 CC segment. The present sequence is an example of a compound SSR primer. The
 CC method represents a modified amplified fragment length polymorphism
 CC assay which is partic. useful for genome fingerprinting, i.e. for
 CC genetic trait marking and germplasm comparisons
 XX Sequence 19 BP; 2 A; 0 C; 7 G; 10 T; 0 U; 0 Other;
 SQ Query Match 1.8%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1799 TGTGTGTGTGTGTGTATAT 1817
 Db 1 TGTGTGTGTGTGTGTATAT 19
 RESULT 143
 AAT66093/c
 ID AAT66093 standard; DNA; 19 BP.
 XX AAT66093;
 XX 25-MAR-2003 (revised)
 DT 18-JUN-1997 (first entry)
 XX Repeat sequence found in the haemoglobin gamma G gene.
 DE Polymorphism; repeat sequence; genetic marker; primer; amplification;
 KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
 KW linkage analysis; genetic disease; animal; plant; breeding; locus;
 KW hybridisation; chromosome; ds.
 XX Homo sapiens.
 OS US5582379-A.
 XX 10-DEC-1996.
 XX 04-APR-1994; 94US-00222177.
 XX 21-APR-1989; 89US-00341562.
 PR 05-SEP-1991; 91US-00754351.
 XX (MARS-) MARSHFIELD CLINIC.
 XX Weber JL;
 XX WPI; 1997-042299/04.
 XX Detection of polymorphic genetic markers of the form (dC-dA)_n(dG-dT)_n -
 PT using novel nucleic acid mols. as primers.
 XX Example 9; Col 59-60; 186pp; English.
 XX The invention relates to the isolation of polymorphic repeat sequences
 CC having the sequence (dC-dA)_n(dG-dT)_n which can be used as genetic
 CC markers. Primers based on these sequences can be used to detect these
 CC repeats, especially for use in e.g. paternity or maternity testing, human
 CC genetic analysis such as linkage analysis of genetic disease, commercial

Best Local Similarity 100.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811
Db 19 TGTGTGTGTGTGTGTGT 1

RESULT 148
ADD69517
ID ADD69517 standard; DNA; 19 BP.
XX
AC ADD69517;
XX
DT 15-JAN-2004 (first entry)
XX
DE ISSR-related PCR primer 4.
XX
KW inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
KW animal; Basmati rice; ss.
XX
OS Unidentified.
XX
PN WO2003085133-A2.
XX
PD 16-OCT-2003.
XX
PF 09-JAN-2003; 2003WO-IB000041.
XX
PR 08-APR-2002; 2002IN-CH000260.
XX
PA (DNAP-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
XX
PI Nagataju JG;
XX
DR WPI; 2003-804317/75.
XX
CC New set of inter-simple sequence repeats (ISSR)-PCR primers for
PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
PT animal systems.
XX
PS Disclosure; Page 19; 60pp; English.
XX
CC The invention relates to a novel set of inter-simple sequence repeats
CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
CC invention may be useful for genotyping diverse genomes of plant and
CC animal systems, in particular for distinguishing Basmati rice varieties
CC from non-Basmati rice varieties and traditional Basmati rice varieties
CC from evolved Basmati rice varieties. The current sequence is that of the
CC ISSR-related PCR primer of the invention.
XX
SQ Sequence 19 BP; 0 A; 0 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811
Db 1 TGTGTGTGTGTGTGTGT 19

RESULT 149
AAF85976
ID AAF85976 standard; DNA; 21 BP.
XX
AC AAF85976;
XX
DT 20-JUN-2001 (first entry)
XX
DE CA repeat fluorogenic probe.
XX
KW Probe; Fluorescein; tetramethyl rhodamine; copy number; ss.

XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "5' end attached to 6-carboxy fluorescein"
FT 21.
FT modified_base /*tag= b
FT /mod_base= OTHER
FT /note= "3' end attached to TAMRA"
XX
XX US6180349-B1.
XX
XX 30-JAN-2001.
XX
XX 18-MAY-1999; 99US-00314246.
XX
XX 18-MAY-1999; 99US-00314246.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Ginzinger DG, Godfrey TE, Jensen RH, Gray JW;
XX WPI; 2001-225787/23.
XX
XX Measuring copy number of a polynucleotide locus in sample useful as
PT diagnostic and prognostic tool, comprises quantifying amount of test
PT locus and reference loci in test and control subject.
XX
XX Claim 25; Col 33; 27pp; English.
XX
XX The present invention relates to measuring the copy number of a locus by
CC amplifying and comparing test and reference loci. The invention is useful
CC as diagnostic and prognostic tools and in correlating abnormal copy
CC number values for specific loci with disease and effectiveness of
CC different treatment options. The present sequence is a CA repeat
CC fluorogenic probe used in the invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 10 G; 9 T; 0 U; 2 Other;

Query Match 1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GGTGTGTGTGTGTGTGT 1812
Db 2 GGTGTGTGTGTGTGTGT 20

RESULT 150
ABL44374
ID ABL44374 standard; DNA; 21 BP.
XX
XX ABL44374;
AC ABL44374;
XX
DT 11-APR-2002 (first entry)
XX
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:1418.
XX
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-00068285.
XX
XX 10-MAR-2000; 2000JP-00066716.
PR

XX (RIKA) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX Arraying genome clones.
XX
XX Claim 4; Page 32; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant amplified product to specify the discrimination Nos. of the multiwell plates containing the clones having said marker sequence; (d) the order of the markers is changed so that the same discrimination Nos. succeed to the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the resultant cultures are amplified by using the above primer; (g) signals are detected from the amplified products; (h) the clones in the multiwell plates are specified from the detected result; and (i) the clones are reconstituted as the positions on the chromosome and arrayed. The microarray is useful for gene analysis. ABL42957 to ABL45322 represent PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634 represent PCR primers for human chromosome 21q22.1, which are specifically claimed for use in the present invention

Sequence 21 BP; 0 A; 2 C; 9 G; 10 T; 0 U; 0 Other;

Query Match 1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 81;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1793 TGTGTGTGTGTGTGTCT 1811
DB 1 TGTGTGTGTGTGTGTGT 19
|||||
|||

RESULT 151
AAZ98503/c
ID ID AAZ98503 standard; DNA; 20 BP.
XX AC AAZ98503;
XX XX
XX DT 19-JUN-2000 (first entry)
XX XX
XX DE H. discus derived sequence #21.
XX XX
XX KW Stellate sequence; DNA fragmentation; microsatellite DNA; DNA marker;
XX KW Haliotis discus; ss.
XX OS Haliotis discus.
XX XX
XX PN WO200011156-A1.
XX XX
XX PD 02-MAR-2000.
XX XX
XX PF 01-JUL-1999; 99WO-JP003551.
XX XX
XX PR 18-AUG-1998; 98JP-00232153.
XX XX
XX FA (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX FI Takahashi H, Sekino M;
XX XX
XX DR WPI; 2000-224692/19.
XX XX
XX PT Isolation of satellite sequences from genomic DNA for use as DNA markers

PT comprises isolating a library with high homogeneity by DNA fragmentation.

XX

XX Example 5; Page 14; 35pp; Japanese.

XX

CC The invention provides a novel method for isolation of satellite

CC sequences from genomic DNA that comprises fragmentation of the DNA by a

CC method which is not dependent on base sequences, then selection of a

CC satellite sequences from the obtained genomic library of high

CC homogeneity. The method is useful for the isolation of microsatellite DNA

CC sequences which can be used as DNA markers. The new method markedly

CC improves the efficiency of isolation of satellite sequences in comparison

CC to prior art methods which are reliant on base sequences. Sequences

CC AZ98483-514 represent sequences from Halliotis discus, used in the method

CC of the invention

XX

XX Sequence 20 BP; 11 A; 9 C; 0 G; 0 T; 0 U; 0 Other;

XX

Qy Query Match 1.8%; Score 18.4; DB 1; Length 20;

XX Best Local Similarity 95.0%; Pred. No. 92;

XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX

Db 1793 TGTGTGTGTGTGTGTGTGTG 1812

XX |||||

XX 20 TGTGTGTGTGTGTGTGTG 1

XX

RESULT 152

XX ABS97833/C

ID ABS97833 standard; DNA; 20 BP.

XX AC ABS97833;

XX

DT 23-DEC-2002 (first entry)

XX

DE Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #41.

XX

KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDL1;

KW Cytochrome P450 A2; CYP450A2; cytochrome P450 02B; CYP45002E1; LTF;

KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;

KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

KW epoxide hydroxylase 2; EPXH2; 5-lipoxygenase activating protein; FLAP;

KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

KW HNMT; kallikrein 2; KHK2; nicotinamide-N-methyl transferase; NNMT;

KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;

KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;

KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;

KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

KW multidrug resistance associated protein 3; cancer; prostate;

KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

KW altered drug metabolism; cardiovascular function; colorectal tumour;

KW central nervous system; pulmonary; immunological; SNP;

XX single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

PN WO200257410-A2.

XX

PD 25-JUL-2002.

XX

PF 28-NOV-2001; 2001WO-US044838.

XX

PR 28-NOV-2000; 2000US-00724389.

XX

PA (DNAS-) DNA SCI LAB INC.

XX

PI Guida M, Hall J;

XX

DR WPI; 2002-698522/75.

XX

PT Isolated nucleic acid molecules having polymorphisms in known human genes

PT e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers

PT for locating, identifying and characterising the genes responsible for

disorder-related traits.

Example 16: Page 131: 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2), cytochrome P450 2E1 (CYP4502E1), adrenergic receptor beta1 (ADRB1), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), catechin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), kallikrein 2) KUK2, nicotinamide -N-methyl transferase (NNMT), NADPH guanine oxidoreductase 2 (NQO2), sulfotransferase themlolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHRM1, CHMR2, CHMR3, CHM4 or CHMR5) sequence. The polymorphic forms of the human genes cited in the invention are useful as genetic linkage markers for locating and characterising the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g. overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1, ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KUK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention.

Sequence 20 BP; 10 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 92;
Matches 19; Conservative 0; Mismatches 1; Indels

[illegible]

Db 20 GTATGTGTGTGTGTGT 1

RESULT 153

ADB25760/C

ID ADB25760 standard; DNA; 20 BP.

AC ADB25760:

20-NOV-2003 (first entry)

XX
DE Mouse connective tissue growth factor antisense oligo DNA (SeqID 153).

antisenese; mouse; murine; ss; connective tissue growth factor; CTGF;
chromosome egsf-1; ctgfract; fibroblast induced secreted protein;
fbsi-1; lvsr; growth factor binding protein-related protein 2; IGFBP-rp2;
IGFBP-8; hcsag; ecogentin; acute lymphoblastic leukemia; gene therapy;
hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis;
scleroderma; atherosclerosis; cytostatic; dermatological; renal fibrosis;
antiarteriosclerotic.

XX
SO
Mus sp.

XX	Key	Location/Qualifiers
PH	modified_base	1..20
FT		/*tag= a
FT		/mod_base= OTHER
FT		/note= "OTHER= phosphorothioate backbone, where 1-5 and
FT		16-20 are 2', methoxyethyl nucleotides. All cytidines are
FT		5-methylcytidines"
XX		
PN	WC2003053340-A2.	
XX		
PD	03-JUL-2003.	
XX		
PF	09-DEC-2002; 2002WO-US038618.	
XX		
PR	10-DEC-2001; 2001US-00006191.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Gaarde WA, Watt AT;	
XX		
DR	WPI; 2003-559091/52.	
XX		
PT	New antisense oligonucleotides for modulating connective tissue growth	
PT	factor expression, particularly useful for treating cancers (e.g. breast	
PT	or prostate cancer), pulmonary or renal fibrosis, scleroderma or	
PT	atherosclerosis.	
XX		
PS	Claim 3; Page 89; 139pp; English.	
XX		
CC	This invention relates to novel methods for modulating the expression of	
CC	connective tissue growth factor (CTGF) by antisense oligonucleotides.	
CC	CTGF has been mapped to human chromosome region 6q23.1, and is also known	
CC	as ctgfract, fibroblast inducible secreted protein, fisp-12, NOV2,	
CC	insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,	
CC	IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and	
CC	promote chemotaxis of fibroblasts; however, it is also upregulated in	
CC	acute lymphoblastic leukaemia and in tumour or endothelial cells	
CC	associated with the vasculature. Accordingly, antisense oligonucleotides	
CC	that inhibit the expression of CTGF in cells or tissues can be used in	
CC	gene therapy to treat various conditions including hyperproliferative	
CC	disorders (particularly cancer, e.g. breast, prostate or renal cancer),	
CC	pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As	
CC	such, the present invention describes these antisense oligos as having	
CC	cytostatic, dermatological and antiarteriosclerotic activities. This	
CC	oligonucleotide sequence is a chimeric phosphorothioate antisense oligo	
CC	with 2' MOE wings and a deoxy gap, which is used to inhibit expression of	
XX	mouse CTGF of the invention.	
XX		
SQ	Sequence 20 BP; 7 A; 3 C; 0 G; 10 T; 0 U; 0 Other;	
	Query Match 1.8%; Score 18.4; DB 1; Length 20;	
	Best Local Similarity 95.0%; Pred.No.92;	
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2247 TAGTTGAAAAATAAAGTGTAT 2266	
DB	20 TAGTTGAAAAATAAAGTATAT 1	
RESULT 154		
AAQ34125		
ID	AAQ34125 standard; DNA; 18 BP.	
XX		
XX	AAQ34125;	
XX		
AC	(revised)	
DT	25-MAR-2003	
DT	02-FEB-1993 (first entry)	
XX		
DE	Sequence of a microsatellite from clone TGLA69.	
XX		
KW	PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;	
KW	genetic mapping; traits; amplification; ss.	

```

XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PS Table 7; Page 381; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100,000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program Optiprim). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
   |||||
Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 155
AAQ33722
ID AAQ33722 standard; DNA; 18 BP.
XX AC AAQ33722;
XX OS Bos taurus.
XX PN WO9213102-A1.
XX DT 25-MAR-2003 (revised)
XX DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA141.
XX PF PCR; selection; primers; Optiprim; breeding; cattle; parentage;
XX KW genetic mapping; traits; amplification; ss.
XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PR 15-JAN-1991; 91US-00642342.

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XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PS Table 7; Page 219; 517pp; English.
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by
XX screening a library of bovine MboI DNA fragments of between 250 and 500
XX bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
XX clones cross-hybridised. Assuming independent distribution of
XX microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
XX in the bovine genome is estimated at >100,000. The sequence information
XX for ca. 230 such bovine microsatellites is summarised in the
XX specification and indexed herein (see below). The sequences upstream and
XX downstream of the microsatellite sequence were used to generate the
XX required PCR primers for in vitro amplification of the corresp.
XX microsatellite (using the program Optiprim). The microsatellites may be
XX used to identify individuals, for parentage testing, and in the genetic
XX mapping of economic trait loci, or genes involved in the determination of
XX economically important traits esp. in cattle, to allow selective
XX breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1811
   |||||
Db 1 GTGTGTGTGTGTGTGTGT 18

RESULT 156
AAQ33950
ID AAQ33950 standard; DNA; 18 BP.
XX AC AAQ33950;
XX DT 25-MAR-2003 (revised)
XX DT 02-FEB-1993 (first entry)
XX DE Microsatellite sequence from clone TGLA346.
XX PF PCR; selection; primers; Optiprim; breeding; cattle; parentage;
XX KW genetic mapping; traits; amplification; ss.
XX OS Bos taurus.
XX PN WO9213102-A1.
XX PD 06-AUG-1992.
XX PF 15-JAN-1992; 92WO-US000340.
XX PR 15-JAN-1991; 91US-00642342.
XX PA (GENM-) GENMARK.
XX PI Georges M, Massey JM;
XX DR WPI; 1992-284684/34.
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene
XX mapping, and selective breeding.
XX PR 15-JAN-1991; 91US-00642342.

```


CC 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
CC FN field.)
XX Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
SQ Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTGT 1811
DB 1 GTGTGTGTGTGTGTGTGT 18
RESULT 159
AAQ46588/c
ID AAQ46588 standard; DNA; 18 BP.
XX AC AAQ46588;
XX 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 23-DEC-1993 (first entry)
XX 23-DEC-1993 (first entry)
DE Simple sequence repeat (CA)9.
XX Microsatellite; simple sequence repeat; SSR; polymorphism; variation;
KW genetic marker; human genome; mapping; ligation reaction; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH repeat_region 1..18
FT /*tag= a
FT /*note= "SSR"
FT repeat_unit 1..2
FT /*tag= b
FT /*rpt_type= TANDEM
XX EP552545-A1.
XX EP552545-A1.
XX 28-JUL-1993.
XX 09-DEC-1992; 92EP-00311242.
XX 17-JAN-1992; 92US-00826930.
XX (PION-) PIONEER HI-BRED INT INC.
XX Grant D;
XX WPI; 1993-236281/30.
XX Detecting genetic variation between organisms - by detecting
XX polymorphisms in simple sequence repeats in DNA of organisms.
XX Disclosure; Page 5; 8pp; English.
XX This (CA)9 simple sequence repeat is used to illustrate the novel method
XX for detecting SSR polymorphisms without the need for direct sequencing or
XX gel electrophoresis. The length of a particular repeat region (i.e.
XX number of repeats) can be highly polymorphic; the sequences flanking the
XX repeat region, however, are conserved. Detection of a SSR of a specific
XX length is achieved by successful ligation of two oligonucleotides, one
XX being exactly complementary to the repeat region and one of its conserved
XX flanking sequences and the other being complementary to the other
XX conserved flanking sequence. (Updated on 10-MAR-2003 to add missing OS
XX field.) (Updated on 25-MAR-2003 to correct PN field.)
SQ Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGT 1810
DB 18 TGTGTGTGTGTGTGTGTGT 1
RESULT 160
AAV21968/c
ID AAV21968 standard; DNA; 18 BP.
XX AC AAV21968;
XX 14-JUL-1998 (first entry)
DT Nuclease resistant antisense oligo NBT 141 targeted against (AC)9.
XX Nuclease resistant; bacterial infection; antibiotic; target;
KW veterinary medicine; treatment; human; industrial process;
KW bacterial control; ss.
XX Synthetic.
XX WO9803533-A1.
XX 29-JAN-1998.
XX 23-JUL-1997; 97WO-US012961.
XX 24-JUL-1996; 96US-00685575.
XX (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX Arrow A, Dale RMK, Thompson TL;
XX WPI; 1998-120687/11.
XX Treating bacterial infections in humans or animals with
XX oligo:nucleotide(s) - resistant to nuclease and targetted to bacterial
XX nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
XX with antibiotics.
XX Claim 49; Page 87; 163pp; English.
XX This antisense oligonucleotide is nuclease resistant and can be used in
XX the treatment of animals, including humans, having a bacterial infection.
XX The treatment comprises administration of such nuclease resistant
XX oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
XX and formulated with a carrier. A compound comprising this nuclease
XX resistant oligonucleotide can be covalently linked to an antibiotic. The
XX method is used to treat infections by a wide variety of Gram-positive and
XX Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
XX The methods are particularly used in immuno-compromised individuals (e.g.
XX patients with acquired immunodeficiency syndrome or those receiving
XX chemotherapy or radiation therapy), optionally in combination with, or
XX fused to, antiviral or other antimicrobial oligonucleotides. Apart from
XX laboratory use, the oligonucleotides can be used to control bacteria in
XX therapeutic cultures, foods, beverages and industrial processes. The
XX oligonucleotides are specific for bacteria, without affecting metabolism
XX in mammalian cells. They may also activate RNase H and have a general,
XX non-specific immune-stimulating effect. The oligonucleotides can be
XX administered orally, intranasally, rectally, topically or by injection,
XX optionally coupled to an agent (e.g. carbohydrate or polyamine) that
XX enhances cellular uptake
SQ Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTGT 1811

Db 18 GTGTGTGTGTGTGTGTGT 1

RESULT 161
AAX77460/c
ID AAX77460 standard; DNA; 18 BP.
XX AC AAX77460;
XX DT 05-AUG-1999 (first entry)
XX DE US912147 primer 4.
XX KW Primer; quantitation; genetic instability; tumour cell; detection;
XX KW neoplastic transformation; carcinogenesis; ss.
XX OS Synthetic.
XX PN US912147-A.
XX PD 15-JUN-1999.
XX PF 22-OCT-1996; 96US-00734973.
XX PR 22-OCT-1996; 96US-00734973.
XX PA (HEAL-) HEALTH RES INC.
XX PI Anderson G, Stoler D, Basik M;
XX WPI; 1999-357197/30.
XX Quantitating genetic instability.
XX Claim 4; Col 17-18; 27pp; English.
XX This invention describes a novel method for quantitating genetic
XX instability independent of microsatellite alterations by treating a
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX from normal cells. The method involves the cells from the same individual
XX with oligonucleotide primers selected from (i) a nucleotide sequence
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
XX 7, (ii) a nucleotide sequence (CG)XY, where Y is as in (i) and Y is a
XX pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
XX a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
XX nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
XX cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
XX (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
XX 16, (vi) a nucleotide sequence (CA)XY, where R is a purine selected from
XX adenine and guanine and Y is a pyrimidine selected from cytosine,
XX thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
XX where R is a purine selected from adenine and guanine and x = 6-16,
XX (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
XX from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
XX of the primers. The method is useful for detecting genomic instability
XX which are commonly associated with the various stages of neoplastic
XX transformation and carcinogenesis. The method is rapid and simple
XX
XX Sequence 18 BP; 9 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
SQ Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTGTGT 1808
DB 18 ATTGTGTGTGTGTGTGTGT 1

RESULT 162
AAX77461/c
ID AAX77461 standard; DNA; 18 BP.
XX

AC AAX77461;
XX 05-AUG-1999 (first entry)
XX US912147 primer 5.
XX KW Primer; quantitation; genetic instability; tumour cell; detection;
XX KW neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
XX OS Synthetic.
XX FH Key
XX misc_RNA 18
XX /tag= a
XX /note= "uracil"
XX
XX US912147-A.
XX PD 15-JUN-1999.
XX PF 22-OCT-1996; 96US-00734973.
XX PR 22-OCT-1996; 96US-00734973.
XX PA (HEAL-) HEALTH RES INC.
XX PI Anderson G, Stoler D, Basik M;
XX WPI; 1999-357197/30.
XX Quantitating genetic instability.
XX Claim 4; Col 17-18; 27pp; English.
XX This invention describes a novel method for quantitating genetic
XX instability independent of microsatellite alterations by treating a
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX from normal cells. The method involves the cells from the same individual
XX with oligonucleotide primers selected from (i) a nucleotide sequence
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
XX 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a
XX pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
XX a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
XX nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
XX cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
XX (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
XX 16, (vi) a nucleotide sequence (CA)XY, where R is a purine selected from
XX adenine and guanine and Y is a pyrimidine selected from cytosine,
XX thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
XX where R is a purine selected from adenine and guanine and x = 6-16,
XX (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
XX from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
XX of the primers. The method is useful for detecting genomic instability
XX which are commonly associated with the various stages of neoplastic
XX transformation and carcinogenesis. The method is rapid and simple
XX
XX Sequence 18 BP; 9 A; 8 C; 0 G; 0 T; 1 U; 0 Other;
SQ Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTGTGT 1808
DB 18 ATTGTGTGTGTGTGTGTGT 1

RESULT 163
AAX76437
ID AAX76437 standard; DNA; 18 BP.
XX AC AAX76437;
XX

XX OS Poaeae.
XX PN NZ509193-A.
XX PD 25-MAY-2001.
XX PF 03-JAN-2001; 2001NZ-00509193.
XX PR 24-DEC-1999; 99AU-00004906.
XX PR 04-MAY-2000; 2000AU-00007310.
XX PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
XX PA (UYSC-) UNIV SOUTHERN CROSS.
XX PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
XX PA (UYAD-) UNIV ADELAIDE.
XX PA (ITWA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX PI Forster JW, Jones ES;
XX DR WPI; 2001-512563/56.
XX PT New simple sequence repeats having 2 or more tandemly repeated nucleotide
PT core elements isolated from ryegrass and fescue, useful for selecting of
PT genes in grass or cereal breeding or profiling grass or cereal species
PT varieties.
XX PS Claim 6; Page 51; 72pp; English.
XX CC The invention relates to a substantially purified or isolated nucleic
CC acid (1) from ryegrass or fescue species including a simple sequence
CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
CC 2-6 nucleotides in length. Also included are a nucleic acid primer
CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
CC library of ryegrass or fescue genomic DNA enriched for SSRs and
CC identifying clones in the library containing SSRs, a library of ryegrass
CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
CC a gene in grass or cereal breeding by identifying an SSR that is closely
CC associated with the gene such that the SSR and the gene are
CC preferentially co-inherited, and selecting for the SSR in the breeding, a
CC method for DNA profiling grass or cereal species varieties by assessing
CC variation between SSR varieties and testing the purity of grass or cereal
CC seed batches by assessing variation within seed batch of an SSR. The SSRs
CC may be used in the selection of genes in grass or cereal breeding, for
CC profiling grass or cereal species varieties, for testing the purity of
CC grass or cereal seed batches, and for DNA profiling to establish the
CC distinct identity, uniformity and/or stability of a cultivar. The present
CC sequence is a ryegrass or fescue SSR
XX SQ Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1793 TGTGCTGTGTGTGTGTG 1810
DB 18 TGTGCTGTGTGTGTGTG 1
RESULT 166
AAS13723/c.
ID ID AAS13723 standard; DNA; 18 BP.
XX AC AAS13723;
XX AC
XX DT 08-MAY-2002 (first entry)
XX DE Simple sequence repeat, SSR, #20.
XX KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
XX KW cereal profiling; grass profiling; seed batch purity testing.
XX

XX NZ509193-A.
 XX
 XX
 XX
 XX 25-MAY-2001.
 XX
 XX 03-JAN-2001; 2001NZ-00509193.
 XX
 XX 24-DEC-1999; 99AU-00004906.
 XX 04-MAY-2000; 2000AU-00007310.
 XX
 XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
 XX (UYSC-) UNIV SOUTHERN CROSS.
 XX (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
 XX (UYAD-) UNIV ADELAIDE.
 XX (ITVA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
 XX
 XX Forster JW, Jones ES;
 XX WPI; 2001-512563/56.
 XX
 XX New simple sequence repeats having 2 or more tandemly repeated nucleotide
 XX core elements isolated from ryegrass and fescue, useful for selecting of
 XX genes in grass or cereal breeding or profiling grass or cereal species
 XX varieties.
 XX
 XX Claim 6; Page 51; 72pp; English.
 XX
 XX The invention relates to a substantially purified or isolated nucleic
 XX acid (1) from ryegrass or fescue species including a simple sequence
 XX repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
 XX 2-6 nucleotides in length. Also included are a nucleic acid primer
 XX suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
 XX library of ryegrass or fescue genomic DNA enriched for SSRs and
 XX identifying clones in the library containing SSRs, a library of ryegrass
 XX or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
 XX a gene in grass or cereal breeding by identifying an SSR that is closely
 XX associated with the gene such that the SSR and the gene are
 XX preferentially co-inherited, and selecting for the SSR in the breeding, a
 XX method for DNA profiling grass or cereal species varieties by assessing
 XX variation between SSR varieties and testing the purity of grass or cereal
 XX seed batches by assessing variation within seed batch of an SSR. The SSRs
 XX may be used in the selection of genes in grass or cereal breeding, for
 XX profiling grass or cereal species varieties, for testing the purity of
 XX grass or cereal seed batches, and for DNA profiling to establish the
 XX distinct identity, uniformity and/or stability of a cultivar. The present
 XX sequence is a ryegrass or fescue SSR
 XX
 XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 1.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTGTGTGT 1811
 Db 1 GTGTGTGTGTGTGTGTGT 18
 RESULT 168
 AAH46012
 ID AAH46012 standard; DNA; 18 BP.
 XX
 XX AC AAH46012;
 XX
 XX DT 12-SEP-2001 (first entry)
 XX
 XX DE Synthetic oligonucleotide 12.
 XX
 XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
 XX cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
 XX tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
 XX lymphoma; ss.
 XX
 XX OS Synthetic.
 XX
 XX PN WO200144465-A2.
 XX
 XX PD 21-JUN-2001.
 XX
 XX PF 12-DEC-2000; 2000WO-CA001467.
 XX
 XX PR 13-DEC-1999; 99US-0170325P.
 XX 29-AUG-2000; 2000US-0228925P.
 XX
 XX (BION-) BIONICHE LIFE SCI INC.
 XX
 XX PI Phillips NC, Fallon MC;
 XX
 XX DR WPI; 2001-398150/42.
 XX
 XX Composition comprising synthetic oligonucleotides which comprise multiple
 XX repeats of dinucleotides such as GT, TG useful for treating cancer by
 XX inducing cell cycle arrest, inhibiting proliferation, activating
 XX caspases.
 XX
 XX Claim 5; Page 17; 77pp; English.
 XX
 XX The present sequence is that of a synthetic oligonucleotide useful to the
 XX invention. The invention relates to a composition, comprises a 2 to 20
 XX base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
 XX repeats of dinucleotides such as GT, TG, etc., according to specific
 XX formula and having cytostatic activity. The oligonucleotide compositions
 XX are useful for inducing cell cycle arrest, inhibition of proliferation,
 XX activation of caspases and induction of apoptosis or production of
 XX cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
 XX necrosis factor (TNF)-alpha by immune system cells, in an animal having
 XX cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
 XX and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
 XX colorectal, ovarian or bone cancer. The compositions induce apoptosis
 XX independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug
 XX resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
 XX and hormone dependence
 XX
 XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 1.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTGTGTGT 1811
 Db 1 GTGTGTGTGTGTGTGTGT 18
 RESULT 169
 AAH46011
 ID AAH46011 standard; DNA; 18 BP.
 XX
 XX AC AAH46011;
 XX
 XX DT 12-SEP-2001 (first entry)
 XX
 XX DE Synthetic oligonucleotide 11.
 XX
 XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
 XX cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
 XX tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
 XX lymphoma; ss.
 XX
 XX OS Synthetic.
 XX
 XX PN WO200144465-A2.
 XX
 XX PD 21-JUN-2001.
 XX
 XX PF 12-DEC-2000; 2000WO-CA001467.

OS Synthetic.
 XX
 XX PN WO200144465-A2.
 XX
 XX PD 21-JUN-2001.
 XX
 XX PF 12-DEC-2000; 2000WO-CA001467.
 XX
 XX PR 13-DEC-1999; 99US-0170325P.
 XX 29-AUG-2000; 2000US-0228925P.
 XX
 XX (BION-) BIONICHE LIFE SCI INC.
 XX
 XX PI Phillips NC, Fallon MC;
 XX
 XX DR WPI; 2001-398150/42.
 XX
 XX Composition comprising synthetic oligonucleotides which comprise multiple
 XX repeats of dinucleotides such as GT, TG useful for treating cancer by
 XX inducing cell cycle arrest, inhibiting proliferation, activating
 XX caspases.
 XX
 XX Claim 5; Page 17; 77pp; English.
 XX
 XX The present sequence is that of a synthetic oligonucleotide useful to the
 XX invention. The invention relates to a composition, comprises a 2 to 20
 XX base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
 XX repeats of dinucleotides such as GT, TG, etc., according to specific
 XX formula and having cytostatic activity. The oligonucleotide compositions
 XX are useful for inducing cell cycle arrest, inhibition of proliferation,
 XX activation of caspases and induction of apoptosis or production of
 XX cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
 XX necrosis factor (TNF)-alpha by immune system cells, in an animal having
 XX cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
 XX and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
 XX colorectal, ovarian or bone cancer. The compositions induce apoptosis
 XX independent of Fas, p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug
 XX resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
 XX and hormone dependence
 XX
 XX SQ Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 1.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTGTGTGT 1811
 Db 1 GTGTGTGTGTGTGTGTGT 18
 RESULT 169
 AAH46011
 ID AAH46011 standard; DNA; 18 BP.
 XX
 XX AC AAH46011;
 XX
 XX DT 12-SEP-2001 (first entry)
 XX
 XX DE Synthetic oligonucleotide 11.
 XX
 XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
 XX cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
 XX tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
 XX lymphoma; ss.
 XX
 XX OS Synthetic.
 XX
 XX PN WO200144465-A2.
 XX
 XX PD 21-JUN-2001.
 XX
 XX PF 12-DEC-2000; 2000WO-CA001467.

XX 13-DEC-1999; 9SUS-017032SP.
 PR 29-AUG-2000; 2000US-022892SP.
 XX (BION-) BIONICHE LIFE SCI INC.
 XX
 XX Phillips NC, Filion MC;
 PI
 DR WPI; 2001-398150/42.
 XX
 XX Composition comprising synthetic oligonucleotides which comprise multiple
 PT repeats of dinucleotides such as GT, TG useful for treating cancer by
 PT inducing cell cycle arrest, inhibiting proliferation, activating
 PT caspases.
 XX
 XX Claim 5; Page 17; 77pp; English.
 PS
 XX The present sequence is that of a synthetic oligonucleotide useful to the
 CC invention. The invention relates to a composition, comprising a 2 to 20
 CC base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple
 CC repeats of dinucleotides such as GT, TG, etc., according to specific
 CC formula and having cytostatic activity. The oligonucleotide compositions
 CC are useful for inducing cell cycle arrest, inhibition of proliferation,
 CC activation of caspases and induction of apoptosis or production of
 CC cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour
 CC necrosis factor (TNF)-alpha by immune system cells, in an animal having
 CC cancer such as primary carcinoma, secondary carcinoma, primary sarcoma
 CC and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,
 CC colorectal, ovarian or bone cancer. The compositions induce apoptosis
 CC independent of Fas, p53/p21, p21/waf-1/Cip, p16(ink4B), drug
 CC resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor
 CC and hormone dependence
 XX
 XX Sequence 18 BP; 0 A; 0 C; 9 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 1.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTG 1810
 DB 1 TGTGTGTGTGTGTGTGTG 18
 RESULT 170
 AA164454/C
 ID AA164454 standard; DNA; 18 BP.
 AC
 AC AA164454;
 XX
 DT 23-NOV-2001 (first entry)
 XX
 DE SSR motif #14.
 XX
 XX Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
 KW trait mapping; marker-assisted selection; gene selection; legume;
 KW DNA profiling; breeding; ds.
 XX
 OS Unidentified.
 XX
 XX NZ509194-A.
 XX
 XX 25-MAY-2001.
 XX
 XX 03-JAN-2001; 2001NZ-00509194.
 PF
 XX 24-DEC-1999; 99AU-00004907.
 PR
 PR 28-MAR-2000; 2000AU-00006520.
 XX
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA
 XX Koelliker R, Forster JW;
 PI

DR WPI; 2001-431058/46.
 XX
 PT Novel simple sequence repeats in clover species useful for selection of
 PT genes in legume breeding, for profiling legume species varieties and for
 PT testing the purity of legume seed batches.
 XX
 XX Claim 6; Page 35; 52pp; English.
 PS
 XX The present invention relates to Simple Sequence Repeats (SSRs) from
 CC clover species. SSRs, also called microsatellites, are based on a 1-7
 CC nucleotide core element which is tandemly repeated. The SSR array is
 CC embedded in complex flanking DNA. SSRs are ideal markers for genome
 CC mapping, trait mapping and marker-assisted selection. The SSRs may be
 CC used in methods for selecting genes in clover/ legume breeding. The SSRs
 CC are also useful for DNA profiling of clover varieties and for testing the
 CC purity of legume seed batches. The present sequence is a SSR motif, which
 CC was used in the present invention
 XX
 XX Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 1.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTG 1810
 DB 18 TGTGTGTGTGTGTGTGTG 1
 RESULT 171
 AAQ49455
 ID AAQ49455 standard; DNA; 20 BP.
 XX
 AC AAQ49455;
 XX
 XX 06-MAY-1994 (first entry)
 DT
 XX
 DE Primer for detecting polymorphisms among highly related plant species.
 XX
 XX Detection; polymorphism; genetic fingerprinting; primer; ss.
 XX
 OS Synthetic.
 XX
 XX JP05244985-A.
 PN
 XX 24-SEP-1993.
 PD
 XX 24-SEP-1991; 91JP-00243122.
 PF
 XX 24-SEP-1991; 91JP-00243122.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX WPI; 1993-338949/43.
 DR
 XX Primer - for detecting polymorphism in DNA among highly interrelated rice
 PT plants or plants of family Brassicace.
 PT
 XX Disclosure; Page 5; 6pp; Japanese.
 PS
 XX The PCR primers (See also AAQ49449-54, AAQ49456) are used to detect
 CC polymorphisms among highly interrelated rice plants or among plants of
 CC family Brassicace. They can also be used for genetic fingerprinting of
 CC plants, allowing detection of polymorphism within one or the same species
 CC of plant
 XX
 XX Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 1.7%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTG 1810

Db 1 TGTGTGTGTGTGTGTG 18

RESULT 172
ADD69468
ID ADD69468 standard; DNA; 20 BP.
XX
AC ADD69468;
XX
DT 15-JAN-2004 (first entry)
XX
DE 3' anchored (ISSR)-PCR primer - SEQ ID 26.
XX
KW inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
KW animal; Basmati rice; ss.
XX
OS Synthetic.
XX
FN WO2003085133-A2.
XX
PD 16-OCT-2003.
XX
PF 09-JAN-2003; 2003WO-IB000041.
XX
PR 08-APR-2002; 2002IN-CH0000260.
XX
PA (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
XX
PI Nagaraju JG;
XX
DR WPI; 2003-804317/75.
XX
XX New set of inter-simple sequence repeats (ISSR)-PCR primers for
PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
PT animal systems.
XX
PS Claim 1; SEQ ID NO 26; 60bp; English.
XX
CC The invention relates to a novel set of inter-simple sequence repeats
CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
CC invention may be useful for genotyping diverse genomes of plant and
CC animal systems, in particular for distinguishing Basmati rice varieties
CC from non-Basmati rice varieties and traditional Basmati rice varieties
CC from evolved Basmati rice varieties. The current sequence is that of the
CC 3' anchored (ISSR)-PCR primer of the invention.
XX
SQ Sequence 20 BP; 1 A; 2 C; 8 G; 9 T; 0 U; 0 Other;
Query Match 1.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1798 GTGTGTGTGTGTGTAT 1815
Db 1 GTGTGTGTGTGTGTAT 18
RESULT 173
AAQ75727
ID AAQ75727 standard; DNA; 21 BP.
XX
AC AAQ75727;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.

PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c) the
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.7%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e-02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTGTTGTTTAAATG 1885
Db 1 TTTTATTGTTTAAATG 21
RESULT 174
ABS97830/c
ID ABS97830 standard; DNA; 21 BP.
XX
AC ABS97830;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #38.
XX
KW Human; ds; cytochrome P450 A1; CYP450A1; UGT2B4; MDRI;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GSTI2; histamine-N-methyl transferase;
KW HMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase; thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B1; uridine receptor; URA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
KW central nervous system; pulmonary; immunological; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
PN WO200257410-A2.
XX
PD 25-JUL-2002.
XX
PF 28-NOV-2001; 2001WO-US044838.


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PR 28-NOV-2000; 2000US-00724389.
XX (DNAS-) DNA SCI LAB INC.
XX Guida M, Hall J;
XX WPI; 2002-698522/75.
XX Isolated nucleic acid molecules having polymorphisms in known human genes
XX e.g. cytochrome P450 A1 and catepsin S useful as genetic linkage markers
XX for locating, identifying and characterizing the genes responsible for
XX disorder-related traits.
XX Example 16; Page 130; 714pp; English.
XX This invention relates to the sequence of an isolated nucleic acid
XX molecule comprising at least one base variation from that of a known
XX human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
XX cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
XX aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
XX (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
XX inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
XX transferase (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
XX transferase (HNMT), kallikrein 2 (KLK2), nicotinamide-N-methyl
XX transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
XX sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
XX (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
XX transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1
XX (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
XX (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
XX receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
XX The polymorphisms in the human genes cited in the invention are useful as
XX genetic linkage markers for locating and characterizing the genes that
XX are responsible for specific traits within the genome and eventually
XX identifying the genes responsible for a variety of disorder-related
XX traits as a result of their e.g., overexpression, constitutive
XX expression, mutation or underexpression, which may be used in diagnosing
XX and/or treating the disorders. The nucleic acid molecules comprising the
XX polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,
XX ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
XX MDR1 and/or MDR3 are useful for screening individuals for altered drug
XX metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
XX AHR, MDR1 and/or MDR3 may also be used to screen individuals for
XX susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
XX used to screen for altered cardiovascular function, in COX2 for altered
XX nervous system function, in FLAP and HNMT for altered pulmonary,
XX immunological or haematological function, in KLK2 for altered serine
XX protease activity in the prostate, in LTF for altered immunological or
XX haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
XX peripheral nervous system function. The present sequence represents a
XX polymorphic DNA sequence of the invention
XX
XX Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.7%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 1.1e-02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1793 TGTGTCGTGTCGTGTCGTGTCGT 1813
XX DB 21 TATGTCGTGTCGTGTCGTGTCGT 1
XX
XX RESULT 175
XX ABS97832/C
XX ID ABS97832 standard; DNA; 21 BP.
XX AC ABS97832;
XX XX
XX XX
XX DT 23-DEC-2002 (first entry)
XX
XX DE Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #40.

```

```

XX Human; ds; cytochrome P450 A1; CYP450A1A1; UGT2B4; MDR1;
XX cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;
XX aryl hydrocarbon receptor nuclear translocator; ARNT; catepsin S; CTSS;
XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
XX epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
XX glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
XX HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
XX NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;
XX UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7; STM;
XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;
XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
XX multidrug resistance associated protein 3; cancer; prostate;
XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
XX altered drug metabolism; cardiovascular function; colorectal tumour;
XX central nervous system; pulmonary; immunological; SNP;
XX single nucleotide polymorphism.
XX Homo sapiens.
XX WO200257410-A2.
XX 25-JUL-2002.
XX 28-NOV-2001; 2001WO-US044838.
XX 28-NOV-2000; 2000US-00724389.
XX (DNAS-) DNA SCI LAB INC.
XX Guida M, Hall J;
XX WPI; 2002-698522/75.
XX Isolated nucleic acid molecules having polymorphisms in known human genes
XX e.g. cytochrome P450 and catepsin S useful as genetic linkage markers
XX for locating, identifying and characterizing the genes responsible for
XX disorder-related traits.
XX Example 16; Page 131; 714pp; English.
XX This invention relates to the sequence of an isolated nucleic acid
XX molecule comprising at least one base variation from that of a known
XX human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
XX cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),
XX aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
XX (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
XX inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
XX protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
XX transferase (HNMT), kallikrein 2 (KLK2), nicotinamide-N-methyl
XX transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
XX sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
XX (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
XX transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1
XX (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
XX (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
XX receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
XX The polymorphisms in the human genes cited in the invention are useful as
XX genetic linkage markers for locating and characterizing the genes that
XX are responsible for specific traits within the genome and eventually
XX identifying the genes responsible for a variety of disorder-related
XX traits as a result of their e.g., overexpression, constitutive
XX expression, mutation or underexpression, which may be used in diagnosing
XX and/or treating the disorders. The nucleic acid molecules comprising the
XX polymorphic sequences contained in CYP450A1, CYP450A2, CYP45002E1,
XX ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
XX MDR1 and/or MDR3 are useful for screening individuals for altered drug
XX metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
XX AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug
XX metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
XX AHR, MDR1 and/or MDR3 may also be used to screen individuals for
XX susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
XX used to screen for altered cardiovascular function, in COX2 for altered
XX nervous system function, in FLAP and HNMT for altered pulmonary,
XX immunological or haematological function, in KLK2 for altered serine
XX protease activity in the prostate, in LTF for altered immunological or
XX haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
XX peripheral nervous system function. The present sequence represents a
XX polymorphic DNA sequence of the invention
XX
XX Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.7%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 1.1e-02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1793 TGTGTCGTGTCGTGTCGTGTCGT 1813
XX DB 21 TATGTCGTGTCGTGTCGTGTCGT 1
XX
XX RESULT 175
XX ABS97832/C
XX ID ABS97832 standard; DNA; 21 BP.
XX AC ABS97832;
XX XX
XX XX
XX DT 23-DEC-2002 (first entry)
XX
XX DE Human NADPH quinone oxidoreductase 2 (NQO2) polymorphic sequence #40.

```


CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KIX2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention
 XX
 SQ Sequence 21 BP; 10 A; 9 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 1.7%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.1e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
 DB 21 TGTATGTGTGTGTGTGTGTGTGT 1

RESULT 176
 AAQ33888
 ID AAQ33888 standard; DNA; 22 BP.
 XX
 AC AAQ33888;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 DE Microsatellite sequence from clone TGLA306.
 XX
 KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 PN W09213102-A1.
 XX
 PD 06-AUG-1992.
 XX
 PF 15-JAN-1992; 92WO-US000340.
 XX
 PR 15-JAN-1991; 91US-00642342.
 XX
 PA (GENM-) GENMARK.
 XX
 PI Georges M, Massey JM;
 XX
 DR WPI; 1992-284684/34.
 XX
 PT Polymorphic bovine DNA markers - used in genetic identification, gene
 mapping, and selective breeding.
 XX
 PS Table 7; Page 285; 517pp; English.
 XX
 CC The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 22 BP; 1 A; 0 C; 11 G; 10 T; 0 U; 0 Other;
 Query Match 1.7%; Score 17.8; DB 1; Length 22;
 Best Local Similarity 90.5%; Pred. No. 1.1e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 90.5%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
 DB 1 TGTGGATGTGTGTGTGTGTGTGT 21

RESULT 177
 AA164468/C
 ID AA164468 standard; DNA; 22 BP.
 XX
 AC AA164468;
 XX
 DT 23-NOV-2001 (first entry)
 XX
 DE SSR motif #18.
 XX
 KW Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
 KW trait mapping; marker-assisted selection; gene selection; legume;
 KW DNA profiling; breeding; ds.
 XX
 OS Unidentified.
 XX
 PN NZ509194-A.
 XX
 PD 25-MAY-2001.
 XX
 PF 03-JAN-2001; 2001NZ-00509194.
 XX
 PR 24-DEC-1999; 99AU-00004907.
 PR 28-MAR-2000; 2000AU-00006520.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX
 PI Koelliker R, Forster JW;
 XX
 DR WPI; 2001-431058/46.
 XX
 PT Novel simple sequence repeats in clover species useful for selection of
 PT genes in legume breeding, for profiling legume species varieties and for
 PT testing the purity of legume seed batches.
 XX
 PS Example 1; Page 19; 52pp; English.
 XX
 CC The present invention relates to Simple Sequence Repeats (SSRs) from
 CC clover species. SSRs, also called microsatellites, are based on a 1-7
 CC nucleotide core element which is tandemly repeated. The SSR array is
 CC embedded in complex flanking DNA. SSRs are ideal markers for genome
 CC mapping, trait mapping and marker-assisted selection. The SSRs may be
 CC used in methods for selecting genes in clover/ legume breeding. The SSRs
 CC are also useful for DNA profiling of clover varieties and for testing the
 CC purity of legume seed batches. The present sequence is a SSR motif, which
 CC was used in the present invention
 XX
 SQ Sequence 22 BP; 10 A; 10 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 1.7%; Score 17.8; DB 1; Length 22;
 Best Local Similarity 90.5%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
 DB 21 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 178
 ABS97834/c
 ID ABS97834 standard; DNA; 22 BP.
 XX
 AC ABS97834;
 XX
 DT 23-DEC-2002 (first entry)

CC ARNT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HMMT for altered strine
 CC immunological or haematological function, in KLX2 for altered strine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention

XX SQ Sequence 20 BP; 10 A; 8 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 1.7%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811
 |||||
 Db 19 TGTATGTGTGTGTGTGT 1

RESULT 182

AAQ34164
 ID AAQ34164 standard; DNA; 17 BP.

XX AAQ34164;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Sequence of a microsatellite from clone TGLA84.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 XX genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 XX mapping, and selective breeding.

XX Table 7; Page 396; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved the determination of

CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 17 BP; 0 A; 0 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809

|||||

Db 1 TGTGTGTGTGTGTGTGT 17

RESULT 183

AAQ33783

ID AAQ33783 standard; DNA; 17 BP.

XX AAQ33783;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA188.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 XX genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 XX mapping, and selective breeding.

XX Table 7; Page 242; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 17 BP; 0 A; 0 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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OS Synthetic.
XX US955597-A.
XX
XX
XX
XX 21-SEP-1999.
XX
XX 30-JUN-1997; 97US-00885126.
XX
XX 16-NOV-1993; 93US-00154013.
XX 21-NOV-1994; 94US-00343018.
XX
XX (GENT-) GENTA INC.
XX
XX Schwartz DA, Vagnefi MM, Riley TA, Arnold LJ, Reynolds MA;
XX
XX WPI; 1999-539600/45.
XX
XX Oligomers made using chirally pure nucleoside dimers, trimers, or
XX tetramers with enhanced binding affinities.
XX
XX Example 19; Col 39-40; 30pp; English.
XX
XX The invention provides methods for preparing oligomers having phosphonate
XX internucleosidyl linkages of a preselected chirality which hybridize to a
XX target RNA sequence. The method of making comprises: (a) synthesizing a
XX nucleoside dimer, trimer, or tetramer with racemic internucleosidyl
XX phosphonate linkages; (b) purifying the racemic nucleoside to a chirally
XX pure nucleoside; and (c) sequentially linking at least 2 of the chirally
XX pure nucleosides to form a synthetic oligomer that is enriched for
XX phosphonate internucleosidyl linkages of a preselected chirality and is
XX complementary to an RNA target sequence. The methods are useful for
XX providing chirally enriched synthetic oligomers. Rp chirally enriched
XX synthetic oligomers have enhanced binding affinities for RNA compared to
XX oligomers with racemic all methylphosphonate internucleosidyl linkages.
XX Sequences AAX91054-75 represent oligomers chemically synthesised using
XX the method of the invention
XX
XX Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 17; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1798 GTGTGTGTGTGTGTGTGT 1814
XX 1 GTGTGTGTGTGTGTGTGT 17
XX
XX RESULT 187
XX AAD17594
XX ID AAD17594 standard; DNA; 17 BP.
XX
XX AC AAD17594;
XX
XX 10-DEC-2001 (first entry)
XX
XX 5' variation generator oligonucleotide PCR primer #9.
XX
XX Genomic DNA analysis; 5' variation generator; 3' fragment generator;
XX endangered animal identification; PCR primer; ss.
XX
XX Unidentified.
XX
XX EP1130114-A1.
XX
XX 05-SEP-2001.
XX
XX 03-MAR-2000; 2000EP-00200757.
XX
XX 03-MAR-2000; 2000EP-00200757.
XX
XX (VHAE-) VAN HAERINGEN LAB BV.
XX

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PI Van Haringen H, Van Haringen WA;
XX
XX WPI; 2001-572636/65.
XX
XX Analyzing genomic DNA in a sample, useful for analyzing genes of
XX organisms (e.g. a species or individual) or identifying endangered
XX animals or plants, by using oligonucleotide primers comprising universal
XX variable fragments.
XX
XX Example 1; Page 6; 23pp; English.
XX
XX The patent discloses a method and associated kit for analysing genomic
XX DNA in a sample. The method comprises conducting a nucleic acid
XX amplification on the genomic DNA in the sample using both first and
XX second oligonucleotide primer to produce DNA fragments based on repeat
XX sequences on at least one end of the genomic DNA. The first primer is a
XX 5' variation generator including a repeat sequence and at least one non-
XX repeat nucleotide. The second oligonucleotide primer is a 3' fragment
XX generator starting within such a genetic distance that amplification of
XX the genomic DNA can be performed and preferably includes inosine. The
XX method is useful for the genetic analysis of an individual organism,
XX particularly of a species or individual. It is also useful for the rapid
XX and straight forward identification of endangered animals or plants. The
XX present DNA sequence is a 5' variation generator oligonucleotide PCR
XX primer
XX
XX Sequence 17 BP; 0 A; 0 C; 8 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 17; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1792 TTGTGTGTGTGTGTGTGT 1808
XX 1 TTGTGTGTGTGTGTGTGT 17
XX
XX RESULT 188
XX ADB45728
XX ID ADB45728 standard; DNA; 17 BP.
XX
XX AC ADB45728;
XX
XX 18-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #6051.
XX
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX primer; probe; tumour suppression; tumour reversion; apoptosis;
XX virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX diagnosis.
XX
XX Homo sapiens.
XX
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001PR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX Disclosure; Page 739; 771pp; French.
XX

```

XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

XX Sequence 17 BP; 3 A; 4 C; 2 G; 8 T; 0 U; 0 Other;
 SQ Query Match 1.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2141 GATCAGTTTTTCACT 2157
 Db 1 GATCAGTTTTTCACT 17

RESULT 189
 AAX77487/C
 ID AAX77487 standard; DNA; 18 BP.
 AC AAX77487;
 XX 05-AUG-1999 (first entry)
 XX US5912147 primer 31.
 XX Primer; quantitation; genetic instability; tumour cell; detection;
 KW neoplastic transformation; carcinogenesis; ss.
 KW Synthetic.
 OS US5912147-A.
 PN 15-JUN-1999.
 PD 22-OCT-1996; 96US-00734973.
 XX 22-OCT-1996; 96US-00734973.
 XX (HEAL-) HEALTH RES INC.
 PA Anderson G, Stoler D, Basik M;
 PI WPI; 1999-357197/30.
 DR Quantitating genetic instability.
 XX Claim 4; Col 29-30; 27pp; English.

XX This invention describes a novel method for quantitating genetic
 CC instability independent of microsatellite alterations by treating a
 CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
 CC from normal cells. The method involves the cells from the same individual
 CC with oligonucleotide primers selected from (i) a nucleotide sequence
 CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
 CC 7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a
 CC adenine and guanine and Y is a pyrimidine selected from cytosine,

CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
 CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
 CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
 CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
 CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
 CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from
 CC adenine and guanine and Y is a pyrimidine selected from cytosine,
 CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
 CC where R is a purine selected from adenine and guanine and x = 6-16,
 CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
 CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
 CC of the primers. The method is useful for detecting genomic instability
 CC which are commonly associated with the various stages of neoplastic
 CC transformation and carcinogenesis. The method is rapid and simple

XX Sequence 18 BP; 8 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
 SQ Query Match 1.6%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1810
 Db 17 GTGTGTGTGTGTGTGTG 1

RESULT 190
 AAX77486/C
 ID AAX77486 standard; DNA; 18 BP.
 AC AAX77486;
 XX 05-AUG-1999 (first entry)
 XX US5912147 primer 30.

XX Primer; quantitation; genetic instability; tumour cell; detection;
 KW neoplastic transformation; carcinogenesis; ss.
 KW Synthetic.
 OS US5912147-A.
 PN 15-JUN-1999.
 PD 22-OCT-1996; 96US-00734973.
 XX 22-OCT-1996; 96US-00734973.
 XX (HEAL-) HEALTH RES INC.
 PA Anderson G, Stoler D, Basik M;
 PI WPI; 1999-357197/30.
 DR Quantitating genetic instability.
 XX Claim 4; Col 29-30; 27pp; English.

XX This invention describes a novel method for quantitating genetic
 CC instability independent of microsatellite alterations by treating a
 CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
 CC from normal cells. The method involves the cells from the same individual
 CC with oligonucleotide primers selected from (i) a nucleotide sequence
 CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
 CC 7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a
 CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
 CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
 CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
 CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
 CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
 CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from
 CC adenine and guanine and Y is a pyrimidine selected from cytosine,

CC thymine, and uracil, and x = 6-16. (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from adenine and guanine and x = 6-16. (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple

XX
SQ Sequence 18 BP; 8 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1810
DB 17 GTGTGTGTGTGTGTG 1

RESULT 191
AAX77484/C
ID AAX77484 standard; DNA; 18 BP.
XX
AC AAX77484;
XX
DT 05-AUG-1999 (first entry)
XX
DE US5912147 primer 28.
XX
KW Primer; quantitation; genetic instability; tumour cell; detection;
neoplastic transformation; carcinogenesis; ss.
XX
OS Synthetic.
XX
PN US5912147-A.
XX
PD 15-JUN-1999.
XX
PF 22-OCT-1996; 96US-00734973.
XX
PR 22-OCT-1996; 96US-00734973.
XX
PA (HEAL-) HEALTH RES INC.
XX
PI Anderson G, Stoler D, Basik M;
XX
DR WPI; 1999-357197/30.
XX
PT Quantitating genetic instability.
XX
PS Claim 4; Col 27-28; 27pp; English.
XX
CC This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from (i) a nucleotide sequence (CA)xRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)xYY, where Y is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CG)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-16, (vi) a nucleotide sequence (CA)xYY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from adenine and guanine and x = 6-16, (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple

XX
SQ Sequence 18 BP; 10 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1808
DB 17 TTGTGTGTGTGTGTG 1

RESULT 192
AAX77459/C
ID AAX77459 standard; DNA; 18 BP.
XX
AC AAX77459;
XX
DT 05-AUG-1999 (first entry)
XX
DE US5912147 primer 3.
XX
KW Primer; quantitation; genetic instability; tumour cell; detection;
neoplastic transformation; carcinogenesis; ss.
XX
OS Synthetic.
XX
PN US5912147-A.
XX
PD 15-JUN-1999.
XX
PF 22-OCT-1996; 96US-00734973.
XX
PR 22-OCT-1996; 96US-00734973.
XX
PA (HEAL-) HEALTH RES INC.
XX
PI Anderson G, Stoler D, Basik M;
XX
DR WPI; 1999-357197/30.
XX
PT Quantitating genetic instability.
XX
PS Claim 4; Col 17-18; 27pp; English.
XX
CC This invention describes a novel method for quantitating genetic instability independent of microsatellite alterations by treating a comparison pair comprising genomic DNA from tumour cells and genomic DNA from normal cells. The method involves the cells from the same individual with oligonucleotide primers selected from (i) a nucleotide sequence (CA)xRG, where R is a purine selected from adenine and guanine and x = 3-7, (ii) a nucleotide sequence (CG)xYY, where R is as in (i) and Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii) a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a nucleotide sequence (CG)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-16, (vi) a nucleotide sequence (CA)xYY, where R is a purine selected from adenine and guanine and Y is a pyrimidine selected from cytosine, thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR, where R is a purine selected from adenine and guanine and x = 6-16, (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination of the primers. The method is useful for detecting genomic instability which are commonly associated with the various stages of neoplastic transformation and carcinogenesis. The method is rapid and simple

XX
SQ Sequence 18 BP; 9 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTG 1808
DB 17 TTGTGTGTGTGTGTGTG 1

RESULT 193
AAAX77488/c
ID AAX77488 standard; DNA; 18 BP.
XX AC AAX77488;
XX DT 05-AUG-1999. (first entry)
XX DE US5912147 primer 32.
XX KW Primer; quantitation; genetic instability; tumour cell; detection;
XX KW neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT misc_RNA 18
FT /*tag= a
FT /note= "uracil"
XX US5912147-A.
XX 15-JUN-1999.
XX PD 22-OCT-1996; 96US-00734973.
XX PF 22-OCT-1996; 96US-00734973.
XX PR (HEAL-) HEALTH RES INC.
XX PA Anderson G, Stoler D, Basik M;
XX PI WPI; 1999-357197/30.
XX DR Quantitating genetic instability.
XX PT Claim 4; Col 29-30; 27pp; English.
XX PS This invention describes a novel method for quantitating genetic
CC instability independent of microsatellite alterations by treating a
CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
CC from normal cells. The method involves the cells from the same individual
CC with oligonucleotide primers selected from (i) a nucleotide sequence
CC (CG)XRG where R is a purine selected from adenine and guanine and x = 3-
CC 7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,
CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
CC of the primers. The method is useful for detecting genomic instability
CC which are commonly associated with the various stages of neoplastic
CC transformation and carcinogenesis. The method is rapid and simple
XX SQ Sequence 18 BP; 8 A; 9 C; 0 G; 0 T; 1 U; 0 Other;
Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1810
DB 17 TTGTGTGTGTGTGTGTG 1

DB 17 GTGTGTGTGTGTGTGTG 1

RESULT 194
AAAX77457/c
ID AAX77457 standard; DNA; 18 BP.
XX AC AAX77457;
XX DT 05-AUG-1999 (first entry)
XX DE US5912147 primer 1.
XX KW Primer; quantitation; genetic instability; tumour cell; detection;
XX KW neoplastic transformation; carcinogenesis; ss.
XX OS Synthetic.
XX FN US5912147-A.
XX 15-JUN-1999.
XX PD 22-OCT-1996; 96US-00734973.
XX PF 22-OCT-1996; 96US-00734973.
XX PR (HEAL-) HEALTH RES INC.
XX PA Anderson G, Stoler D, Basik M;
XX PI WPI; 1999-357197/30.
XX DR Quantitating genetic instability.
XX PT Claim 4; Col 15-16; 27pp; English.
XX PS This invention describes a novel method for quantitating genetic
CC instability independent of microsatellite alterations by treating a
CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
CC from normal cells. The method involves the cells from the same individual
CC with oligonucleotide primers selected from (i) a nucleotide sequence
CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
CC 7, (ii) a nucleotide sequence (CG)XRY, where R is as in (i) and Y is a
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,
CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
CC of the primers. The method is useful for detecting genomic instability
CC which are commonly associated with the various stages of neoplastic
CC transformation and carcinogenesis. The method is rapid and simple
XX SQ Sequence 18 BP; 9 A; 8 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTG 1808
DB 17 TTGTGTGTGTGTGTGTG 1

RESULT 195
AAQ75581
ID AAQ75581 standard; DNA; 20 BP.
XX

AC AAQ75581;
 XX
 DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 XX JP06303997-A.
 PN
 XX
 XX 01-NOV-1994.
 PD
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX
 XX WPI; 1995-018287/03.
 DR
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 XX Disclosure; Page 5; 11pp; Japanese.
 PS
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 XX
 SQ Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.6%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1865 TTTTATTTTGTGTTTAAAT 1884
 DB 1 TTTTATTTTGTGTTTAAAT 20
 RESULT 196
 AAA73096
 ID AAA73096 standard; DNA; 20 BP.
 XX
 AC AAA73096;
 XX
 XX 24-NOV-2000 (first entry)
 DT
 XX Human MC1R gene related TATA box oligonucleotide SEQ ID NO:15.
 DE
 XX Human; melanocortin-1 receptor; MC1R; promoter; regulation; detection;
 KW melanin; ds.
 XX
 OS Homo sapiens.
 XX
 XX JP2000166563-A.
 PN
 XX
 PD 20-JUN-2000.
 XX
 XX 04-DEC-1998; 98JP-00345881.
 PF
 XX 04-DEC-1998; 98JP-00345881.
 PR
 XX (SHIS) SHISEIDO CO LTD.
 PA
 XX
 XX WPI; 2000-485552/43.
 DR
 XX
 XX Upstream controlling sequence of melanocortin1 receptor and its
 PT application.
 PT
 XX
 PS Disclosure; Page 4; 21pp; Japanese.
 XX
 XX The present invention describes a control-active polynucleotide derived
 CC from the human melanocortin-1 receptor (MC1R) gene upstream controlling
 CC sequence. Also described is a method for detecting a substance affecting
 CC synthesis of melanin in which a host transformed by an expression vector,
 CC comprising a control active polynucleotide derived from MC1R, is cultured
 CC in the presence of a sample to be tested and a signal formed by the
 CC expression of said reporter gene is detected. The control-active
 CC polynucleotide is used for the detection of a substance affecting
 CC expression of said reporter gene is detected. The control-active
 CC polynucleotide is used for the detection of a substance affecting
 CC synthesis of melanin. The present sequence represents a human
 CC melanocortin-1 receptor gene TATA box oligonucleotide, which is given in
 CC the exemplification of the present invention

DR WPI; 2000-485552/43.
 XX
 XX Upstream controlling sequence of melanocortin1 receptor and its
 PT application.
 PT
 XX
 PS Disclosure; Page 4; 21pp; Japanese.
 XX
 XX The present invention describes a control-active polynucleotide derived
 CC from the human melanocortin-1 receptor (MC1R) gene upstream controlling
 CC sequence. Also described is a method for detecting a substance affecting
 CC synthesis of melanin in which a host transformed by an expression vector,
 CC comprising a control active polynucleotide derived from MC1R, is cultured
 CC in the presence of a sample to be tested and a signal formed by the
 CC expression of said reporter gene is detected. The control-active
 CC polynucleotide is used for the detection of a substance affecting
 CC expression of said reporter gene is detected. The control-active
 CC polynucleotide is used for the detection of a substance affecting
 CC synthesis of melanin. The present sequence represents a human
 CC melanocortin-1 receptor gene TATA box oligonucleotide, which is given in
 CC the exemplification of the present invention
 XX
 SQ Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
 Query Match 1.6%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1811 TGTATATATATATATATGTA 1830
 DB 1 TATATATATATATATATATA 20
 RESULT 197
 AAA73096/c
 ID AAA73096 standard; DNA; 20 BP.
 XX
 AC AAA73096;
 XX
 XX 24-NOV-2000 (first entry)
 DT
 XX Human MC1R gene related TATA box oligonucleotide SEQ ID NO:15.
 DE
 XX Human; melanocortin-1 receptor; MC1R; promoter; regulation; detection;
 KW melanin; ds.
 XX
 OS Homo sapiens.
 XX
 XX JP2000166563-A.
 PN
 XX
 PD 20-JUN-2000.
 XX
 XX 04-DEC-1998; 98JP-00345881.
 PF
 XX 04-DEC-1998; 98JP-00345881.
 PR
 XX (SHIS) SHISEIDO CO LTD.
 PA
 XX
 XX WPI; 2000-485552/43.
 DR
 XX
 XX Upstream controlling sequence of melanocortin1 receptor and its
 PT application.
 PT
 XX
 PS Disclosure; Page 4; 21pp; Japanese.
 XX
 XX The present invention describes a control-active polynucleotide derived
 CC from the human melanocortin-1 receptor (MC1R) gene upstream controlling
 CC sequence. Also described is a method for detecting a substance affecting
 CC synthesis of melanin in which a host transformed by an expression vector,
 CC comprising a control active polynucleotide derived from MC1R, is cultured
 CC in the presence of a sample to be tested and a signal formed by the
 CC expression of said reporter gene is detected. The control-active
 CC polynucleotide is used for the detection of a substance affecting
 CC expression of said reporter gene is detected. The control-active
 CC polynucleotide is used for the detection of a substance affecting
 CC synthesis of melanin. The present sequence represents a human
 CC melanocortin-1 receptor gene TATA box oligonucleotide, which is given in
 CC the exemplification of the present invention

XX SQ Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 1.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1811 TGTATATATATATATATGTA 1830
DB 20 TATATATATATATATATATA 1
RESULT 198
AAL50667
ID AAL50667 standard; DNA; 20 BP.
XX
AC AAL50667;
DT 16-JAN-2003 (first entry)
XX
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #1.
KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW drug dosage optimisation; xenobiotic sensitivity.
XX
OS Homo sapiens.
XX
PN US2002115097-A1.
XX
PD 22-AUG-2002.
XX
PF 01-FEB-2002; 2002US-00061693.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Rienzo AD, Iyer L, Ratain MJ;
XX
DR WPI; 2002-740095/80.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient, involves
PT determining number of thymidine-adenine repeats in the promoter.
XX
PS Claim 8; Page 9; 13pp; English.
XX
CC The invention comprises a method for detecting polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
CC UGT1A1). The method involves determining the number of thymidine-adenine
CC (TA) repeats in the promoter - as the number of TA repeats correlates
CC with expression of the UGT gene. The method of the invention is useful
CC for detecting polymorphisms in a UGT gene promoter. The method of the
CC invention is also useful in optimising drug dosages and predicting an
CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
CC TA repeat polymorphism
XX
SQ Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 1.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1811 TGTATATATATATATATGTA 1830
DB 1 TATATATATATATATATATA 20
RESULT 199
AAL50667/c
ID AAL50667 standard; DNA; 20 BP.

XX AAL50667;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #1.
KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW drug dosage optimisation; xenobiotic sensitivity.
XX
OS Homo sapiens.
XX
PN US2002115097-A1.
XX
PD 22-AUG-2002.
XX
PF 01-FEB-2002; 2002US-00061693.
XX
PR 16-FEB-1999; 99US-00251274.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Rienzo AD, Iyer L, Ratain MJ;
XX
DR WPI; 2002-740095/80.
XX
PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient, involves
PT determining number of thymidine-adenine repeats in the promoter.
XX
PS Claim 8; Page 9; 13pp; English.
XX
CC The invention comprises a method for detecting polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
CC UGT1A1). The method involves determining the number of thymidine-adenine
CC (TA) repeats in the promoter - as the number of TA repeats correlates
CC with expression of the UGT gene. The method of the invention is useful
CC for detecting polymorphisms in a UGT gene promoter. The method of the
CC invention is also useful in optimising drug dosages and predicting an
CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
CC TA repeat polymorphism
XX
SQ Sequence 20 BP; 10 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
Query Match 1.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1811 TGTATATATATATATATGTA 1830
DB 20 TATATATATATATATATATA 1
RESULT 200
ABZ91716
ID ABZ91716 standard; DNA; 20 BP.
XX
AC ABZ91716;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.


```
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate backbone, where 1-5 and
FT 16-20 are 2' methoxyethyl nucleotides. All cytidines are
FT 5-methylcytidines"
XX
XX WO2003053340-A2.
XX
XX 03-JUL-2003.
XX
XX 09-DEC-2002; 2002WO-US038618.
XX
XX 10-DEC-2001; 2001US-00006191.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Gaarde WA, Watt AT;
XX WPI; 2003-559091/52.
XX
XX New antisense oligonucleotides for modulating connective tissue growth
XX factor expression, particularly useful for treating cancers (e.g. breast
XX or prostate cancer), pulmonary or renal fibrosis, scleroderma or
XX atherosclerosis.
XX
XX Claim 3; Page 89; 139pp; English.
XX
XX This invention relates to novel methods for modulating the expression of
XX connective tissue growth factor (CTGF) by antisense oligonucleotides.
XX CTGF has been mapped to human chromosome region 6q23.1, and is also known
XX as ctgfact, fibroblast inducible secreted protein, fisp-12, NOV2,
XX insulin-like growth factor binding protein-related protein 2, IGFBP-rp2,
XX IGFBP-8, Hs24 and ecogenin. It is known to stimulate DNA synthesis and
XX promote chemotaxis of fibroblasts, however, it is also upregulated in
XX acute lymphoblastic leukaemia and in tumour or endothelial cells
XX associated with the vasculature. Accordingly, antisense oligonucleotides
XX that inhibit the expression of CTGF in cells or tissues can be used in
XX gene therapy to treat various conditions including hyperproliferative
XX disorders (particularly cancer, e.g. breast, prostate or renal cancer),
XX pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As
XX such, the present invention describes these antisense oligos as having
XX cytostatic, dermatological and antiarteriosclerotic activities. This
XX oligonucleotide sequence is a chimeric phosphorothioate antisense oligo
XX with 2' MOE wings and a deoxy gap, which is used to inhibit expression of
XX mouse CTGF of the invention.
XX
XX Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 16.8; DB 1; Length 20;
XX Best Local Similarity 90.0%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1675 ATTCTGATTCGATGACACT 1694
XX |||||
XX DB 20 ATTCTGATTCGATGACACT 1
XX
XX RESULT 203
XX AAQ75729
XX ID AAQ75729 standard; DNA; 21 BP.
XX
XX AC AAQ75729;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX the double-stranded cDNAs with restriction enzyme and; (c)
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PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 16.8; DB 1; Length 21;
XX Best Local Similarity 90.0%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1865 TTTTATTTTGTGTTTAAAT 1884
XX |||||
XX DB 1 TTTTATTTTGTGTTTAAAT 20
XX
XX RESULT 204
XX AAQ75730
XX ID AAQ75730 standard; DNA; 21 BP.
XX
XX AC AAQ75730;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
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CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
    Query Match 1.6%; Score 16.8; DB 1; Length 21;
    Best Local Similarity 90.0%; Pred. No. 1.4e+02;
    Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTAAAT 1884
DB 1 TTTTATTTTGTGTTTAAAT 20

RESULT 205
AAQ75728
ID AAQ75728 standard; DNA; 21 BP.
XX
AC AAQ75728;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JF06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
    Query Match 1.6%; Score 16.8; DB 1; Length 21;
    Best Local Similarity 90.0%; Pred. No. 1.4e+02;
    Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTAAAT 1884
DB 1 TTTTATTTTGTGTTTAAAT 20

RESULT 206
AAZ60082/c
ID AAZ60082 standard; DNA; 21 BP.
XX
AC AAZ60082;
XX
DT 25-APR-2000 (first entry)

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XX Reverse PCR primer -439/MIP-3beta used to amplify MIP-3beta ORF.
DE
XX Chemokine; PCR primer; macrophage inflammation protein 3beta;
KW dendritic cell; disease treatment; MIP-3beta; infection; cancer; allergy;
KW immune response initiation; autoimmune disease; tissue rejection; ss.
XX
OS Homo sapiens.
XX
FN EP974357-A1.
XX
PD 26-JAN-2000.
XX
PF 16-JUL-1998; 98EP-00401799.
XX
PR 16-JUL-1998; 98EP-00401799.
XX
PA (SCHE ) SCHERING-PLOUGH.
XX
FI Caux C, Vanbervliet B, Lebecque S, Vicari A, Dieu M;
DR WPI; 2000-118300/11.
XX
PT Use of chemokines capable of directing migration of dendritic cells,
PT useful for treating microbial infections, cancer and autoimmune diseases.
XX
PS Disclosure; Col 13; 16pp; English.
XX
SQ Sequence 21 BP; 8 A; 11 C; 0 G; 2 T; 0 U; 0 Other;
    Query Match 1.6%; Score 16.8; DB 1; Length 21;
    Best Local Similarity 90.0%; Pred. No. 1.4e+02;
    Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGTGTGTGT 1813
DB 21 GTGTGTGTGTGTGTGTGTGTGTGTGT 2

RESULT 207
ABK47993/c
ID ABK47993 standard; DNA; 21 BP.
XX
AC ABK47993;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human MIP-3 beta RT-PCR primer -439/MIP-3 beta.
XX
KW Human; chemokine; MCP-4; hMCP-4; ss; 6CKine; dendritic cell; renal;
KW autoimmune disease; tissue rejection; allergy; cancer; hepatocellular;
KW melanoma; breast; pancreas; colon; glioma; endometrium; intestine; lung;
KW prostate; thyroid; ovary; testis; liver; head; neck; colorectal; bladder;
KW oesophagus; stomach; eye; glioblastoma; gastric; metastatic carcinoma;
KW immunosuppressive; anti-allergic; cytostatic; rectum; RT-PCR; primer;
KW reverse transcriptase; macrophage inflammatory protein 3 beta;

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XX MIP-3 beta.
XX Homo sapiens.
XX US2002034494-A1.
XX 21-MAR-2002.
XX 24-JAN-2001; 2001US-00768917.
XX 24-JAN-2001; 2001US-00768917.
XX (VICARI) VICARI A P.
XX (CAUX/) CAUX C.
XX (LAFACE) LAFACE D.
XX Vicari AP, Caux C, Laface D;
XX WPI; 2002-351086/38.
XX Using chemokine MCP-4 or 6CKine to attract dendritic cells to the site of
XX an antigen is useful to treat disease states, particularly autoimmune
XX disease, tissue rejection, allergy and cancer.
XX Example; Page 7; 29pp; English.
XX The invention relates to a method for enhancing an immune response in a
XX mammal, comprising administering chemokine MCP-4 or 6CKine or their
XX biologically active fragments. The chemokines are capable of directing
XX the migration of dendritic cells to manufacture a medicament for a
XX disease state. The invention is used to treat disease states, including
XX an autoimmune disease, tissue rejection or an allergy, or a cancer,
XX particularly melanoma, breast, pancreatic, colon, lung, glioma,
XX hepatocellular, endometrial, gastric, intestinal, renal, prostate,
XX thyroid, ovarian, testicular, liver, head and neck, colorectal,
XX cesophagus, stomach, eye or bladder cancer, glioblastoma or metastatic
XX carcinoma. This sequence represents an Rn-PCR primer for macrophage
XX inflammatory protein 3 beta (MIP-3 beta), used in analysis of
XX responsiveness to chemokines
XX
XX Sequence 21 BP; 8 A; 11 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 16.8; DB 1; Length 21;
XX Best Local Similarity 90.0%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
XX 21 GTGTGTGTGTGTGTGTGTGT 2
XX
XX RESULT 208
XX AAT30425
XX ID AAT30425 standard; DNA; 24 BP.
XX AC AAT30425;
XX 28-JAN-1997 (first entry)
XX
XX Compound simple sequence repeat primer (CA)4.5(TA)7.5.
XX
XX Detection; polymorphism; perfect compound simple sequence repeat;
XX adaptor directed primer; genome; genetic; fingerprinting;
XX amplified fragment length polymorphism assay; microsatellite region;
XX genetic trait marking; germplasm comparisons; compound; ss.
XX
XX Synthetic.
XX WO9617082-A2.
XX 06-JUN-1996.
XX 21-NOV-1995; 95WO-US015150.

XX 28-NOV-1994; 94US-00346456.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Morgante M, Vogel JM;
XX WPI; 1996-277795/28.
XX Modified amplified fragment length polymorphism assay - for detection of
XX polymorphism esp. in microsatellite regions.
XX Disclosure; Fig 1c; 173pp; English.
XX Detecting polymorphisms between 2 nucleic acid samples, esp. in
XX microsatellite regions, comprises digesting the nucleic acid to generate
XX fragments, ligating adaptor segments to their ends, amplifying them using
XX primer directed amplification and comparing the prods. to detect
XX differences. The primers used in the amplification comprise a primer
XX consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor
XX directed primer, comprising a sequence complementary to an adaptor
XX segment. The present sequence is an example of a compound SSR primer. The
XX method represents a modified amplified fragment length polymorphism
XX assay, which is partic. useful for genome fingerprinting, i.e. for
XX genetic trait marking and germplasm comparisons
XX
XX Sequence 24 BP; 12 A; 4 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 16.8; DB 1; Length 24;
XX Best Local Similarity 90.0%; Pred. No. 1.6e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1813 TATATATATATATATGTACA 1832
XX 1 TATATATATATATATACACA 20
XX
XX RESULT 209
XX ADD69518
XX ID ADD69518 standard; DNA; 17 BP.
XX AC ADD69518;
XX 15-JAN-2004 (first entry)
XX ISSR-related PCR primer 5.
XX inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
XX animal; Basmati rice; ss.
XX Unidentified.
XX WO2003085133-A2.
XX 16-OCT-2003.
XX 09-JAN-2003; 2003WO-IB000041.
XX 08-APR-2002; 2002IN-CH000260.
XX (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
XX Nagaraju JG;
XX WPI; 2003-804317/75.
XX New set of inter-simple sequence repeats (ISSR)-PCR primers for
XX genotyping eukaryotes, useful for genotyping diverse genomes of plant and
XX animal systems.
XX Disclosure; Page 19; 60pp; English.
XX The invention relates to a novel set of inter-simple sequence repeats

CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
 CC invention may be useful for genotyping diverse genomes of plant and
 CC animal systems, in particular for distinguishing Basmati rice varieties
 CC from non-Basmati rice varieties and traditional Basmati rice varieties
 CC from evolved Basmati rice varieties. The current sequence is that of the
 CC ISSR-related PCR primer of the invention.

XX Sequence 17 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 1 Other;

Query Match 1.6%; Score 16.6; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 1; Mismatches 0;

QY 1794 GTGTGTGTGTGTGTGTG 1810

DB 1 GTGTGTGTGTGTGTGTG 17

RESULT 210

AAQ33786

ID AAQ33786 standard; DNA; 18 BP.

XX AAQ33786;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone TGLA189.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;

KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

XX W09213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 mapping, and selective breeding.

XX Table 7; Page 244; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T)₆n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 18 BP; 1 A; 0 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1;

QY 1794 GTGTGTGTGTGTGTGTG 1811

DB 1 GTGTGTGTGTGTGTGTG 18

RESULT 211

AA119941

ID AA119941 standard; DNA; 18 BP.

XX AA119941;

XX 14-JUN-1999 (first entry)

XX Primer SEQ ID NO:1 from JP11075880.

XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX Synthetic.

XX JP11075880-A.

XX 23-MAR-1999.

XX 10-JUL-1998; 98JP-00195719.

XX 14-JUL-1997; 97JP-00205378.

XX (KAGA) ZH KAGAKU & KESSEI RYOCHO KENKYUSHO.

XX WPI; 1999-257710/22.

XX Labelling of an oligonucleotide - useful for detecting genes.

XX Example 1; Page 7; 10pp; Japanese.

XX A method has been developed for labelling an oligonucleotide having a
 CC repeated sequence of (XY)_n (where X and Y consists of a combination of
 CC adenine and thymine or uracil or guanine and cytosine, and n is an
 CC integer of 1 or more) at the 3' terminal side in which the repeated
 CC sequence is added and extended using a labelled body of the nucleotide
 CC constituting the repeated sequence and a DNA polymerase lacking in 5' to
 CC 3' exonuclease activity. The method can be used for detecting a gene. The
 CC method can detect a gene in a sensitivity up to ten times higher than
 CC prior art methods. The present sequence represents a primer used in an
 CC example from the present invention

XX Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1;

QY 1813 TATATATATATATATGTA 1830

DB 1 TATATATATATATATATA 18

RESULT 212

AA119941/C

ID AA119941 standard; DNA; 18 BP.

XX AA119941;

XX 14-JUN-1999 (first entry)

XX Primer SEQ ID NO:1 from JP11075880.

XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX Synthetic.

XX JP11075880-A.
 XX 23-MAR-1999.
 XX 10-JUL-1998; 98JP-00195719.
 XX 14-JUL-1997; 97JP-00205378.
 XX (KAGA) ZH KAGAKU & KESSSEI RYOHO KENKYUSHO.
 XX WPI; 1999-257710/22.
 XX Labelling of an oligonucleotide - useful for detecting genes.
 XX Example 1; Page 7; 10pp; Japanese.
 XX A method has been developed for labelling an oligonucleotide having a
 CC repeated sequence of (XY)_n (where X and Y consists of a combination of
 CC adenine and thymine or uracil or guanine and cytosine, and n is an
 CC integer of 1 or more) at the 3'-terminal side in which the repeated
 CC sequence is added and extended using a labelled body of the nucleotide
 CC constituting the repeated sequence and a DNA polymerase lacking in 5' to
 CC 3' exonuclease activity. The method can be used for detecting a gene. The
 CC method can detect a gene in a sensitivity up to ten times higher than
 CC prior art methods. The present sequence represents a primer used in an
 CC example from the present invention

XX SQ Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
 Query Match 1.6%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.4e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
 DB 18 TATATATATATATATA 1

RESULT 213
 AAX77485/C
 ID AAX77485 standard; DNA; 18 BP.
 AC AAX77485;
 DT 05-AUG-1999 (first entry)
 DE US5912147 primer 29.
 XX Primer; quantitation; genetic instability; tumour cell; detection;
 XX neoplastic transformation; carcinogenesis; ss.
 OS Synthetic.
 XX US5912147-A.
 XX 15-JUN-1999.
 XX 22-OCT-1996; 96US-00734973.
 XX 22-OCT-1996; 96US-00734973.
 XX (HEAL-) HEALTH RES INC.
 XX Anderson G, Stoler D, Basik M;
 XX WPI; 1999-357197/30.
 XX Quantitating genetic instability.
 XX Claim 4; Col 27-28; 27pp; English.
 XX This invention describes a novel method for quantitating genetic

CC instability independent of microsatellite alterations by treating a
 CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
 CC from normal cells. The method involves the cells from the same individual
 CC with oligonucleotide primers selected from (i) a nucleotide sequence
 CC (CG)XRg, where R is a purine selected from adenine and guanine and x = 3-
 CC 7, (ii) a nucleotide sequence (CG)XYR, where R is as in (i) and Y is a
 CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
 CC a nucleotide sequence (CG)XRg, where R is as in (i) and x = 3-7, (iv) a
 CC nucleotide sequence (CG)XYR, where Y is a pyrimidine selected from
 CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
 CC (CA)XRg, where R is a purine selected from adenine and guanine and x = 6-
 CC 16, (vi) a nucleotide sequence (CA)XYR, where R is a purine selected from
 CC adenine and guanine and Y is a pyrimidine selected from cytosine,
 CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRr,
 CC where R is a purine selected from adenine and guanine and x = 6-16,
 CC (viii) a nucleotide sequence (CA)XYR, where Y is a pyrimidine selected
 CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
 CC of the primers. The method is useful for detecting genomic instability
 CC which are commonly associated with the various stages of neoplastic
 CC transformation and carcinogenesis. The method is rapid and simple

XX SQ Sequence 18 BP; 9 A; 8 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 1.6%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.4e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
 DB 18 TCTGTGTGTGTGTGTGTG 1

RESULT 214
 AAX77494/C
 ID AAX77494 standard; DNA; 18 BP.
 AC AAX77494;
 DT 05-AUG-1999 (first entry)
 DE US5912147 primer 38.
 XX Primer; quantitation; genetic instability; tumour cell; detection;
 XX neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
 OS Synthetic.
 XX Key Location/Qualifiers
 XX misc_RNA 17..18
 XX /*tag= a
 XX /*note= "uracil"
 XX US5912147-A.
 XX 15-JUN-1999.
 XX 22-OCT-1996; 96US-00734973.
 XX 22-OCT-1996; 96US-00734973.
 XX (HEAL-) HEALTH RES INC.
 XX Anderson G, Stoler D, Basik M;
 XX WPI; 1999-357197/30.
 XX Quantitating genetic instability.
 XX Claim 4; Col 31-32; 27pp; English.
 XX This invention describes a novel method for quantitating genetic
 CC instability independent of microsatellite alterations by treating a
 CC comparison pair comprising genomic DNA from tumour cells and genomic DNA

CC from normal cells. The method involves the cells from the same individual
CC with oligonucleotide primers selected from (i) a nucleotide sequence
CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
CC 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,
CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
CC of the primers. The method is useful for detecting genomic instability
CC which are commonly associated with the various stages of neoplastic
CC transformation and carcinogenesis. The method is rapid and simple
CC
XX
SQ Sequence 18 BP; 8 A; 8 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
| | | | | | | | | | | | | | | | | |
Db 18 AATGTGTGTGTGTGTG 1

RESULT 215
AA77493/C
ID AAX77493 standard; DNA; 18 BP.

XX AC AAX77493;
XX DT 05-AUG-1999 (first entry)
XX DE US5912147 primer 37.

XX KW Primer; quantitation; genetic instability; tumour cell; detection;
XX KW neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT misc_RNA 17 /*tag= a
XX FT /*note= "uracil"
XX FT

XX PN US5912147-A.
XX PD 15-JUN-1999.
XX PF 22-OCT-1996; 96US-00734973.

XX PR 22-OCT-1996; 96US-00734973.
XX PA (HEAL-) HEALTH RES INC.

XX PI Anderson G, Stoler D, Basik M;
XX DR WPI; 1999-357197/30.

XX PT Quantitating genetic instability.
XX PS Claim 4; Col 31-32; 27pp; English.

XX CC This invention describes a novel method for quantitating genetic
XX CC instability independent of microsatellite alterations by treating a
XX CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX CC from normal cells. The method involves the cells from the same individual
XX CC with oligonucleotide primers selected from (i) a nucleotide sequence

CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
CC 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)XRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,
CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
CC of the primers. The method is useful for detecting genomic instability
CC which are commonly associated with the various stages of neoplastic
CC transformation and carcinogenesis. The method is rapid and simple
XX
SQ Sequence 18 BP; 8 A; 8 C; 0 G; 1 T; 1 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
| | | | | | | | | | | | | | | | | |
Db 18 AATGTGTGTGTGTGTG 1

RESULT 216
AA77464/C
ID AAX77464 standard; DNA; 18 BP.

XX AC AAX77464;
XX DT 05-AUG-1999 (first entry)
XX DE US5912147 primer 8.

XX KW Primer; quantitation; genetic instability; tumour cell; detection;
XX KW neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT misc_RNA 18 /*tag= a
XX FT /*note= "uracil"
XX FT

XX PN US5912147-A.
XX PD 15-JUN-1999.
XX PF 22-OCT-1996; 96US-00734973.

XX PR 22-OCT-1996; 96US-00734973.
XX PA (HEAL-) HEALTH RES INC.

XX PI Anderson G, Stoler D, Basik M;
XX DR WPI; 1999-357197/30.

XX PT Quantitating genetic instability.
XX PS Claim 4; Col 19-20; 27pp; English.

XX CC This invention describes a novel method for quantitating genetic
XX CC instability independent of microsatellite alterations by treating a
XX CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX CC from normal cells. The method involves the cells from the same individual
XX CC with oligonucleotide primers selected from (i) a nucleotide sequence
XX CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
XX CC 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a

CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
CC a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a
CC nucleotide sequence (CG)xY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,
CC (viii) a nucleotide sequence (CA)xY, where Y is a pyrimidine selected
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
CC of the primers. The method is useful for detecting genomic instability
CC which are commonly associated with the various stages of neoplastic
CC transformation and carcinogenesis. The method is rapid and simple
CC
XX
SQ Sequence 18 BP; 8 A; 8 C; 1 G; 0 T; 1 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 ACTGTGTGTGTGTGTG 1

RESULT 217
AAAX77491/C
ID AAX77491 standard; DNA; 18 BP.
XX
XX AAX77491;
AC AAX77491;
XX
XX 05-AUG-1999 (first entry)
DT
DE US5912147 primer 35.
XX
XX Primer; quantitation; genetic instability; tumour cell; detection;
KW neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
XX
XX Synthetic.
OS
XX
XX
XX Key Location/Qualifiers
FH 18
FT misc_RNA /tag= a
FT /note= "uracil"
FT
XX
XX US5912147-A.
XX
XX 15-JUN-1999.
XX
XX 22-OCT-1996; 96US-00734973.
XX
XX 22-OCT-1996; 96US-00734973.
XX
XX (HEAL-) HEALTH RES INC.
XX
XX Anderson G, Stoler D, Basik M;
XX
XX WPI; 1999-357197/30.
XX
XX Quantitating genetic instability.
XX
XX Claim 4; Col 31-32; 27pp; English.
XX
XX
XX This invention describes a novel method for quantitating genetic
CC instability independent of microsatellite alterations by treating a
CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
CC from normal cells. The method involves the cells from the same individual
CC with oligonucleotide primers selected from (i) a nucleotide sequence
CC (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-
CC 7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
CC a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a
CC nucleotide sequence (CG)xY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,

CC nucleotide sequence (CG)xY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,
CC (viii) a nucleotide sequence (CA)xY, where Y is a pyrimidine selected
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
CC of the primers. The method is useful for detecting genomic instability
CC which are commonly associated with the various stages of neoplastic
CC transformation and carcinogenesis. The method is rapid and simple
CC
XX
SQ Sequence 18 BP; 8 A; 8 C; 0 G; 1 T; 1 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 AATGTGTGTGTGTGTG 1

RESULT 218
AAAX77489/C
ID AAX77489 standard; DNA; 18 BP.
XX
XX AAX77489;
AC AAX77489;
XX
XX 05-AUG-1999 (first entry)
DT
DE US5912147 primer 33.
XX
XX Primer; quantitation; genetic instability; tumour cell; detection;
KW neoplastic transformation; carcinogenesis; ss.
XX
XX Synthetic.
OS
XX
XX
XX US5912147-A.
XX
XX 15-JUN-1999.
XX
XX 22-OCT-1996; 96US-00734973.
XX
XX 22-OCT-1996; 96US-00734973.
XX
XX (HEAL-) HEALTH RES INC.
XX
XX Anderson G, Stoler D, Basik M;
XX
XX WPI; 1999-357197/30.
XX
XX Quantitating genetic instability.
XX
XX Claim 4; Col 29-30; 27pp; English.
XX
XX
XX This invention describes a novel method for quantitating genetic
CC instability independent of microsatellite alterations by treating a
CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
CC from normal cells. The method involves the cells from the same individual
CC with oligonucleotide primers selected from (i) a nucleotide sequence
CC (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-
CC 7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
CC a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a
CC nucleotide sequence (CG)xY, where Y is a pyrimidine selected from
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
CC (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-
CC 16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from
CC adenine and guanine and Y is a pyrimidine selected from cytosine,
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR,
CC where R is a purine selected from adenine and guanine and x = 6-16,

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1810
DB 18 TGTGTGTGTGTGTGTG 1

RESULT 221
AAS13764
ID AAS13764 standard; DNA; 18 BP.
XX AC AAS13764;
XX DT 08-MAY-2002 (first entry)
XX DE Simple sequence repeat, SSR, #36.
XX KW Simple sequence repeat; plant; ds, SSR; ryegrass; fescue; tandem repeat;
XX KW cereal profiling; grass profiling; seed batch purity testing.
XX OS Lolium rigidum.
XX PN NZ509193-A.
XX PD 25-MAY-2001.
XX PF 03-JAN-2001; 2001NZ-00509193.
XX PR 24-DEC-1999; 99AU-00004906.
XX PR 04-MAY-2000; 2000AU-00007310.
XX PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
XX PA (UYSC-) UNIV SOUTHERN CROSS.
XX PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
XX PA (UVAD-) UNIV ADELAIDE.
XX PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX PI Forster JW, Jones ES;
XX DR WPI; 2001-512563/56.
XX PS New simple sequence repeats having 2 or more tandemly repeated nucleotide
XX PT core elements isolated from ryegrass and fescue, useful for selecting of
XX PT genes in grass or cereal breeding or profiling grass or cereal species
XX PT varieties.
XX PS Example 1; Fig 6; 72pp; English.
XX CC The invention relates to a substantially purified or isolated nucleic
XX CC acid (1) from ryegrass or fescue species including a simple sequence
XX CC repeat (SSR) having 2 or more tandemly repeated nucleotide core elements
XX CC 2-6 nucleotides in length. Also included are a nucleic acid primer
XX CC suitable for amplifying an SSR, identifying (M) an SSR by preparing a
XX CC library of ryegrass or fescue genomic DNA enriched for SSRs and
XX CC identifying clones in the library containing SSRs, a library of ryegrass
XX CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
XX CC a gene in grass or cereal breeding by identifying an SSR that is closely
XX CC associated with the gene such that the SSR and the gene are
XX CC preferentially co-inherited, and selecting for the SSR in the breeding, a
XX CC method for DNA profiling grass or cereal species varieties by assessing
XX CC variation between SSR varieties and testing the purity of grass or cereal
XX CC seed batches by assessing variation within seed batch of an SSR. The SSRs
XX CC may be used in the selection of genes in grass or cereal breeding, for
XX CC profiling grass or cereal species varieties, for testing the purity of
XX CC grass or cereal seed batches, and for DNA profiling to establish the
XX CC distinct identity, uniformity and/or stability of a cultivar. The present
XX CC sequence is a ryegrass or fescue SSR
XX
XX Sequence 18 BP; 0 A; 1 C; 8 G; 9 T; 0 U; 0 Other;
Query Match 1.6%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1811
DB 1 GTCTGTGTGTGTGTGTG 18

RESULT 222
AAI64450/C
ID AAI64450 standard; DNA; 18 BP.
XX AC AAI64450;
XX DT 23-NOV-2001 (first entry)
XX DE SSR motif #10.
XX KW Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;
XX KW trait mapping; marker-assisted selection; gene selection; legume;
XX KW DNA profiling; breeding; ds.
XX OS Unidentified.
XX PN NZ509194-A.
XX PD 25-MAY-2001.
XX PF 03-JAN-2001; 2001NZ-00509194.
XX PR 24-DEC-1999; 99AU-00004907.
XX PR 28-MAR-2000; 2000AU-00006520.
XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX PI Koelliker R, Forster JW;
XX DR WPI; 2001-431058/46.
XX PS Novel simple sequence repeats in clover species useful for selection of
XX PT genes in legume breeding, for profiling legume species varieties and for
XX PT testing the purity of legume seed batches.
XX PS Claim 6; Page 35; 52pp; English.
XX CC The present invention relates to Simple Sequence Repeats (SSRs) from
XX CC clover species. SSRs, also called microsatellites, are based on a 1-7
XX CC nucleotide core element which is tandemly repeated. The SSR array is
XX CC embedded in complex flanking DNA. SSRs are ideal markers for genome
XX CC mapping, trait mapping and marker-assisted selection. The SSRs may be
XX CC used in methods for selecting genes in clover/ legume breeding. The SSRs
XX CC are also useful for DNA profiling of clover varieties and for testing the
XX CC purity of legume seed batches. The present sequence is a SSR motif, which
XX CC was used in the present invention
XX
XX Sequence 18 BP; 8 A; 10 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1810
DB 18 TGTGTGTGTGTGTGTG 1

RESULT 223
ABX79779
ID ABX79779 standard; cDNA; 18 BP.
XX AC ABX79779;
XX DT 17-APR-2003 (first entry)

```
XX DE EST polymorphic DNA repeat polynucleotide #104.
XX KW EST: expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
XX KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX KW Homo sapiens.
XX OS US6472154-B1.
XX PN 29-OCT-2002.
XX PD 31-DEC-1999; 99US-00475947.
XX PF 31-DEC-1999; 99US-00475947.
XX PR 31-DEC-1999; 99US-00475947.
XX PS (TEXA ) UNIV TEXAS SYSTEM.
XX PA Garner HR, Wren JD, Minna JD, Fondon JW;
XX PI WPI; 2003-208818/20.
XX DR Identifying a candidate polymorphic repeat within a coding sequence, for
XX PT understanding or treating genetic disease, comprises detecting tandem
XX PT repeats in a target coding sequence and scoring the repeats for
XX PT polymorphic probability.
XX PS Example; Col 385; 589pp; English.
XX SS The invention discloses a method for identifying a candidate polymorphic
XX CC repeat within a coding sequence (expressed sequence tag, EST), which
XX CC comprises detecting tandem repeats in a target coding sequence, scoring
XX CC the repeats for polymorphic probability and generating a dataset
XX CC correlating the repeats with polymorphic probability to identify a
XX CC candidate polymorphic repeat. The computational methods (polymorphic
XX CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
XX CC useful for identifying and detecting candidate polymorphic repeats in
XX CC human genes, which can be used to understand, treat or eliminate genetic
XX CC diseases, predispositions or adverse drug-treatment reactions. Examples
XX CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxia,
XX CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX CC the polymorphic repeats identified for a search of human ESTs
XX SQ Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;
XX Query Match 1.6%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.4e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1810 GTGTATATATATATATAT 1827
DB 1 GTATATATATATATATAT 18

RESULT 224
ABX79779/c
ID ABX79779 standard; cDNA; 18 BP.
XX AC ABX79779;
XX AC 17-APR-2003 (first entry)
XX DT
XX DE EST polymorphic DNA repeat polynucleotide #104.
XX KW EST: expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
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KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX KW Homo sapiens.
XX OS US6472154-B1.
XX PN 29-OCT-2002.
XX PD 31-DEC-1999; 99US-00475947.
XX PF 31-DEC-1999; 99US-00475947.
XX PR 31-DEC-1999; 99US-00475947.
XX PS (TEXA ) UNIV TEXAS SYSTEM.
XX PA Garner HR, Wren JD, Minna JD, Fondon JW;
XX PI WPI; 2003-208818/20.
XX DR Identifying a candidate polymorphic repeat within a coding sequence, for
XX PT understanding or treating genetic disease, comprises detecting tandem
XX PT repeats in a target coding sequence and scoring the repeats for
XX PT polymorphic probability.
XX PS Example; Col 385; 589pp; English.
XX SS The invention discloses a method for identifying a candidate polymorphic
XX CC repeat within a coding sequence (expressed sequence tag, EST), which
XX CC comprises detecting tandem repeats in a target coding sequence, scoring
XX CC the repeats for polymorphic probability and generating a dataset
XX CC correlating the repeats with polymorphic probability to identify a
XX CC candidate polymorphic repeat. The computational methods (polymorphic
XX CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
XX CC useful for identifying and detecting candidate polymorphic repeats in
XX CC human genes, which can be used to understand, treat or eliminate genetic
XX CC diseases, predispositions or adverse drug-treatment reactions. Examples
XX CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxia,
XX CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX CC the polymorphic repeats identified for a search of human ESTs
XX SQ Sequence 18 BP; 8 A; 0 C; 1 G; 9 T; 0 U; 0 Other;
XX Query Match 1.6%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.4e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTAC 1831
DB 18 ATATATATATATATAC 1

RESULT 225
AAH91159/c
ID AAH91159 standard; DNA; 19 BP.
XX AC AAH91159;
XX AC 09-OCT-2001 (first entry)
XX DT
XX DE Human inflammatory bowel disease associated polymorphic site #234.
XX KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX OS Homo sapiens.
XX PS Key Location/Qualifiers
XX FT misc_feature 9 /*tag= a
XX FT
```

FT /note= "SNP, optional deletion at this position"

XX WO200142511-A2.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033632.

XX 10-DEC-1999; 99US-0170257P.

XX 10-APR-2000; 2000US-0196046P.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX WPI; 2001-367874/38.

XX Testing for the presence of polymorphisms associated with inflammatory

XX bowel disease, using a hybridization assay.

XX Claim 1; Page 48; 463pp; English.

XX The present invention describes a method for detecting the presence of

XX polymorphisms associated with inflammatory bowel diseases such as

XX ulcerative colitis and Crohn's disease. The methods can be used to detect

XX the presence of genetic polymorphisms associated with inflammatory bowel

XX disease and correlating their occurrence with disease states. They may be

XX used in this way for phenotypic correlations, forensics, paternity

XX testing, medicine and genetic analysis. The present sequence is a

XX polymorphic site described in the exemplification of the invention

XX Sequence 19 BP; 9 A; 4 C; 0 G; 5 T; 0 U; 1 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1802 GTGTGTGTGTGTATATATA 1820

DB 19 GTATGTGTGTATATATA 1

RESULT 226

ABK90423

ID ABK90423 standard; DNA; 19 BP.

AC ABK90423;

XX 05-NOV-2002 (first entry)

DT Human UGT1A1 promoter polymorphism (TA)8 repeat region.

DE Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;

XX uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;

KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;

KW TAS-103; xenobiotic.

XX Homo sapiens.

OS US6395481-B1.

XX 28-MAY-2002.

XX 16-FEB-1999; 99US-00251274.

XX 16-FEB-1999; 99US-00251274.

XX (ARCH-) ARCH DEV CORP.

PA Di Rienzo A, Iyer L, Ratain MJ;

XX WPI; 2002-588597/63.

XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase

PT gene promoter, useful for optimizing drug dosages for a patient,

PT comprises determining the presence of five thymidine-adenine repeats in

PT the promoter.

XX Example 6; Col 11; 13pp; English.

XX The invention relates to detecting (M1) polymorphisms in a uridine

XX diphosphate glucuronosyltransferase (UGT) gene promoter by determining

XX the presence of five thymidine-adenine (TA) repeats in the promoter,

XX where the presence of the five TA repeats correlates with increased

XX expression of the gene. The method is used for detecting polymorphisms in

XX a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is

XX useful for screening individuals for variation in glucuronidation

XX activity, for optimizing drug dosages for a patient, where the drugs

XX (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably

XX UGT1A1) and the activity of the drug is effected by its level of

XX glucuronidation. The method preferably involves obtaining DNA from an

XX individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene

XX promoter) contained in the DNA and determining the number of TA repeats

XX in the promoter. Thus the DNA being amplified comprises all or part of

XX UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and

XX the number of TA repeats is determined by gel electrophoresis or by

XX sequencing the amplified DNA. The polymorphism comprises an allele

XX consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA

XX repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,

XX (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or

XX (TA)8/(TA)8. (M1) is also useful for predicting an individual's

XX sensitivity to xenobiotics that are glucuronidated by a UGT (preferably

XX UGT1A1) gene product, the method comprising determining the number of TA

XX repeats in a UGT gene promoter, where the number of TA repeats correlates

XX with expression of the UGT gene, and the individuals sensitivity to

XX xenobiotics is effected by glucuronidation activity. The methods

XX preferably involve determining the presence of five, six or seven TA

XX repeats in the promoter. Defects in glucuronidation is associated with

XX Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The

XX present sequence is the UGT1A1 promoter (TA)8 repeat region

XX Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.6%; Score 16.4; DB 1; Length 19;

Best Local Similarity 94.4%; Pred. No. 1.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830

DB 1 TATATATATATATATATA 18

RESULT 227

ABK90423/c

ID ABK90423 standard; DNA; 19 BP.

AC ABK90423;

XX 05-NOV-2002 (first entry)

DT Human UGT1A1 promoter polymorphism (TA)8 repeat region.

DE Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;

XX uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;

KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;

KW TAS-103; xenobiotic.

XX Homo sapiens.

OS US6395481-B1.

XX 28-MAY-2002.

XX 16-FEB-1999; 99US-00251274.

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PR 16-FEB-1999; 99US-00251274.
XX (ARCH-) ARCH DEV CORP.
PA Di Rienzo A, Iyer L, Ratain MJ;
XX WPI; 2002-588597/63.
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
XX gene promoter; useful for optimizing drug dosages for a patient, involves
XX comprises determining the presence of five thymidine-adenine repeats in
XX the promoter.
XX Example 6; Col 11; 13pp; English.
XX The invention relates to detecting (M1) polymorphisms in a uridine
XX diphosphate glucuronosyltransferase (UGT) gene promoter by determining
XX the presence of five thymidine-adenine (TA) repeats in the promoter,
XX where the presence of the five TA repeats correlates with increased
XX expression of the gene. The method is used for detecting polymorphisms in
XX a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is
XX useful for screening individuals for variation in glucuronidation
XX activity, for optimising drug dosages for a patient, where the drugs
XX (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
XX UGT1A1) and the activity of the drug is effected by its level of
XX glucuronidation. The method preferably involves obtaining DNA from an
XX individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
XX promoter) contained in the DNA and determining the number of TA repeats
XX in the promoter. Thus the DNA being amplified comprises all or part of
XX UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
XX the number of TA repeats is determined by gel electrophoresis or by
XX sequencing the amplified DNA. The polymorphism comprises an allele
XX consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
XX repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
XX (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
XX (TA)8/(TA)8. (M1) is also useful for predicting an individual's
XX sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
XX UGT1A1) gene product, the method comprising determining the number of TA
XX repeats in a UGT gene promoter, where the number of TA repeats correlates
XX with expression of the UGT gene, and the individual's sensitivity to
XX xenobiotics is effected by glucuronidation activity. The methods
XX preferably involve determining the presence of five, six or seven TA
XX repeats in the promoter. Defects in glucuronidation is associated with
XX Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
XX present sequence is the UGT1A1 promoter (TA)8 repeat region
XX Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
XX Query Match 1.6%; Score 16.4; DB 1; Length 19;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 18 TATATATATATATATATA 1

RESULT 228
AAL50681
ID AAL50681 standard; DNA; 19 BP.
XX AAL50681;
XX AC AAL50681;
XX DT 16-JAN-2003 (first entry)
XX DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.
XX KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
XX uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
XX drug dosage optimisation; xenobiotic sensitivity.
XX OS Homo sapiens.
XX PN US2002115097-A1.
XX PD 22-AUG-2002.
XX PF 01-FEB-2002; 2002US-00061693.
XX PR 16-FEB-1999; 99US-00251274.
XX (ARCH-) ARCH DEV CORP.
XX Riienzo AD, Iyer L, Ratain MJ;
XX WPI; 2002-740095/80.
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
XX gene promoter; useful for optimizing drug dosages for a patient, involves
XX determining number of thymidine-adenine repeats in the promoter.
XX Example 6; Page 3; 13pp; English.
XX The invention comprises a method for detecting polymorphisms in a uridine
XX diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
XX UGT1A1). The method involves determining the number of thymidine-adenine
XX (TA) repeats in the promoter - as the number of TA repeats correlates
XX with expression of the UGT gene. The method of the invention is useful
XX for detecting polymorphisms in a UGT gene promoter. The method of the
XX invention is also useful in optimising drug dosages and predicting an
XX individual's sensitivity to xenobiotics for drugs and xenobiotics that
XX are glucuronidated by UGT. The present DNA sequence represents a UGT gene
XX TA repeat polymorphism
XX Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
XX Query Match 1.6%; Score 16.4; DB 1; Length 19;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 1 TATATATATATATATATA 18

RESULT 229
AAL50681/c
ID AAL50681 standard; DNA; 19 BP.
XX AAL50681;
XX AC AAL50681;
XX DT 16-JAN-2003 (first entry)
XX DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.
XX KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
XX uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
XX drug dosage optimisation; xenobiotic sensitivity.
XX OS Homo sapiens.
XX PN US2002115097-A1.
XX PD 22-AUG-2002.
XX PF 01-FEB-2002; 2002US-00061693.
XX PR 16-FEB-1999; 99US-00251274.
XX (ARCH-) ARCH DEV CORP.
XX Riienzo AD, Iyer L, Ratain MJ;
XX WPI; 2002-740095/80.
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase

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PN US2002115097-A1.
XX 22-AUG-2002.
XX PF 01-FEB-2002; 2002US-00061693.
XX PR 16-FEB-1999; 99US-00251274.
XX (ARCH-) ARCH DEV CORP.
XX Riienzo AD, Iyer L, Ratain MJ;
XX WPI; 2002-740095/80.
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
XX gene promoter; useful for optimizing drug dosages for a patient, involves
XX determining number of thymidine-adenine repeats in the promoter.
XX Example 6; Page 3; 13pp; English.
XX The invention comprises a method for detecting polymorphisms in a uridine
XX diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
XX UGT1A1). The method involves determining the number of thymidine-adenine
XX (TA) repeats in the promoter - as the number of TA repeats correlates
XX with expression of the UGT gene. The method of the invention is useful
XX for detecting polymorphisms in a UGT gene promoter. The method of the
XX invention is also useful in optimising drug dosages and predicting an
XX individual's sensitivity to xenobiotics for drugs and xenobiotics that
XX are glucuronidated by UGT. The present DNA sequence represents a UGT gene
XX TA repeat polymorphism
XX Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
XX Query Match 1.6%; Score 16.4; DB 1; Length 19;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 1 TATATATATATATATATA 18

RESULT 229
AAL50681/c
ID AAL50681 standard; DNA; 19 BP.
XX AAL50681;
XX AC AAL50681;
XX DT 16-JAN-2003 (first entry)
XX DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #15.
XX KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
XX uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
XX drug dosage optimisation; xenobiotic sensitivity.
XX OS Homo sapiens.
XX PN US2002115097-A1.
XX PD 22-AUG-2002.
XX PF 01-FEB-2002; 2002US-00061693.
XX PR 16-FEB-1999; 99US-00251274.
XX (ARCH-) ARCH DEV CORP.
XX Riienzo AD, Iyer L, Ratain MJ;
XX WPI; 2002-740095/80.
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase

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PT gene promoter, useful for optimizing drug dosages for a patient, involves
 PT determining number of thymidine-adenine repeats in the promoter.
 XX
 PS Example 6; Page 3; 13pp; English.

XX The invention comprises a method for detecting polymorphisms in a uridine
 CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
 CC UGT1A1). The method involves determining the number of thymidine-adenine
 CC (TA) repeats in the promoter - as the number of TA repeats correlates
 CC with expression of the UGT gene. The method of the invention is useful
 CC for detecting polymorphisms in a UGT gene promoter. The method of the
 CC invention is also useful in optimising drug dosages and predicting that
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
 CC TA repeat polymorphism

XX
 SQ Sequence 19 BP; 10 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
 Query Match 1.6%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
 Db 18 TATATATATATATATA 1

RESULT 230
 ABA99798
 ID ABA99798 standard; DNA; 20 BP.
 XX
 AC ABA99798;
 XX
 DT 11-JUN-2002 (first entry)
 XX
 DE Murine capn12 exon 7 splice donor site.
 XX
 KW Calpain protease; murine; gene therapy; screening; diagnosis; capn12; ss.
 XX
 OS Mus sp.

XX Key Location/Qualifiers
 FH exon 1..10
 FT /*tag= a
 FT /number= 7
 FT intron 11..20
 FT /*tag= b
 FT /number= 7

XX DB10031932-A1.
 XX
 XX 10-JAN-2002.
 XX
 XX 30-JUN-2000; 2000DB-01031932.
 XX
 XX 30-JUN-2000; 2000DB-01031932.
 XX
 XX (BADI) BASF AG.
 XX
 XX WPI; 2002-115441/16.
 XX

XX New calpain protein 12 with cysteine protease activity, useful for
 PT treating specific deficiency disorders.
 PT
 PS Disclosure; Fig 2c; 36pp; German.
 XX
 XX This invention describes a novel murine calpain protease 12 (capn12). The
 CC calpain protease of the invention, related proteins and nucleic acid that
 CC encodes it, are useful for treatment (including gene therapy) of diseases
 CC associated with insufficient expression of the calpain protease. The
 CC protein is also used to screen for calpain protein effectors and to raise
 CC specific immunoglobulins (Ig) useful for diagnosis. Also the
 CC polynucleotide encoding capn12 is useful, e.g. as primers and probes, for

CC diagnosis of diseases, or predisposition to them, and for recombinant
 CC production of capn12. This sequence represents the murine calpain 12,
 CC capn12 exon 7 splice donor site described in the disclosure of the
 CC invention
 XX
 SQ Sequence 20 BP; 5 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
 Query Match 1.6%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1589 AGTGACAGCTAGGATGCTG 1606
 Db 3 AGTGACAGCTAGGATGGG 20

RESULT 231
 AAQ33743
 ID AAQ33743 standard; DNA; 16 BP.
 XX
 AC AAQ33743;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 XX Microsatellite sequence from clone TGLA159.
 XX
 XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KW genetic mapping; traits; amplification; ss.
 XX
 OS Bos taurus.
 XX
 XX WO9213102-A1.
 XX
 XX 06-AUG-1992.
 XX
 XX 15-JAN-1992; 92WO-US000340.
 XX
 XX 15-JAN-1991; 91US-00642342.
 XX
 XX (GENM-) GENMARK.
 XX
 XX Georges M, Massey JM;
 XX
 XX WPI; 1992-284684/34.
 XX
 XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX
 XX Table 7; Page 227; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obtd. by
 CC screening a library of bovine MboI DNA fragments of between 250 and 500
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved in the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
 SQ

XX Query Match 1.5%; Score 16; DB 1; Length 16;
 XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1793 TGTGTGTGTGTGTGTG 1808
DB 1 TGTGTGTGTGTGTGTG 16

RESULT 232
AAQ33749
ID AAQ33749 standard; DNA; 16 BP.
XX
AC AAQ33749;
XX
AC 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA160.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
XX
XX WO9213102-A1.
PN
XX 06-AUG-1992.
PD
XX 15-JAN-1992; 92WO-US000340.
PF
XX 15-JAN-1991; 91US-00642342.
PR
XX (GENM-) GENMARK.
PA
XX Georges M, Massey JM;
PI
XX WPI; 1992-284684/34.
DR
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
ET
XX Table 7; Page 229; 517pp; English.
PS
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
DB 1 GTGTGTGTGTGTGTGT 16

RESULT 233
AAQ33903
ID AAQ33903 standard; DNA; 16 BP.
XX
AC AAQ33903;
XX
AC 25-MAR-2003 (revised)
DT 16-FEB-1995 (first entry)
XX
DE Purine-pyrimidine contg. ribooligonucleoside R138.
XX
XX Purine; pyrimidine; methylphosphonate; MP; triple helix; translation;
KW oligonucleoside; ss.
XX
```

```
AC AAQ33903;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA311.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
XX
XX WO9213102-A1.
PN
XX 06-AUG-1992.
PD
XX 15-JAN-1992; 92WO-US000340.
PF
XX 15-JAN-1991; 91US-00642342.
PR
XX (GENM-) GENMARK.
PA
XX Georges M, Massey JM;
PI
XX WPI; 1992-284684/34.
DR
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
ET
XX Table 7; Page 291; 517pp; English.
PS
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
DB 1 GTGTGTGTGTGTGTGT 16

RESULT 234
AAQ68236/c
ID AAQ68236 standard; RNA; 16 BP.
XX
AC AAQ68236;
XX
XX 25-MAR-2003 (revised)
DT 16-FEB-1995 (first entry)
XX
DE Purine-pyrimidine contg. ribooligonucleoside R138.
XX
XX Purine; pyrimidine; methylphosphonate; MP; triple helix; translation;
KW oligonucleoside; ss.
XX
```

OS Synthetic.
 XX WO9413326-A1.
 PN
 XX
 PD 23-JUN-1994.
 XX
 PF 08-DEC-1993; 93WO-US011986.
 XX
 PR 08-DEC-1992; 92US-00987746.
 XX
 PA (GENT-) GENTA INC.
 XX
 PI Arnold LJ, Reynolds MA;
 XX
 DR WPI; 1994-217542/26.
 XX
 PT Detection, recognition, inhibition and alteration of single and double
 PT stranded target nucleic acid sequences - by formation of a triple helix
 PT structure using 2 oligomers which block translation.
 XX
 PS Example 2; Page 37; 67pp; English.
 XX
 CC Two sets of methylphosphonate oligonucleosides ("MP oligomers") and
 CC complementary ribooligonucleosides ("RNA oligomers") contg. alternating
 CC purines and pyrimidines were examined for their ability to form triple
 CC helix complexes. (Set 1:G2019 and R138; Set 2:G2018 and R139 - see
 CC AAQ68235-38). It was shown that MP oligomers contg. alternating purines
 CC and pyrimidines are capable of forming triple stranded complexes with
 CC complementary RNA oligomers. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 16 BP; 8 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1793 TGTGTGTGTGTGTGTG 1808
 D 16 TGTGTGTGTGTGTGTG 1
 RESULT 235
 AAQ68235
 ID AAQ68235 standard; DNA; 16 BP.
 XX
 AC AAQ68235;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-FEB-1995 (first entry)
 XX
 DE Purine-pyrimidine contg. methylphosphonate oligonucleoside G2019.
 XX
 KW Purine; pyrimidine; methylphosphonate; MP; triple helix; translation;
 KW oligonucleoside; ss.
 XX
 OS Synthetic.
 XX
 PN WO9413326-A1.
 XX
 PD 23-JUN-1994.
 XX
 PF 08-DEC-1993; 93WO-US011986.
 XX
 PR 08-DEC-1992; 92US-00987746.
 XX
 PA (GENT-) GENTA INC.
 XX
 PI Arnold LJ, Reynolds MA;
 XX
 DR WPI; 1994-217542/26.
 XX
 PT Detection, recognition, inhibition and alteration of single and double

PT stranded target nucleic acid sequences - by formation of a triple helix
 PT structure using 2 oligomers which block translation.
 XX
 PS Example 2; Page 37; 67pp; English.
 XX
 CC Two sets of methylphosphonate oligonucleosides ("MP oligomers") and
 CC complementary ribooligonucleosides ("RNA oligomers") contg. alternating
 CC purines and pyrimidines were examined for their ability to form triple
 CC helix complexes. (Set 1:G2019 and R138; Set 2:G2018 and R139 - see
 CC AAQ68235-38). It was shown that MP oligomers contg. alternating purines
 CC and pyrimidines are capable of forming triple stranded complexes with
 CC complementary RNA oligomers. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 16 BP; 0 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
 Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y 1794 GTGTGTGTGTGTGTGTG 1809
 D 1 GTGTGTGTGTGTGTGTG 16
 RESULT 236
 AAQ68238
 ID AAQ68238 standard; RNA; 16 BP.
 XX
 AC AAQ68238;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-FEB-1995 (first entry)
 XX
 DE Purine-pyrimidine contg. ribooligonucleoside R139.
 XX
 KW Purine; pyrimidine; methylphosphonate; MP; triple helix; translation;
 KW oligonucleoside; ss.
 XX
 OS Synthetic.
 XX
 PN WO9413326-A1.
 XX
 PD 23-JUN-1994.
 XX
 PF 08-DEC-1993; 93WO-US011986.
 XX
 PR 08-DEC-1992; 92US-00987746.
 XX
 PA (GENT-) GENTA INC.
 XX
 PI Arnold LJ, Reynolds MA;
 XX
 DR WPI; 1994-217542/26.
 XX
 PT Detection, recognition, inhibition and alteration of single and double
 PT stranded target nucleic acid sequences - by formation of a triple helix
 PT structure using 2 oligomers which block translation.
 XX
 PS Example 2; Page 37; 67pp; English.
 XX
 CC Two sets of methylphosphonate oligonucleosides ("MP oligomers") and
 CC complementary ribooligonucleosides ("RNA oligomers") contg. alternating
 CC purines and pyrimidines were examined for their ability to form triple
 CC helix complexes. (Set 1:G2019 and R138; Set 2:G2018 and R139 - see
 CC AAQ68235-38). It was shown that MP oligomers contg. alternating purines
 CC and pyrimidines are capable of forming triple stranded complexes with
 CC complementary RNA oligomers. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 16 BP; 0 A; 0 C; 8 G; 0 T; 8 U; 0 Other;
 Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 16; Gaps 0;
 Y 1793 TGTGTGTGTGTGTGTG 1808
 D 16 TGTGTGTGTGTGTGTG 1

Best Local Similarity 50.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
 Matches 8; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
 Db 1 UGUGUGUGUGUGUGUG 16

RESULT 237
 AAQ68237/C
 ID AAQ68237 standard; DNA; 16 BP.
 AC AAQ68237;
 XX
 XX 25-MAR-2003 (revised)
 DT 16-FEB-1995 (first entry)
 XX
 XX Purine-pyrimidine contg. methylphosphonate oligonucleoside G2018.
 XX
 XX Purine, pyrimidine; methylphosphonate; MP; triple helix; translation;
 KW oligonucleoside; ss.
 XX
 XX Synthetic.
 OS
 XX W09413326-A1.
 PN
 XX 23-JUN-1994.
 PD
 XX 08-DEC-1993; 93WO-US011986.
 PF
 XX 08-DEC-1992; 92US-00987746.
 PR
 XX (GENT-) GENTA INC.
 PA
 XX Arnold LJ, Reynolds MA;
 PI
 XX WPI; 1994-217542/26.
 DR
 XX
 XX Detection, recognition, inhibition and alteration of single and double
 PT stranded target nucleic acid sequences - by formation of a triple helix
 PT structure using 2 oligomers which block translation.
 XX
 FS Example 2; Page 37; 67pp; English.

Two sets of methylphosphonate oligonucleosides ("MP oligomers") and
 complementary ribooligonucleosides ("RNA oligomers") contg. alternating
 purines and pyrimidines were examined for their ability to form triple
 helix complexes. (Set 1: G2019 and R138; Set 2: G2018 and R139 - see
 CC AAQ68235-38). It was shown that MP oligomers contg. alternating purines
 CC and pyrimidines are capable of forming triple stranded complexes with
 CC complementary RNA oligomers. (Updated on 25-MAR-2003 to correct PN
 CC field.)

SQ Sequence 16 BP; 8 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1809
 Db 16 GTGTGTGTGTGTGTGT 1

RESULT 238
 AAT66090/C
 ID AAT66090 standard; DNA; 16 BP.
 XX
 XX AAT66090;
 AC
 XX 25-MAR-2003 (revised)
 DT 18-JUN-1997 (first entry)
 XX

DE Repeat sequence found in ADP/ATP translocase gene.
 XX Polymorphism; repeat sequence; genetic marker; primer; amplification;
 KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
 KW linkage analysis; genetic disease; animal; plant; breeding; locus;
 KW hybridisation; chromosome; ds.
 XX
 OS Homo sapiens.
 XX
 XX US5582979-A.
 PN
 XX 10-DEC-1996.
 PD
 XX 04-APR-1994; 94US-00222177.
 PF
 XX 21-APR-1989; 89US-00341562.
 PR
 XX 05-SEP-1991; 91US-00754351.
 XX
 XX (MARS-) MARSHFIELD CLINIC.
 PA
 XX Weber JL;
 PI
 XX WPI; 1997-042299/04.
 DR
 XX
 XX Detection of polymorphic genetic markers of the form (dc-da)n(dg-dt)n -
 PT using novel nucleic acid mols. as primers.
 PT
 XX Example 9; Col 59-60; 186pp; English.
 PS
 XX The invention relates to the isolation of polymorphic repeat sequences
 CC having the sequence (dc-da)n.(dg-dt)n which can be used as genetic
 CC markers. Primers based on these sequences can be used to detect these
 CC repeats, especially for use in e.g. paternity or maternity testing, human
 CC genetic analysis such as linkage analysis of genetic disease, commercial
 CC animal or plant breeding or pedigree analysis. The sequences AAT66084-
 CC T66107 represent repeat sequences of low informativeness found in
 CC specific human genes. This repeat sequence is found in the ADP/ATP
 CC translocase gene. The sequence is amplified by primers AAT66091-2.
 CC (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 16 BP; 8 A; 8 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.5%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
 Db 16 TGTGTGTGTGTGTGTG 1

RESULT 239
 AAZ98508/C
 ID AAZ98508 standard; DNA; 16 BP.
 XX
 XX AAZ98508;
 AC
 XX 19-JUN-2000 (first entry)
 DT
 XX H. discus derived sequence #26.
 DE
 XX
 XX Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
 KW Haliotis discus; ss.
 KW
 XX Haliotis discus.
 OS
 XX W020001156-A1.
 PN
 XX 02-MAR-2000.
 PD
 XX 01-JUL-1999; 99WO-JP003551.
 PF
 XX 18-AUG-1998; 98JP-00232153.
 PR

XX PA (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.

XX PI Takahashi H, Sekino M;

XX DR WPI; 2000-224692/19.

XX PT Isolation of satellite sequences from genomic DNA for use as DNA markers

XX PT comprises isolating a library with high homogeneity by DNA fragmentation.

XX PS Example 5; Page 14; 35pp; Japanese.

XX CC The invention provides a novel method for isolation of satellite
 CC sequences from genomic DNA that comprises fragmentation of the DNA by a
 CC method which is not dependent on base sequence, then selection of the
 CC satellite sequences from the obtained genomic library of high
 CC homogeneity. The method is useful for the isolation of microsatellite DNA
 CC sequences which can be used as DNA markers. The new method markedly
 CC improves the efficiency of isolation of satellite sequences in comparison
 CC to prior art methods which are reliant on base sequences. Sequences
 CC AA298483-514 represent sequences from *Halotis* discus, used in the method
 CC of the invention

XX SQ Sequence 16 BP; 8 A; 8 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808

DB 16 TGTGTGTGTGTGTGTG 1

RESULT 240

AAAD17599/c

ID AAAD17599 standard; DNA; 17 BP.

XX AC AAAD17599;

XX DT 10-DEC-2001 (first entry)

XX DE 5' variation generator oligonucleotide PCR primer #14.

XX KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;

XX KW endangered animal identification; PCR primer; ss.

XX OS Unidentified.

XX PN EP1130114-A1.

XX PD 05-SEP-2001.

XX PF 03-MAR-2000; 2000EP-00200757.

XX PR 03-MAR-2000; 2000EP-00200757.

XX PA (VHAE-) VAN HAERINGEN LAB BV.

XX PI Van Haringen H, Van Haringen WA;

XX DR WPI; 2001-572636/65.

XX PT Analyzing genomic DNA in a sample, useful for analyzing genes of

XX PT organisms (e.g. a species or individual) or identifying endangered

XX PT animals or plants, by using oligonucleotide primers comprising universal

XX PT variable fragments.

XX PS Example 1; Page 6; 23pp; English.

XX CC The patent discloses a method and associated kit for analysing genomic

XX CC DNA in a sample. The method comprises conducting a nucleic acid

XX CC amplification on the genomic DNA in the sample using both first and

CC second oligonucleotide primer to produce DNA fragments based on repeat
 CC sequences on at least one end of the genomic DNA. The first primer is a
 CC 5' variation generator including a repeat sequence and at least one non-
 CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment
 CC generator starting within such a genetic distance that amplification of
 CC the genomic DNA can be performed and preferably includes inosine. The
 CC method is useful for the genetic analysis of an individual organism,
 CC particularly of a species or individual. It is also useful for the rapid
 CC and straight forward identification of endangered animals or plants. The
 CC present DNA sequence is a 5' variation generator oligonucleotide PCR
 CC primer

XX SQ Sequence 17 BP; 8 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808

DB 17 TGTGTGTGTGTGTGTG 2

RESULT 241

AAAD17597/c

ID AAAD17597 standard; DNA; 17 BP.

XX AC AAAD17597;

XX DT 10-DEC-2001 (first entry)

XX DE 5' variation generator oligonucleotide PCR primer #12.

XX KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;

XX KW endangered animal identification; PCR primer; ss.

XX OS Unidentified.

XX PN EP1130114-A1.

XX PD 05-SEP-2001.

XX PF 03-MAR-2000; 2000EP-00200757.

XX PR 03-MAR-2000; 2000EP-00200757.

XX PA (VHAE-) VAN HAERINGEN LAB BV.

XX PI Van Haringen H, Van Haringen WA;

XX DR WPI; 2001-572636/65.

XX PT Analyzing genomic DNA in a sample, useful for analyzing genes of

XX PT organisms (e.g. a species or individual) or identifying endangered

XX PT animals or plants, by using oligonucleotide primers comprising universal

XX PT variable fragments.

XX PS Example 1; Page 6; 23pp; English.

XX CC The patent discloses a method and associated kit for analysing genomic

XX CC DNA in a sample. The method comprises conducting a nucleic acid

XX CC amplification on the genomic DNA in the sample using both first and

XX CC second oligonucleotide primer to produce DNA fragments based on repeat

XX CC sequences on at least one end of the genomic DNA. The first primer is a

XX CC 5' variation generator including a repeat sequence and at least one non-

XX CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment

XX CC generator starting within such a genetic distance that amplification of

XX CC the genomic DNA can be performed and preferably includes inosine. The

XX CC method is useful for the genetic analysis of an individual organism,

XX CC particularly of a species or individual. It is also useful for the rapid

XX CC and straight forward identification of endangered animals or plants. The

XX CC present DNA sequence is a 5' variation generator oligonucleotide PCR

XX CC primer

```

XX SQ Sequence 17 BP; 8 A; 9 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
DB 17 TGTGTGTGTGTGTGTG 2

RESULT 242
AAD17595
ID AAD17595 standard; DNA; 17 BP.
XX AC AAD17595;
XX DT 10-DEC-2001 (first entry)
XX DE 5' variation generator oligonucleotide PCR primer #10.
XX KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;
XX KW endangered animal identification; PCR primer; ss.
XX OS Unidentified.
XX PN EP1130114-A1.
XX PD 05-SEP-2001.
XX PF 03-MAR-2000; 2000EP-00200757.
XX PR 03-MAR-2000; 2000EP-00200757.
XX PR 03-MAR-2000; 2000EP-00200757.
XX PA (VHAE-) VAN HAERINGEN LAB BV.
XX PI Van Haringen H, Van Haringen WA;
XX DR WPI; 2001-572636/65.
XX PT Analyzing genomic DNA in a sample, useful for analyzing genes of
XX PT organisms (e.g. a species or individual) or identifying endangered
XX PT animals or plants, by using oligonucleotide primers comprising universal
XX PT variable fragments.
XX PS Example 1; Page 6; 23pp; English.
XX CC The patent discloses a method and associated kit for analysing genomic
XX CC DNA in a sample. The method comprises conducting a nucleic acid
XX CC amplification on the genomic DNA in the sample using both first and
XX CC second oligonucleotide primer to produce DNA fragments based on repeat
XX CC sequences on at least one end of the genomic DNA. The first primer is a
XX CC 5' variation generator including a repeat sequence and at least one non-
XX CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment
XX CC generator starting within such a genetic distance that amplification of
XX CC the genomic DNA can be performed and preferably includes inosine. The
XX CC method is useful for the genetic analysis of an individual organism,
XX CC particularly of a species or individual. It is also useful for the rapid
XX CC and straight forward identification of endangered animals or plants. The
XX CC present DNA sequence is a 5' variation generator oligonucleotide PCR
XX CC primer
XX SQ Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
DB 2 TGTGTGTGTGTGTGTG 17

RESULT 244
AAD17598/c
ID AAD17598 standard; DNA; 17 BP.
XX AC AAD17598;
XX DT 10-DEC-2001 (first entry)
XX DE 5' variation generator oligonucleotide PCR primer #13.
XX
```

```

RESULT 243
AAD17596
ID AAD17596 standard; DNA; 17 BP.
XX AC AAD17596;
XX DT 10-DEC-2001 (first entry)
XX DE 5' variation generator oligonucleotide PCR primer #11.
XX KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;
XX KW endangered animal identification; PCR primer; ss.
XX OS Unidentified.
XX PN EP1130114-A1.
XX PD 05-SEP-2001.
XX PF 03-MAR-2000; 2000EP-00200757.
XX PR 03-MAR-2000; 2000EP-00200757.
XX PR (VHAE-) VAN HAERINGEN LAB BV.
XX PI Van Haringen H, Van Haringen WA;
XX DR WPI; 2001-572636/65.
XX PT Analyzing genomic DNA in a sample, useful for analyzing genes of
XX PT organisms (e.g. a species or individual) or identifying endangered
XX PT animals or plants, by using oligonucleotide primers comprising universal
XX PT variable fragments.
XX PS Example 1; Page 6; 23pp; English.
XX CC The patent discloses a method and associated kit for analysing genomic
XX CC DNA in a sample. The method comprises conducting a nucleic acid
XX CC amplification on the genomic DNA in the sample using both first and
XX CC second oligonucleotide primer to produce DNA fragments based on repeat
XX CC sequences on at least one end of the genomic DNA. The first primer is a
XX CC 5' variation generator including a repeat sequence and at least one non-
XX CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment
XX CC generator starting within such a genetic distance that amplification of
XX CC the genomic DNA can be performed and preferably includes inosine. The
XX CC method is useful for the genetic analysis of an individual organism,
XX CC particularly of a species or individual. It is also useful for the rapid
XX CC and straight forward identification of endangered animals or plants. The
XX CC present DNA sequence is a 5' variation generator oligonucleotide PCR
XX CC primer
XX SQ Sequence 17 BP; 0 A; 1 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
DB 2 TGTGTGTGTGTGTGTG 17

RESULT 244
AAD17598/c
ID AAD17598 standard; DNA; 17 BP.
XX AC AAD17598;
XX DT 10-DEC-2001 (first entry)
XX DE 5' variation generator oligonucleotide PCR primer #13.
XX
```

KW Genomic DNA analysis; 5' variation generator; 3' fragment generator;
 KW endangered animal identification; PCR primer; ss.
 OS Unidentified.
 XX EP1130114-A1.
 PN
 XX 05-SEP-2001.
 PD
 XX
 PF 03-MAR-2000; 2000EP-00200757.
 XX
 PR 03-MAR-2000; 2000EP-00200757.
 XX
 PA (VHAE-) VAN HAERINGEN LAB BV.
 XX
 PI Van Haringen H, Van Haringen WA;
 XX
 DR WPI; 2001-572636/65.
 XX
 XX Analyzing genomic DNA in a sample, useful for analyzing genes of
 PT organisms (e.g. a species or individual) or identifying endangered
 PT animals or plants, by using oligonucleotide primers comprising universal
 PT variable fragments.
 XX
 XX Example 1; Page 6; 23pp; English.
 PS
 CC The patent discloses a method and associated kit for analysing genomic
 CC DNA in a sample. The method comprises conducting a nucleic acid
 CC amplification on the genomic DNA in the sample using both first and
 CC second oligonucleotide primer to produce DNA fragments based on repeat
 CC sequences on at least one end of the genomic DNA. The first primer is a
 CC 5' variation generator including a repeat sequence and at least one non-
 CC repeat nucleotide. The second oligonucleotide primer is a 3' fragment
 CC generator starting within such a genetic distance that amplification of
 CC the genomic DNA can be performed and preferably includes inosine. The
 CC method is useful for the genetic analysis of an individual organism,
 CC particularly of a species or individual. It is also useful for the rapid
 CC and straight forward identification of endangered animals or plants. The
 CC present DNA sequence is a 5' variation generator oligonucleotide PCR
 CC primer
 XX
 SQ Sequence 17 BP; 8 A; 8 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 1.5%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1793 TGTGTGTGTGTGTGTG 1808
 Db 17 TGTGTGTGTGTGTGTG 2
 RESULT 245
 AAX77462/C
 ID AAX77462 standard; DNA; 18 BP.
 AC AAX77462;
 XX
 DT 05-AUG-1999 (first entry)
 XX
 DE US5912147 primer 6.
 XX
 XX US5912147 primer 6.
 XX
 KW Primer; quantitation; genetic instability; tumour cell; detection;
 KW neoplastic transformation; carcinogenesis; ss.
 XX
 OS Synthetic.
 XX
 PN US5912147-A.
 XX
 PD 15-JUN-1999.
 XX
 PF 22-OCT-1996; 96US-00734973.
 XX
 PR (HEAL-) HEALTH RES INC.
 XX
 PA Anderson G, Stoler D, Basik M;
 XX
 PI WPI; 1999-357197/30.
 XX

PR 22-OCT-1996; 96US-00734973.
 XX (HEAL-) HEALTH RES INC.
 PA
 XX Anderson G, Stoler D, Basik M;
 PI
 XX WPI; 1999-357197/30.
 DR
 XX
 XX Quantitating genetic instability.
 PT
 XX
 PS Claim 4; Col 17-18; 27pp; English.
 XX
 CC This invention describes a novel method for quantitating genetic
 CC instability independent of microsatellite alterations by treating a
 CC comparison pair comprising genomic DNA from tumour cells and genomic DNA
 CC from normal cells. The method involves the cells from the same individual
 CC with oligonucleotide primers selected from (i) a nucleotide sequence
 CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
 CC 7, (ii) a nucleotide sequence (CG)XY, where R is as in (i) and Y is a
 CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
 CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
 CC nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
 CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
 CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
 CC 16, (vi) a nucleotide sequence (CA)XY, where R is a purine selected from
 CC adenine and guanine and Y is a pyrimidine selected from cytosine,
 CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
 CC where R is a purine selected from adenine and guanine and x = 6-16,
 CC (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
 CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
 CC of the primers. The method is useful for detecting genomic instability
 CC which are commonly associated with the various stages of neoplastic
 CC transformation and carcinogenesis. The method is rapid and simple
 XX
 SQ Sequence 18 BP; 8 A; 9 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 1.5%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1793 TGTGTGTGTGTGTGTG 1808
 Db 16 TGTGTGTGTGTGTGTG 1
 RESULT 246
 AAX77458/C
 ID AAX77458 standard; DNA; 18 BP.
 XX
 AC AAX77458;
 XX
 DT 05-AUG-1999 (first entry)
 XX
 DE US5912147 primer 2.
 XX
 XX US5912147 primer 2.
 KW Primer; quantitation; genetic instability; tumour cell; detection;
 KW neoplastic transformation; carcinogenesis; ss.
 XX
 OS Synthetic.
 XX
 PN US5912147-A.
 XX
 PD 15-JUN-1999.
 XX
 PF 22-OCT-1996; 96US-00734973.
 XX
 PR 22-OCT-1996; 96US-00734973.
 XX
 PA (HEAL-) HEALTH RES INC.
 XX
 PI Anderson G, Stoler D, Basik M;
 XX
 DR WPI; 1999-357197/30.
 XX

```

XX Quantitating genetic instability.
PT Claim 4; Col 17-18; 27pp; English.
PS
XX
XX This invention describes a novel method for quantitating genetic
XX instability independent of microsatellite alterations by treating a
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX from normal cells. The method involves the cells from the same individual
XX with oligonucleotide primers selected from (i) a nucleotide sequence
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
XX 7, (ii) a nucleotide sequence (CG)XY, where Y is as in (i) and Y is a
XX pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
XX a nucleotide sequence (CG)XRY, where R is as in (i) and x = 3-7, (iv) a
XX nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
XX cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
XX (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
XX 16, (vi) a nucleotide sequence (CA)XY, where Y is a purine selected from
XX adenine and guanine and Y is a pyrimidine selected from cytosine,
XX thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
XX where R is a purine selected from adenine and guanine and x = 6-16,
XX (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
XX from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
XX of the primers. The method is useful for detecting genomic instability
XX which are commonly associated with the various stages of neoplastic
XX transformation and carcinogenesis. The method is rapid and simple
XX
SQ Sequence 18 BP; 8 A; 8 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
DB 16 TGTGTGTGTGTGTGTG 1
RESULT 247
AAX77492/C
ID AAX77492 standard; DNA; 18 BP.
XX
XX AAX77492;
AC AAX77492;
XX
XX 05-AUG-1999 (first entry)
DT
XX
XX US5912147 primer 36.
DE
XX
XX Primer; quantitation; genetic instability; tumour cell; detection;
XX neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
XX
XX Synthetic.
OS
XX
XX US5912147-A.
PN
XX
XX 15-JUN-1999.
PD
XX
XX 22-OCT-1996; 96US-00734973.
PF
XX
XX 22-OCT-1996; 96US-00734973.
PR
XX
XX (HEAL-) HEALTH RES INC.
PA
XX
XX Anderson G, Stoler D, Basik M;
PI
XX
XX WPI; 1999-357197/30.
DR
XX
XX Quantitating genetic instability.
PT
XX
XX Claim 4; Col 29-30; 27pp; English.
XX
XX This invention describes a novel method for quantitating genetic
XX instability independent of microsatellite alterations by treating a
XX comparison pair comprising genomic DNA from tumour cells and genomic DNA
XX from normal cells. The method involves the cells from the same individual
XX with oligonucleotide primers selected from (i) a nucleotide sequence
XX (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
XX 7, (ii) a nucleotide sequence (CG)XY, where Y is as in (i) and Y is a
XX pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
XX a nucleotide sequence (CG)XRY, where R is as in (i) and x = 3-7, (iv) a
XX nucleotide sequence (CG)XY, where Y is a pyrimidine selected from
XX cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
XX (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
XX 16, (vi) a nucleotide sequence (CA)XY, where Y is a purine selected from
XX adenine and guanine and Y is a pyrimidine selected from cytosine,
XX thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
XX where R is a purine selected from adenine and guanine and x = 6-16,
XX (viii) a nucleotide sequence (CA)XY, where Y is a pyrimidine selected
XX from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
XX of the primers. The method is useful for detecting genomic instability
XX which are commonly associated with the various stages of neoplastic
XX transformation and carcinogenesis. The method is rapid and simple
XX
SQ Sequence 18 BP; 8 A; 8 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
DB 16 TGTGTGTGTGTGTGTG 1
RESULT 247
AAX77492/C
ID AAX77492 standard; DNA; 18 BP.
XX
XX AAX77492;
AC AAX77492;
XX
XX 05-AUG-1999 (first entry)
DT
XX
XX US5912147 primer 36.
DE
XX
XX Primer; quantitation; genetic instability; tumour cell; detection;
XX neoplastic transformation; carcinogenesis; DNA/RNA hybrid; ss.
XX
XX Synthetic.
OS
XX
XX US5912147-A.
PN
XX
XX 15-JUN-1999.
PD
XX
XX 22-OCT-1996; 96US-00734973.
PF
XX
XX 22-OCT-1996; 96US-00734973.
PR
XX
XX (HEAL-) HEALTH RES INC.
PA
XX
XX Anderson G, Stoler D, Basik M;
PI
XX
XX WPI; 1999-357197/30.
DR
XX
XX Quantitating genetic instability.
PT

```


CC with oligonucleotide primers selected from (i) a nucleotide sequence
 CC (CG)XRG, where R is a purine selected from adenine and guanine and x = 3-
 CC 7, (ii) a nucleotide sequence (CG)XYR, where R is as in (i) and Y is a
 CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)
 CC a nucleotide sequence (CG)XRR, where R is as in (i) and x = 3-7, (iv) a
 CC nucleotide sequence (CG)XXY, where Y is a pyrimidine selected from
 CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence
 CC (CA)XRG, where R is a purine selected from adenine and guanine and x = 6-
 CC 16, (vi) a nucleotide sequence (CA)XYR, where R is a purine selected from
 CC adenine and guanine and Y is a pyrimidine selected from cytosine,
 CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)XRR,
 CC where R is a purine selected from adenine and guanine and x = 6-16,
 CC (viii) a nucleotide sequence (CA)XXY, where Y is a pyrimidine selected
 CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination
 CC of the primers. The method is useful for detecting genomic instability
 CC which are commonly associated with the various stages of neoplastic
 CC transformation and carcinogenesis. The method is rapid and simple
 XX
 SQ Sequence 18 BP; 8 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
 DB 16 TGTGTGTGTGTGTGTG 1

RESULT 249
 ABZ89513
 ID ABZ89513 standard; DNA; 20 BP.
 AC ABZ89513;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 FN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPTG-) EPIGENESIS PHARM INC.
 PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 4755; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 20 BP; 3 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 1.5%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
 DB 1 TTTTATTTTGTGTTT 16

RESULT 250
 AAQ75552
 ID AAQ75552 standard; DNA; 19 BP.
 AC AAQ75552;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.5%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1865 TTTTATTTTTGTTTTTAA 1883
||||| ||||| |||||
1 TTTTATTTTTTTTTTAA 19

RESULT 251
AAQ34094/c
AAQ34094 standard; DNA; 40 BP.
AAQ34094;
XX XX
25-MAR-2003 (revised)
02-FEB-1993 (first entry)
XX XX
Sequence of a microsatellite from clone TGLA53.
XX XX
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
XX XX
Bos taurus.
XX XX
W09213102-A1.
XX XX
06-AUG-1992.
XX XX
15-JAN-1992; 92WO-US000340.
XX XX
15-JAN-1991; 91US-00642342.
XX XX
(GENN-) GENMARK.
XX XX
Georges M, Massey JM;
XX XX
WPI; 1992-284684/34.
XX XX
Polymorphic bovine DNA markers - used in genetic identification, gene
mapping, and selective breeding.
XX XX
Table 7; Page 369; 517pp; English.
XX XX
The sequence is that of a bovine microsatellite sequence obt'd. by
screening a library of bovine MbolI DNA fragments of between 250 and 500
bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
clones cross-hybridised. Assuming independent distribution of
microsatellites and MbolI sites, the frequency of (T)n > 9 microsatellites
in the bovine genome is estimated at >100, 000. The sequence information
for ca. 230 such bovine microsatellites is summarised in the
specification and indexed herein (see below). The sequences upstream and
downstream of the microsatellite sequence were used to generate the
required PCR primers for in vitro amplification of the corresp.
microsatellite (using the program OPTIPRIM). The microsatellites may be
used to identify individuals, for parentage testing, and in the genetic
mapping of economic trait loci, or genes involved in the determination of
economically important traits esp. in cattle, to allow selective
breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
field.)
XX XX
Sequence 40 BP; 7 A; 1 C; 13 G; 19 T; 0 U; 0 Other;
XX XX

Query Match 1.5%; Score 15.8; DE 1; Length 40;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1814 ATATATATATATATGTCACA 1832
||||| ||||| |||||
39 ATATATATATATATACACA 21

QY
Db

RESULT 252
AAT27914

AAT27914 standard; DNA; 18 BP.

AAT27914;

28-JAN-1997 (first entry)

5'-anchored simple sequence repeat primer HVH(TG)7.5.

Detection; polymorphism; perfect compound simple sequence repeat; adaptor directed primer; genome; genetic; fingerprinting; amplified fragment length polymorphism assay; microsatellite region; genetic trait marking; germplasm comparisons; 5'-anchored; ss.

Synthetic.

MO9617082-A2.

06-JUN-1996.

21-NOV-1995; 95WO-USO15150.

28-NOV-1994; 94US-00346456.

(DUPO) DU PONT DE NEMOURS & CO E I.

Morgante M, Vogel JM;

WFI; 1996-277795/28.

Modified amplified fragment length polymorphism assay - for detection of polymorphism esp. in micro:satellite regions.

Example 1; Page 77; 173pp; English.

Detecting polymorphisms between 2 nucleic acid samples, esp. in microsatellite regions, comprises digesting the nucleic acid to generate fragments, ligating adaptor segments to their ends, amplifying them using primer directed amplification and comparing the prods. to detect differences. The primers used in the amplification comprise a primer consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor directed primer, comprising a sequence complementary to an adaptor segment. The present sequence is an example of a SSR primer, which is flanked at its 5'-end by degenerate nucleotides. The method represents a modified amplified fragment length polymorphism assay, which is partic. useful for genome fingerprinting, i.e. for genetic trait marking and germplasm comparisons

Sequence 18 BP; 0 A; 0 C; 7 G; 8 T; 0 U; 3 Other;

Query Match 1.5%; Score 15.6; DB 1; Length 18;
Best Local Similarity 83.3%; Pred.No.1.8e+02;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1790 TATTGTGTGTGTGTGT 1807
:::|||||

DB 1 HVHTGTGTGTGTGT 18

RESULT 253
AAV91399
ID AAV91399 standard; RNA; 17 BP.
XX
AC AAV91399;
XX
DT 18-FEB-1999 (first entry)
XX
DE Human C-raf target site nucleotide position 2899.
XX
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; Genetic drift;
KW restenosis; rheumatoid arthritis; ss.

XX OS Homo sapiens.
 XX PN WO9850530-A2.
 XX PD 12-NOV-1998.
 XX PF 05-MAY-1998; 98WO-US009249.
 XX PR 09-MAY-1997; 97US-0046059P.
 XX PR 09-JUN-1997; 97US-0049002P.
 XX PR 03-JUL-1997; 97US-0051718P.
 XX PR 22-AUG-1997; 97US-0056808P.
 XX PR 02-OCT-1997; 97US-0061321P.
 XX PR 02-OCT-1997; 97US-0061324P.
 XX PR 05-NOV-1997; 97US-0064866P.
 XX PR 19-DEC-1997; 97US-0068212P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 XX PI Parry T, Beigelman L, Meswigen JA, Karpelisky A, Burgin A;
 XX PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX DR WPI; 1999-009494/01.
 XX PS Identifying new catalytic nucleic acid that modulates selected processes
 XX PT - especially ribozymes that cleave Raf RNA for treating cancer.
 XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 XX PT used as antiviral agents and synthons.
 XX PS Claim 177; Page 154; 259pp; English.
 XX CC A method has been developed for the identification of a nucleic acid
 XX CC capable of modulating a process in a biological system. The method
 XX CC comprises: (a) introducing into the system a random library of nucleic
 XX CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 XX CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 XX CC in systems where modulation has occurred and/or determining the sequence
 XX CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 XX CC endonuclease activity and catalytic activity, from the present invention,
 XX CC are used to modulate gene expression in plant and mammalian cells and to
 XX CC cleave target nucleic acid, particularly for treating systemic diseases
 XX CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 XX CC ascites and infection. They may also be used to detect genetic drift and
 XX CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
 XX CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 XX CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 XX CC generally any condition associated with the level of c-rat. Introduction
 XX CC of sugar/phosphate modifications increases stability against nuclease and
 XX CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 XX CC method, specifically for modulating the expression of a Raf gene
 XX SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;
 Query Match 1.5%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 17.6%; Pred. No. 1.8e+02;
 Matches 3; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
 QY 1866 TTTTATTTTGTGTTTA 1882
 Db 1 UUUUAUUUUUUUUU 17
 RESULT 254
 AAV21967
 ID AAV21967 standard; DNA; 18 BP.
 XX AC AAV21967;
 XX DT 14-JUL-1998 (first entry)
 XX DE Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.

XX KW Nuclease resistant; bacterial infection; antibiotic; target;
 KW veterinary medicine; treatment; human; industrial process;
 KW bacterial control; ss.
 XX OS Synthetic.
 XX PN WO9803533-A1.
 XX PD 29-JAN-1998.
 XX PF 23-JUL-1997; 97WO-US012961.
 XX PR 24-JUL-1996; 96US-00685575.
 XX PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
 XX PI Arrow A, Dale RMK, Thompson TL;
 XX DR WPI; 1998-120687/11.
 XX PT Treating bacterial infections in humans or animals with
 XX PT oligo:nucleotide(s) resistant to nuclease and targeted to bacterial
 XX PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
 XX PT with antibiotics.
 XX PS Claim 49; Page 87; 163pp; English.
 XX CC This antisense oligonucleotide is nuclease resistant and can be used in
 XX CC the treatment of animals, including humans, having a bacterial infection.
 XX CC The treatment comprises administration of such nuclease resistant
 XX CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
 XX CC and formulated with a carrier. A compound comprising this nuclease
 XX CC resistant oligonucleotide can be covalently linked to an antibiotic. The
 XX CC method is used to treat infections by a wide variety of Gram-positive and
 XX CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
 XX CC The methods are particularly used in immuno-compromised individuals (e.g.
 XX CC patients with acquired immunodeficiency syndrome or those receiving
 XX CC chemotherapy or radiation therapy), optionally in combination with, or
 XX CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from
 XX CC therapeutic use, the oligonucleotides can be used to control bacteria in
 XX CC laboratory cultures, foods, beverages and industrial processes. The
 XX CC oligonucleotides are specific for bacteria, without affecting metabolism
 XX CC in mammalian cells. They may also activate RNase H and have a general,
 XX CC non-specific immune-stimulating effect. The oligonucleotides can be
 XX CC administered orally, intranasally, rectally, topically or by injection,
 XX CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that
 XX CC enhances cellular uptake
 XX SQ Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
 Query Match 1.5%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1814 ATATATATATATATGTA 1830
 Db 1 ATATATATATATATATA 17
 RESULT 255
 AAV21967/c
 ID AAV21967 standard; DNA; 18 BP.
 XX AC AAV21967;
 XX DT 14-JUL-1998 (first entry)
 XX DE Nuclease resistant antisense oligo NBT 140 targeted against (AT)9.
 XX KW Nuclease resistant; bacterial infection; antibiotic; target;
 KW veterinary medicine; treatment; human; industrial process;
 KW bacterial control; ss.

XX OS Synthetic.
 XX PN WO9803533-A1.
 XX PD 29-JAN-1998.
 XX PF 23-JUL-1997; 97WO-US012961.
 XX PR 24-JUL-1996; 96US-00685575.
 XX PA (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
 XX PI Arrow A, Dale RMK, Thompson TL;
 XX DR WPI; 1998-120687/11.
 XX PT Treating bacterial infections in humans or animals with
 PT oligonucleotide(s) - resistant to nuclease and targetted to bacterial
 PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
 PT with antibiotics.
 XX PS Claim 49; Page 87; 163pp; English.
 XX CC This antisense oligonucleotide is nuclease resistant and can be used in
 CC the treatment of animals, including humans, having a bacterial infection.
 CC The treatment comprises administration of such nuclease resistant
 CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
 CC and formulated with a carrier. A compound comprising this nuclease
 CC resistant oligonucleotide can be covalently linked to an antibiotic. The
 CC method is used to treat infections by a wide variety of Gram-positive and
 CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
 CC The methods are particularly used in immuno-compromised individuals (e.g.
 CC patients with acquired immunodeficiency syndrome or those receiving
 CC chemotherapy or radiation therapy), optionally in combination with, or
 CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from
 CC therapeutic use, the oligonucleotides can be used to control bacteria in
 CC laboratory cultures, foods, beverages and industrial processes. The
 CC oligonucleotides are specific for bacteria, without affecting metabolism
 CC in mammalian cells. They may also activate RNase H and have a general,
 CC non-specific immune-stimulating effect. The oligonucleotides can be
 CC administered orally, intranasally, rectally, topically or by injection,
 CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that
 CC enhances cellular uptake
 XX SQ Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
 Query Match 1.5%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1814 ATATATATATATATGTA 1830
 DB 18 ATATATATATATATATA 2
 RESULT 256
 AAH37514
 ID AAH37514 standard; DNA; 18 BP.
 XX AC AAH37514;
 XX DT 14-AUG-2001 (first entry)
 XX DE SNP specific lower PCR primer SEQ ID 310.
 XX KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNPs; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.

OS Homo sapiens.
 XX PN WO200129262-A2.
 XX PD 26-APR-2001.
 XX PF 13-OCT-2000; 2000WO-US028436.
 XX PR 15-OCT-1999; 99US-0160096P.
 XX PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX PI Picoult-Newburg L, Pohl M;
 XX DR WPI; 2001-290930/30.
 XX PT New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX PS Claim 1; Page 51; 83pp; English.
 XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence
 XX SQ Sequence 18 BP; 0 A; 2 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 1.5%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTGTGTG 1810
 DB 1 GTGTGTGTGTGTGTGCG 17
 RESULT 257
 ABL38718
 ID ABL38718 standard; DNA; 18 BP.
 XX AC ABL38718;
 XX DT 16-APR-2002 (first entry)
 XX DE Immunostimulatory nucleic acid SEQ ID NO: 85.
 XX KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers

modified_base 1..18
 /*tag= a
 /mod_base= OTHER
 /note= "phosphorothioate backbone"

WO200197843-A2.
 27-DEC-2001.
 22-JUN-2001; 2001WO-US020154.
 22-JUN-2000; 2000US-0213346P.
 (IOWA) UNIV IOWA RES FOUND.
 Weiner G, Hartmann G;
 WPI; 2002-154611/20.

Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of developing cancer.

Disclosure; Page 116; 312pp; English.

The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention

Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.5%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830
 |||||
 Db 1 ATATATATATATATA 17

RESULT 258
 ABL38718/c
 ID ABL38718 standard; DNA; 18 BP.
 AC ABL38718;
 DT 16-APR-2002 (first entry)
 DE Immunostimulatory nucleic acid SEQ ID NO: 85.
 XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH modified_base 1..18
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"

PN WO200197843-A2.
 XX 27-DEC-2001.
 PD 22-JUN-2001; 2001WO-US020154.
 XX 22-JUN-2000; 2000US-0213346P.
 XX (IOWA) UNIV IOWA RES FOUND.
 PA Weiner G, Hartmann G;
 PI WPI; 2002-154611/20.
 DR Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of developing cancer.

Disclosure; Page 116; 312pp; English.

The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention

Sequence 18 BP; 9 A; 0 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.5%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.9e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATGTA 1830
 |||||
 Db 18 ATATATATATATATA 2

RESULT 259
 AAT27912/c
 ID AAT27912 standard; DNA; 18 BP.
 XX AAT27912;
 AC AAT27912;
 DT 28-JAN-1997 (first entry)
 DE 5'-anchored simple sequence repeat primer DBD(AC)7.5.
 XX Detection; polymorphism; perfect compound simple sequence repeat;
 KW adaptor directed primer; genome; genetic; fingerprinting;
 KW amplified fragment length polymorphism assay; microsatellite region;
 KW genetic trait marking; germplasm comparisons; 5'-anchored; ss.
 XX Synthetic.
 OS WO9617082-A2.
 XX 06-JUN-1996.
 PD 21-NOV-1995; 95WO-US015150.
 XX 28-NOV-1994; 94US-00346456.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA

Db 1 GTGTGTGTGTGTGTG 15

RESULT 262

AAH31678

ID AAX31678 standard; DNA; 15 BP.

XX AC AAX31678;

XX 21-MAY-1999 (first entry)

XX Tag sequence of a transcript increased in pancreatic cancer.

XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;

XX diagnosis; prognosis; treatment; ss.

XX Homo sapiens.

XX WO9853319-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US010277.

XX 21-MAY-1997; 97US-0047352P.

XX (UJJO) UNIV JOHNS HOPKINS.

XX Vogelstein B, Kinzler KW;

XX WPI; 1999-070161/06.

XX Use of isolated gene transcripts - useful for developing products for the

XX diagnosis, prognosis and treatment of cancers, particularly colon and

XX pancreatic cancer.

XX Claim 13; Page 69; 120pp; English.

XX AAX30947-31815 represent tag sequences of transcripts that are

XX differentially expressed in colorectal cancer, in pancreatic cancer, or

XX in both. The tag sequences can be used to identify genes by matching the

XX tag to a gen data base member, or by using the tag sequences as probes to

XX isolate unidentified genes from cDNA libraries. The tag sequences can

XX also be used in a method for diagnosing colon or pancreatic cancer in a

XX sample suspected of being neoplastic. The method comprises comparing the

XX level of at least one transcript in a first sample of a tissue to a

XX second sample, where the first sample is a colonic tissue suspected of

XX being neoplastic and the second sample is a normal human colonic tissue.

XX The transcript is identified by a tag selected from AAX30947-31815. The

XX methods of the invention can be used in the diagnosis, prognosis and

XX treatment of cancer

XX Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other;

XX Query Match 1.4%; Score 15; DB 1; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2231 CATGTTTGCACCTTT 2245

Db 1 CATGTTTGCACCTTT 15

RESULT 263

AAH46010

ID AAH46010 standard; DNA; 15 BP.

XX AC AAH46010;

XX 12-SEP-2001 (first entry)

XX Synthetic oligonucleotide 10.

KW Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;

KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;

KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;

XX lymphoma; ss.

XX Synthetic.

XX WO200144465-A2.

XX 21-JUN-2001.

XX 12-DEC-2000; 2000WO-CA001467.

XX 13-DEC-1999; 99US-0170325P.

XX 29-AUG-2000; 2000US-0228925P.

XX (BION-) BIONICHE LIFE SCI INC.

XX Phillips NC, Filion MC;

XX WPI; 2001-398150/42.

XX Composition comprising synthetic oligonucleotides which comprise multiple

XX repeats of dinucleotides such as GT, TG useful for treating cancer by

XX inducing cell cycle arrest, inhibiting proliferation, activating

XX caspases.

XX Claim 5; Page 17; 77pp; English.

XX The present sequence is that of a synthetic oligonucleotide useful to the

XX invention. The invention relates to a composition, comprising a 2 to 20

XX base 3'-OH, 5'-OH synthetic oligonucleotide which comprises multiple

XX repeats of dinucleotides such as GT, TG, etc. according to specific

XX formula and having cytostatic activity. The oligonucleotide compositions

XX are useful for inducing cell cycle arrest, inhibition of proliferation,

XX activation of caspases and induction of apoptosis or production of

XX cytokines such as interleukin (IL)-1-beta, IL-6, IL-10, IL-12 and tumour

XX necrosis factor (TNF)-alpha by immune system cells, in an animal having

XX cancer such as primary carcinoma, secondary carcinoma, primary sarcoma

XX and secondary sarcoma such as, leukemia, lymphoma, breast, prostate,

XX colorectal, ovarian or bone cancer. The compositions induce apoptosis

XX independent of Fas, p53/p21, p21/waf-1/Cip, p15(Ink4B), p16(Ink4), drug

XX resistance, caspase 3, transforming growth factor (TGF)-beta 1 receptor

XX and hormone dependence

XX Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;

XX Query Match 1.4%; Score 15; DB 1; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTG 1808

Db 1 GTGTGTGTGTGTGTG 15

RESULT 264

ABK32632

ID ABK32632 standard; DNA; 15 BP.

XX AC ABK32632;

XX 23-APR-2002 (first entry)

XX Human pancreatic cancer SAGE tag #184.

XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;

XX serial analysis of gene expression; diagnostic; prognostic; probe;

XX cancer marker; ss.

XX Homo sapiens.

XX US6333152-B1.

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XX PD 25-DEC-2001.
XX PF 20-MAY-1998; 98US-00081645.
XX PR 20-MAY-1998; 98US-00081645.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;
XX DR WPI; 2002-153821/20.
XX PT New human nucleic acid containing specific SAGE tags, useful as
XX PT diagnostic markers for cancer, also derived probes.
XX PS Disclosure; Col 83; 161pp; English.
XX CC The invention relates to an isolated, purified human nucleic acid (I)
XX CC that has the same sequence as a mRNA found in humans and is a SAGE
XX CC (serial analysis of gene expression) tag comprising a single stranded
XX CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
XX CC diagnostic and prognostic markers of cancer, especially of the colon and
XX CC pancreas. ABK1900-ABK3270 represent human colon and pancreatic cancer
XX CC SAGE tags of the invention
XX CC
XX CC Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2231 CATGTTGCACCTTT 2245
XX DB 1 CATGTTGCACCTTT 15
XX
XX RESULT 265
XX ID ABK90419 standard; DNA; 16 BP.
XX AC ABK90419;
XX DT 05-NOV-2002 (first entry)
XX DE Human UGT1A1 promoter polymorphism (TA)8 repeat.
XX KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
XX KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
XX KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
XX KW TAS-103; xenobiotic.
XX OS Homo sapiens.
XX PN US6395481-B1.
XX XX 28-MAY-2002.
XX PF 16-FEB-1999; 99US-00251274.
XX PR 16-FEB-1999; 99US-00251274.
XX PA (ARCH-) ARCH DEV CORP.
XX PI Di Rienzo A, Iyer L, Ratain MJ;
XX DR WPI; 2002-588597/63.
XX PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
XX PT gene promoter, useful for optimizing drug dosages for a patient,
XX PT comprises determining the presence of five thymidine-adenine repeats in
XX PT the promoter.

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PS Claim 7; Col 17; 13pp; English.
XX
XX CC The invention relates to detecting (M1) polymorphisms in a uridine
XX CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
XX CC the presence of five thymidine-adenine (TA) repeats in the promoter,
XX CC where the presence of the five TA repeats correlates with increased
XX CC expression of the gene. The method is used for detecting polymorphisms in
XX CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is
XX CC useful for screening individuals for variation in glucuronidation
XX CC activity, for optimising drug dosages for a patient, where the drugs
XX CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
XX CC UGT1A1) and the activity of the drug is effected by its level of
XX CC glucuronidation. The method preferably involves obtaining DNA from an
XX CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
XX CC promoter) contained in the DNA and determining the number of TA repeats
XX CC in the promoter. Thus the DNA being amplified comprises all or part of
XX CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
XX CC the number of TA repeats is determined by gel electrophoresis or by
XX CC sequencing the amplified DNA. The polymorphism comprises an allele
XX CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
XX CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
XX CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
XX CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's
XX CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
XX CC UGT1A1) gene product, the method comprising determining the number of TA
XX CC repeats in a UGT gene promoter, where the number of TA repeats correlates
XX CC with expression of the UGT gene, and the individuals sensitivity to
XX CC xenobiotics is effected by glucuronidation activity. The methods
XX CC preferably involve determining the presence of five, six or seven TA
XX CC repeats in the promoter. Defects in glucuronidation is associated with
XX CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
XX CC present sequence is the UGT1A1 promoter (TA)8 repeat
XX
XX CC Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 1.4%; Score 15; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1813 TATATATATATATAT 1827
XX DB 1 TATATATATATATAT 15
XX
XX RESULT 266
XX ID ABK90419/C
XX AC ABK90419;
XX DT 05-NOV-2002 (first entry)
XX DE Human UGT1A1 promoter polymorphism (TA)8 repeat.
XX KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
XX KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
XX KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
XX KW TAS-103; xenobiotic.
XX OS Homo sapiens.
XX PN US6395481-B1.
XX XX 28-MAY-2002.
XX PF 16-FEB-1999; 99US-00251274.
XX PR 16-FEB-1999; 99US-00251274.
XX PA (ARCH-) ARCH DEV CORP.
XX PI Di Rienzo A, Iyer L, Ratain MJ;
XX DR WPI; 2002-588597/63.
XX PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
XX PT gene promoter, useful for optimizing drug dosages for a patient,
XX PT comprises determining the presence of five thymidine-adenine repeats in
XX PT the promoter.

```


CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
 CC UGT1A1). The method involves determining the number of thymidine-adenine
 CC (TA) repeats in the promoter - as the number of TA repeats correlates
 CC with expression of the UGT gene. The method of the invention is useful
 CC for detecting polymorphisms in a UGT gene promoter. The method of the
 CC invention is also useful in optimizing drug dosages and predicting an
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
 CC TA repeat polymorphism

XX
 SQ Sequence 16 BP; 8 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
 |||||
 DB 16 TATATATATATATAT 2

RESULT 269
 ABK90422
 ID ABK90422 standard; DNA; 17 BP.
 XX AC ABK90422;
 XX 05-NOV-2002 (first entry)
 XX Human UGT1A1 promoter polymorphism (TA)7 repeat region.
 XX Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
 KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
 KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
 KW TAS-103; xenobiotic.
 XX Homo sapiens.
 OS US6395481-B1.
 PN 28-MAY-2002.
 XX 16-FEB-1999; 99US-00251274.
 XX 16-FEB-1999; 99US-00251274.
 XX (ARCH-) ARCH DEV CORP.
 PA Di Rienzo A, Iyer L, Ratain MJ;
 PI WPI; 2002-588597/63.
 XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
 PT gene promoter, useful for optimizing drug dosages for a patient,
 PT comprises determining the presence of five thymidine-adenine repeats in
 PT the promoter.
 XX Example 6; Col 11; 13pp; English.

CC The invention relates to detecting (M1) polymorphisms in a uridine
 CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
 CC the presence of five thymidine-adenine (TA) repeats in the promoter,
 CC where the presence of the five TA repeats correlates with increased
 CC expression of the gene. The method is used for detecting polymorphisms in
 CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is
 CC useful for screening individuals for variation in glucuronidation
 CC activity, for optimising drug dosages for a patient, where the drugs
 CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
 CC UGT1A1) and the activity of the drug is affected by its level of
 CC glucuronidation. The method preferably involves obtaining DNA from an
 CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
 CC promoter) contained in the DNA and determining the number of TA repeats
 CC in the promoter. Thus the DNA being amplified comprises all or part of

CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
 CC the number of TA repeats is determined by gel electrophoresis or by
 CC sequencing the amplified DNA. The polymorphism comprises an allele
 CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
 CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
 CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
 CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's
 CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
 CC UGT1A1) gene product, the method comprising determining the number of TA
 CC repeats in a UGT gene promoter, where the number of TA repeats correlates
 CC with expression of the UGT gene, and the individual's sensitivity to
 CC xenobiotics is affected by glucuronidation activity. The methods
 CC preferably involve determining the presence of five, six or seven TA
 CC repeats in the promoter. Defects in glucuronidation is associated with
 CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
 CC present sequence is the UGT1A1 promoter (TA)7 repeat region

XX
 SQ Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
 Query Match 1.4%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
 |||||
 DB 1 TATATATATATATAT 15

RESULT 270
 ABK90422/c
 ID ABK90422 standard; DNA; 17 BP.
 XX AC ABK90422;
 XX 05-NOV-2002 (first entry)
 XX Human UGT1A1 promoter polymorphism (TA)7 repeat region.
 XX Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
 KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
 KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
 KW TAS-103; xenobiotic.
 XX Homo sapiens.
 OS US6395481-B1.
 PN 28-MAY-2002.
 XX 16-FEB-1999; 99US-00251274.
 XX 16-FEB-1999; 99US-00251274.
 XX (ARCH-) ARCH DEV CORP.
 PA Di Rienzo A, Iyer L, Ratain MJ;
 PI WPI; 2002-588597/63.
 XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
 PT gene promoter, useful for optimizing drug dosages for a patient,
 PT comprises determining the presence of five thymidine-adenine repeats in
 PT the promoter.
 XX Example 6; Col 11; 13pp; English.

CC The invention relates to detecting (M1) polymorphisms in a uridine
 CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
 CC the presence of five thymidine-adenine (TA) repeats in the promoter,
 CC where the presence of the five TA repeats correlates with increased
 CC expression of the gene. The method is used for detecting polymorphisms in
 CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is
 CC useful for screening individuals for variation in glucuronidation

activity, for optimising drug dosages for a patient, where the drugs (e.g. irinotecan or TAS-103) are glucuronidated by UGT (preferably UGT1A1) and the activity of the drug is effected by its level of glucuronidation. The method preferably involves obtaining DNA from an individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene promoter) contained in the DNA and determining the number of TA repeats in the promoter. Thus the DNA being amplified comprises all or part of UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and the number of TA repeats is determined by gel electrophoresis or by sequencing the amplified DNA. The polymorphism comprises an allele consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5, (TA)5/(TA)6, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or (TA)8/(TA)8. (M1) is also useful for predicting an individual's sensitivity to xenobiotics that are glucuronidated by a UGT (preferably UGT1A1) gene product, the method comprising determining the number of TA repeats in a UGT gene promoter, where the number of TA repeats correlates with expression of the UGT gene, and the individuals sensitivity to xenobiotics is effected by glucuronidation activity. The methods preferably involve determining the presence of five, six or seven TA repeats in the promoter. Defects in glucuronidation is associated with Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The present sequence is the UGT1A1 promoter (TA)7 repeat region

XX Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1813 TATATATATATATAT 1827
DB 15 TATATATATATAT 2

RESULT 271
AAL50679
ID AAL50679 standard; DNA; 17 BP.
XX
AC AAL50679;
XX
XX 16-JAN-2003 (first entry)
XX
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #13.
XX
XX Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW drug dosage optimisation; xenobiotic sensitivity.
XX
XX Homo sapiens.
XX
XX US2002115097-A1.
XX
XX 22-AUG-2002.

XX
XX 01-FEB-2002; 2002US-00061693.
XX
XX 16-FEB-1999; 99US-00251274.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Rienzo AD, Iyer L, Ratain MJ;
XX
XX WPI; 2002-740095/80.
XX
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient, involves
PT determining number of thymidine-adenine repeats in the promoter.
XX
XX Example 6; Page 2; 13pp; English.
XX
XX The invention comprises a method for detecting polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably

CC UGT1A1). The method involves determining the number of thymidine-adenine
CC (TA) repeats in the promoter - as the number of TA repeats correlates
CC with expression of the UGT gene. The method of the invention is useful
CC for detecting polymorphisms in a UGT gene promoter. The method of the
CC invention is also useful in optimising drug dosages and predicting an
CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
CC TA repeat polymorphism
XX
XX Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1813 TATATATATATATAT 1827

DB 1 TATATATATATAT 15

RESULT 272
AAL50679/c
ID AAL50679 standard; DNA; 17 BP.
XX
XX AAL50679;
XX
XX 16-JAN-2003 (first entry)
XX
DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #13.
XX
XX Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
KW drug dosage optimisation; xenobiotic sensitivity.
XX
XX Homo sapiens.
XX
XX US2002115097-A1.
XX
XX 22-AUG-2002.

XX 01-FEB-2002; 2002US-00061693.
XX
XX 16-FEB-1999; 99US-00251274.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Rienzo AD, Iyer L, Ratain MJ;
XX
XX WPI; 2002-740095/80.
XX
XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
PT gene promoter, useful for optimizing drug dosages for a patient, involves
PT determining number of thymidine-adenine repeats in the promoter.
XX
XX Example 6; Page 2; 13pp; English.
XX
XX The invention comprises a method for detecting polymorphisms in a uridine
CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably

XX Sequence 17 BP; 9 A; 0 C; 0 G; 8 T; 0 U; 0 Other;
SQ

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
 |||||
Db . 16 TATATATATATAT 2

RESULT 273

ABZ60766
ID ABZ60766 standard; RNA; 17 BP.
XX AC
XX AC
XX XX
DT TT
TT DT
XX XX
DE Human K-Ras DNase substrate #878.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.
OS OS
XX WO200297114-A2.
PN PN
XX PD
PD O5-DEC-2002.
XX XX
PF 29-MAY-2002; 2002WO-USO16840.
XX PF
PR 29-MAY-2001; 2001US-0294140P.
PR PR
PR 06-JUN-2001; 2001US-0296249P.
PR PR
PR 10-SEP-2001; 2001US-0318471P.
XX XX
(RIBO-) RIBOZYME PHARM INC.
PA PA
XX PP
PI Mcswiggen J;
XX XX
DR DR
DX WFI; 2003-140484/13.
XX XX

Novel short interfering RNA and enzymatic nucleic acid useful for treating cancer, modulates the expression of a nucleic acid encoding HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

Claim 58; Page 101; 185pp; English.

The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytostatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ6520 - ABZ6524, ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention

Sequence 17 BP; 5 A; 3 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 66.7%; Pred.No.2e+02;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1391 TGTTAAGACTTGACA 1405
 ::::|||:
Dd 2 UGUUAAACUGUCAGA 16

RESULT 274
AAT27913/C
ID AAT27913 standard; DNA; 18 BP.
XX XX
XX AAT27913;
AC AC

PD 06-JUN-1996.
 XX 21-NOV-1995; 95WO-US015150.
 PF 28-NOV-1994; 94US-00346456.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Morgante M, Vogel JM;
 PI WPI; 1996-277795/28.
 DR Modified amplified fragment length polymorphism assay - for detection of
 PT polymorphism esp. in micro:satellite regions.
 XX Example 1; Page 77; 173pp; English.
 CC Detecting polymorphisms between 2 nucleic acid samples, esp. in
 CC microsatellite regions, comprises digesting the nucleic acid to generate
 CC fragments, ligating adaptor segments to their ends, amplifying them using
 CC primer directed amplification and comparing the prods. to detect
 CC differences. The primers used in the amplification comprise a primer
 CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor
 CC directed primer, comprising a sequence complementary to an adaptor
 CC segment. The present sequence is an example of a SSR primer, which is
 CC flanked at its 5'-end by degenerate nucleotides. The method represents a
 CC modified amplified fragment length polymorphism assay, which is partic.
 CC useful for genome fingerprinting, i.e. for genetic trait marking and
 CC germplasm comparisons
 XX Sequence 18 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 3 Other;
 XX
 Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTGTG 1808
 DB 4 GTGTGTGTGTGTGTG 18
 RESULT 276
 ABZ11102
 ID ABZ11102 standard; DNA; 18 BP.
 XX ABZ11102;
 AC
 XX 16-JAN-2003 (first entry)
 DT
 XX Haematopoietic cell proliferation disorder related oligonucleotide #1242.
 DE
 XX Human; haematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; probe; primer; ss.
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO200277272-A2.
 PN
 XX 03-OCT-2002.
 PD
 XX 26-MAR-2002; 2002WO-EP003401.
 PF
 XX 26-MAR-2001; 2001US-0278333P.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu B;
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwope I, Ziebarth H;
 XX

DR WPI; 2003-016942/01.
 XX Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.
 XX Claim 15; Page 69; 117pp; English.
 PS
 XX The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;
 XX
 Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1867 TTTATTTTGTGTTT 1881
 DB 1 TTTATTTTGTGTTT 15
 RESULT 277
 ABZ10510
 ID ABZ10510 standard; DNA; 18 BP.
 XX ABZ10510;
 AC
 XX 16-JAN-2003 (first entry)
 DT
 XX Haematopoietic cell proliferation disorder related oligonucleotide #650.
 DE
 XX Human; haematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; probe; primer; ss.
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO200277272-A2.
 PN
 XX 03-OCT-2002.
 PD
 XX 26-MAR-2002; 2002WO-EP003401.
 PF
 XX 26-MAR-2001; 2001US-0278333P.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu B;
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwope I, Ziebarth H;
 XX

XX WPI; 2003-018942/01.
 XX
 XX Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.
 XX
 XX Claim 15; Page 47; 117pp; English.
 PS
 XX The present invention describes a method for detecting and
 CC differentiating between hematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy hematopoietic cells and proliferative
 CC disorder hematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of hematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of hematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC hematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of hematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 XX Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;
 SQ
 Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1867 TTTATTTTGTGTTT 1881
 DB 1 TTTATTTTGTGTTT 15
 RESULT 278
 ADC70018
 ID ADC70018 standard; DNA; 18 BP.
 AC
 XX ADC70018;
 AC
 XX 18-DEC-2003 (first entry)
 DT
 XX Primer oligo used for analysing CpG islands in genomic DNA (SeqID 507).
 DE PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;
 XX adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;
 KW cytosine methylation state.
 KW
 XX Unidentified.
 OS
 XX WO2003052135-A2.
 XX
 XX 26-JUN-2003.
 PD
 XX 10-DEC-2002; 2002WO-EP014026.
 PF
 XX 14-DEC-2001; 2001DE-01061625.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Burger M, Field JK, Genc B, Lilloglou T, Lipscher E, Maier S;
 PI Nimmrich I;
 PI
 XX WPI; 2003-533029/50.
 DR

XX Detecting and differentiating cytosine methylation state of genomic DNA,
 PT useful for diagnosing, treating prognosticating and/or monitoring lung
 PT cell proliferative disorders e.g. adenocarcinoma and squamous cell
 PT carcinoma.
 XX
 XX Claim 15; SEQ ID NO 507; 58pp; English.
 PS
 XX This invention relates to a novel method for detecting and
 CC differentiating between lung cell proliferative disorders associated with
 CC at least one gene and/or their regulatory regions. Specifically, it
 CC refers to a method comprising contacting a target nucleic acid in a
 CC biological sample with at least one reagent, wherein the reagent is able
 CC to distinguish between methylated and non-methylated CpG dinucleotides
 CC present in the target DNA. As such, it is possible to further
 CC differentiate and diagnose medical conditions including adenocarcinoma
 CC and squamous cell carcinoma, and their respective adjacent lung tissue.
 CC The present invention describes cytostatic oligomers and PNA-oligomers
 CC that are useful as probes for determining the cytosine methylation state
 CC or single nucleotide polymorphisms (SNPs) of the target sequence. This
 CC oligonucleotide sequence is a primer oligomer used for the analysis of
 CC CpG positions within genomic DNA, used in an exemplification of the
 CC invention.
 XX
 XX Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;
 SQ
 Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1867 TTTATTTTGTGTTT 1881
 DB 1 TTTATTTTGTGTTT 15
 RESULT 279
 ADE84378
 ID ADE84378 standard; DNA; 18 BP.
 AC
 XX ADE84378;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX Human lymphoid cell proliferative disorder gene CpG analysis oligo #84.
 DE
 XX Lymphoid cell proliferative disorder; methylation;
 KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
 KW diffuse large B-cell lymphoma; mantle cell lymphoma;
 KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
 KW follicular lymphoma; diagnosis; prognosis; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO2003044226-A2.
 PN
 XX 30-MAY-2003.
 PD
 XX 25-NOV-2002; 2002WO-EP013265.
 PF
 XX 23-NOV-2001; 2001DE-01057491.
 PR
 XX 28-DEC-2001; 2001DE-01064501.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;
 PI WPI; 2003-457621/43.
 PI
 XX Detecting and differentiating between lymphoid cell proliferative
 PT disorders comprises contacting a target nucleic acid with at least one
 PT reagent that distinguishes between methylated and non-methylated CpG
 PT dinucleotides.
 PT
 XX

PS Claim 30; SEQ ID NO 374; 448pp; English.
 XX The invention relates to a method of detecting and differentiating
 CC between lymphoid cell proliferative disorders associated with at least
 CC one gene and/or their regulatory regions in a subject by contacting a
 CC target nucleic acid in a biological sample obtained from the subject with
 CC at least one reagent or series of reagents that distinguish between
 CC methylated and non-methylated CpG dinucleotides within the target nucleic
 CC acid. The genes and/or their regulatory regions are preferably selected
 CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GP1b beta, MYOD1, CDH3,
 CC MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2a, CDKN2B, FOS,
 CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKN1C,
 CC GSK3beta, SR1, AFAF1, BAK1, BAX or HOKAS. Oligomers, peptide nucleic
 CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
 CC of the genes are useful for detecting the methylation state of all the
 CC CpG dinucleotides within one or more the sequences, or their complements,
 CC for determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) and for differentiating at least two of the medical
 CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
 CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
 CC lymphoma. They are also useful for detecting of a predisposition to,
 CC differentiation between subclasses, diagnosis, prognosis, treating and/or
 CC monitoring of lymphoid cell proliferative disorder. This sequence
 CC represents an oligonucleotide used to analyse of CpG positions within the
 CC above mentioned genes.
 XX
 XX Sequence 18 BP; 1 A; 0 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 1.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1867 TTTATTTTCTTTT 1881
 DB 1 TTTATTTTCTTTT 15

RESULT 280
 ABK66312
 ID ABK66312 standard; DNA; 32 BP.
 XX
 AC ABK66312;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human gene specific PCR primer #400.
 KW Primer; ss; DNA microarray; differential expression analysis; human.
 XX Homo sapiens.
 OS
 PN US6352829-B1.
 XX
 PD 05-MAR-2002.
 XX
 PF 05-JAN-1999; 99US-00225928.
 XX
 PR 21-MAY-1997; 97US-00859998.
 XX
 PA (CLON-) CLONTECH LAB INC.
 XX
 PI Chenchik A, Johadze G, Bibilashvili R;
 XX
 DR WPI; 2002-314699/35.
 XX

Producing sub-population of labeled nucleic acids, useful for analyzing
 PT differences in RNA profiles between several different physiological
 PT sources, using set of distinct gene specific primers.
 XX
 PS Example 3; SEQ ID NO 400; 11pp; English.
 XX
 CC The invention relates to producing a sub-population of labeled nucleic
 CC acids (NAs) comprising contacting a NA sample from a physiological

CC source, with a pool of 50 distinct gene specific primers under suitable
 CC conditions to enzymatically generate sub-population of NAs, where each
 CC gene specific primer has a sequence complementary to a distinct mRNA, and
 CC each labeled NA is generated using a single gene specific primer. The
 CC method is useful for producing a sub-population of labeled NAs which is
 CC useful for analysing the differences in the RNA profiles between several
 CC different physiological sources, where the method comprises producing
 CC subpopulation of labeled NAs for the different physiological sources,
 CC comprising the populations for each physiological source to identify
 CC differences in the population, where the comparison is preferably
 CC performed by hybridising the labeled NAs for each of the distinct
 CC physiological sources to an array of probe NAs stably associated with the
 CC surface of a substrate to produce a hybridisation pattern for each of the
 CC sources, and comparing the patterns for each of the sources, where
 CC differential gene expression assays are utilised in differential
 CC expression analysis of diseased a normal tissue e.g. neoplastic a normal
 CC tissue, or different tissue or subtype types. The present sequence is a
 CC human gene specific PCR primer used in the method of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at <http://wipo.segdata.uspto.gov/sequence.html?docID=6352829B1>
 XX
 SQ Sequence 32 BP; 9 A; 8 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 1.4%; Score 15; DB 1; Length 32;
 Best Local Similarity 67.7%; Pred. No. 2.8e+02;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1731 CCTTGGCAGTGAATTGCTGTACCAAG 1761
 DB 2 CCTTGTACAGGCAAAATTCATTGCCACAAG 32

RESULT 281
 AAT94667
 ID AAT94667 standard; DNA; 18 BP.
 XX
 AC AAT94667;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Anchored poly(T) oligonucleotide polyT-AnchA.
 XX
 KW Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
 KW snapdragon; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9732023-A1.
 XX
 PD 04-SEP-1997.
 XX
 PF 28-FEB-1997; 97WO-AU000124.
 XX
 PR 01-MAR-1996; 96AU-00008386.
 XX
 PA (FLOR-) FLORIGENE LTD.
 XX
 PI Brugliera F, Holton TA, Michael MZ;
 XX
 DR WPI; 1997-448691/41.
 XX
 PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
 PT corresponding DNA, used in the manipulation of pigmentation in plants.
 XX
 PS Example 15; Page 59; 234pp; English.

CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
 CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
 CC region of a polyadenylation sequence. They were used to prime cDNA
 CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
 CC were also utilised in the PCR amplification of plant cytochrome P450
 CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding

CC flavonoid 3' hydroxylase (see AA035704) was isolated using a differential
 CC display approach. This can be used to manipulate the pigmentation of
 CC transgenic plants
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1865 TTTTATTTTGTGTTTAA 1882
 |||||
 DB 1 TTTTATTTTGTGTTTAA 18
 RESULT 282
 AA035704
 ID AAX18372 standard; DNA; 18 BP.
 XX
 AC AAX18372;
 XX
 DT 11-MAY-1999 (first entry)
 DE RT-PCR primer of the invention SEQ ID 13.
 DE RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 KW
 XX Synthetic.
 OS
 XX JPA1032765-A.
 PN
 XX 09-FEB-1999.
 PD
 XX 18-JUL-1997; 97JP-00208312.
 PF
 XX 18-JUL-1997; 97JP-00208312.
 PR
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX WPI; 1999-183822/16.
 DR
 XX Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 PT
 XX Disclosure; Page 11; 19pp; Japanese.
 PS
 CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha, beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX
 SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1866 TTTTATTTTGTGTTTAA 1883
 |||||
 DB 1 TTTTATTTTGTGTTTAA 18
 RESULT 283
 AA07067/C
 ID AA07067 standard; DNA; 18 BP.

XX AA07067;
 AC 03-JUL-2000 (first entry)
 XX
 DT Human integrin beta 3 antisense oligonucleotide, SEQ ID NO:40.
 DE
 XX Integrin beta 3; human endothelial glycoprotein; GP3A; GPIIa; ITGB3;
 KW CD61; platelet glycoprotein 3a; cellular adhesion; vitronectin receptor;
 KW fibronectin receptor; expression inhibition; antisense; tumour formation;
 KW cancer invasion; bleeding disorder; inflammation; ss.
 XX
 OS Homo sapiens.
 OS
 XX US6037176-A.
 PN
 XX 14-MAR-2000.
 PD
 XX 25-JUN-1999; 99US-00344520.
 PF
 XX 25-JUN-1999; 99US-00344520.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CP, Cowser LM, Monia BP;
 PI WPI; 2000-246189/21.
 DR
 XX New antisense compound that inhibits human integrin beta3, useful e.g.
 XX for treating or preventing infection, inflammation and tumors.
 PT
 XX Example 15; Col 40; 3pp; English.
 PS
 CC Sequences AA07035-A07074 represent antisense oligonucleotides targetted
 CC to the human integrin beta 3 gene, which inhibit its expression. The
 CC antisense oligonucleotides were designed to target different regions of
 CC the human integrin beta 3 RNA, and were analysed for their effect on
 CC integrin beta 3 mRNA levels by quantitative real-time PCR. GAPDH
 CC (glyceraldehyde-3-phosphate) mRNA levels were measured as a control.
 CC Integrins constitute one of four classes of cellular adhesion molecules,
 CC and play an important role in cell migration, cell anchorage to
 CC substrates and cytoadhesion signalling pathways. They are heterodimeric
 CC cation-dependent membrane glycoproteins composed of an alpha and beta
 CC subunit. Integrin beta 3 (also known as human endothelial glycoprotein,
 CC GP3A, GPIIa, ITGB3, CD61 and platelet glycoprotein 3a) is the common
 CC beta subunit partner of the members of the beta-3 subfamily of integrins.
 CC This family consists of the vitronectin receptor (alpha-v-beta-3) and the
 CC fibronectin receptor (alpha-1b-beta-3). Cells expressing this class of
 CC integrin can adhere to various matrix proteins and participate in various
 CC cytoadhesion-driven cellular responses. Integrin beta 3 is implicated in
 CC conditions such as vascular restenosis, excessive bone resorption,
 CC angiogenesis (in melanoma), tumour invasion, platelet aggregation and
 CC Glanzmann's thrombasthenia. The oligonucleotides of the invention are
 CC useful for diagnosis, prevention and treatment of conditions associated
 CC with integrin beta 3 expression, such as tumour formation, inflammation,
 CC infections and the diseases mentioned above
 XX
 SQ Sequence 18 BP; 10 A; 7 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 1.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.2e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTGTGTGT 1811
 |||||
 DB 18 GTGTGTGTGTGTGTGTGT 1
 RESULT 284
 ADD69515
 ID ADD69515 standard; DNA; 15 BP.
 XX
 AC ADD69515;

XX 15-JAN-2004 (first entry)
 XX ISSR-related PCR primer 2.
 XX inter-simple sequence repeat; ISSR, SSR, PCR; primer; genotyping; plant;
 XX animal; Basmati rice; ss.
 XX Unidentified.
 OS WO2003085133-A2.
 PN 16-OCT-2003.
 XX 09-JAN-2003; 2003WO-IB000041.
 XX 08-APR-2002; 2002IN-CH000260.
 XX (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
 PI Nagaraju JG;
 XX WPI; 2003-804317/75.
 XX New set of inter-simple sequence repeats (ISSR)-PCR primers for
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
 PT animal systems.
 PS Disclosure; Page 19; 60pp; English.
 CC The invention relates to a novel set of inter-simple sequence repeats
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
 CC invention may be useful for genotyping diverse genomes of plant and
 CC animal systems, in particular for distinguishing Basmati rice varieties
 CC from non-Basmati rice varieties and traditional Basmati rice varieties
 CC from evolved Basmati rice varieties. The current sequence is that of the
 CC ISSR-related PCR primer of the invention.
 XX Sequence 15 BP; 0 A; 0 C; 7 G; 7 T; 0 U; 1 Other;
 SQ Query Match 1.4%; Score 14.6; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 2e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX 1792 TTGTGTGTGTGTGTG 1806
 :|||||
 1 TTGTGTGTGTGTGTG 15
 DB
 RESULT 285
 ADD69514
 ID ADD69514 standard; DNA; 15 BP.
 XX AC ADD69514;
 XX 15-JAN-2004 (first entry)
 DE ISSR-related PCR primer 1.
 XX inter-simple sequence repeat; ISSR, SSR, PCR; primer; genotyping; plant;
 XX animal; Basmati rice; ss.
 XX Unidentified.
 OS WO2003085133-A2.
 PN 16-OCT-2003.
 XX 09-JAN-2003; 2003WO-IB000041.
 XX 08-APR-2002; 2002IN-CH000260.
 XX (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.

XX Nagaraju JG;
 PI WPI; 2003-804317/75.
 XX New set of inter-simple sequence repeats (ISSR)-PCR primers for
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
 PT animal systems.
 XX Disclosure; Page 19; 60pp; English.
 CC The invention relates to a novel set of inter-simple sequence repeats
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
 CC invention may be useful for genotyping diverse genomes of plant and
 CC animal systems, in particular for distinguishing Basmati rice varieties
 CC from non-Basmati rice varieties and traditional Basmati rice varieties
 CC from evolved Basmati rice varieties. The current sequence is that of the
 CC ISSR-related PCR primer of the invention.
 XX Sequence 15 BP; 0 A; 0 C; 7 G; 7 T; 0 U; 1 Other;
 SQ Query Match 1.4%; Score 14.6; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 2e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTGTG 1808
 :|||||
 1 TTGTGTGTGTGTGTG 15
 DB
 RESULT 286
 AAQ51146
 ID AAQ51146 standard; DNA; 16 BP.
 XX AC AAQ51146;
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 02-JUN-1994 (first entry)
 XX S. cerevisiae telomeric sequence.
 XX Telomere; budding yeast; eukaryotic; conserved region;
 KW phylogenetic relationship; ss.
 XX Saccharomyces cerevisiae.
 PH Key Location/Qualifiers
 FT misc_feature 4
 FT /*tag= a
 FT /note= "May be absent"
 FT misc_feature 5..16
 FT /*tag= b
 FT /note= "May be truncated by multiples of 2 bp"
 XX WO9323572-A1.
 XX 25-NOV-1993.
 XX 13-MAY-1993; 93WO-US004546.
 XX 13-MAY-1992; 92US-00882438.
 XX 24-MAR-1993; 93US-00038766.
 XX (GERO-) GERON CORP.
 XX (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.
 XX West MD, Shay J, Wright W, Blackburn EH;
 XX WPI; 1993-386602/48.
 XX Therapy and diagnosis of conditions involving telomerase using inhibitor
 PT - partic. for neoplasia, infection with pathogenic parasites and age-

PT related diseases.
 PS Disclosure; Fig 30; 186pp; English.
 XX The sequences given in AA051138-46 represent telomeric sequences derived from various budding yeast species. There is a great variety in the length and sequence complexity of these sequences compared to those of other eukaryotes, yet they all have a 6 base conserved region at the 3' end. The telomeric relationships between these yeasts is fairly consistent with the phylogenetic relationship and it has been shown that CC C. tropicalis contains at least two forms of telomeric sequences. CC (Updated on 25-MAR-2003 to correct FN field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 1.4%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTG 1808
 Db 1 TGGGTGTGTGTGTGTG 16
 RESULT 287
 AA096310
 ID AA096310 standard; DNA; 16 BP.
 AC AA096310;
 XX
 DT 25-MAR-2003 (revised)
 DT 08-APR-1998 (first entry)
 XX
 DE Fungal telomeric nucleic acid sequence.
 XX
 KW Detection; eukaryotic pathogen; telomeric nucleic acid sequence;
 KW telomerase activity; diagnosis; fungal infection; fungus; fungi;
 KW malarial infection; malaria; ss.
 XX
 OS Saccharomyces cerevisiae.
 XX
 FN US5695932-A.
 XX
 PD 09-DEC-1997.
 XX
 PF 13-MAY-1993; 93US-00060952.
 XX
 PR 13-MAY-1992; 92US-00882438.
 PR 24-MAR-1993; 93US-00038766.
 XX
 PA (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Blackburn EH, Shay J, Meeachern MJ, West MD, Wright W;
 XX
 DR WPI; 1998-04:1292/04.
 XX
 PT Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -
 PT by detecting telomerase activity.
 XX
 PS Claim 5; Col 95-96; 82pp; English.
 XX
 CC The present sequence can be used in a novel method for detecting a eukaryotic pathogen in a patient. The method comprises obtaining a sample of somatic tissue or cells from the patient, determining if telomerase activity is present and correlating this with the presence of the pathogen. The method is useful for diagnosis of fungal infections, especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces, Sporothrix, Coccidioides, Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections, especially Plasmodium vivax, P. ovale, P. malariae or P. falciparum. (Updated on 25-MAR-2003 to correct PA field.)

XX
 SQ Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 1.4%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTG 1808
 Db 1 TGGGTGTGTGTGTGTG 16
 RESULT 288
 AA013770
 ID AA013770 standard; DNA; 16 BP.
 XX
 AC AA013770;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Simple sequence repeat, SSR, #42.
 XX
 KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
 KW cereal profiling; grass profiling; seed batch purity testing.
 XX
 OS Phalaris aquatica.
 XX
 FN NZ509193-A.
 XX
 PD 25-MAY-2001.
 XX
 PF 03-JAN-2001; 2001NZ-00509193.
 XX
 PR 24-DEC-1999; 99AU-00004906.
 PR 04-MAY-2000; 2000AU-00007310.
 XX
 PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
 PA (UNSC-) UNIV SOUTHERN CROSS.
 PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
 PA (UYAD-) UNIV ADELAIDE.
 PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
 XX
 PI Forster JW, Jones ES;
 XX
 DR WPI; 2001-512563/56.
 XX
 PT New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.
 XX
 PS Example 1; Fig 6; 72pp; English.
 XX
 CC The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-5 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR identifying (M) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal seed batches by assessing variation within seed batch of an SSR. The SSRs may be used in the selection of genes in grass or cereal breeding, for profiling grass or cereal species varieties, for testing the purity of grass or cereal seed batches, and for DNA profiling to establish the distinct identity, uniformity and/or stability of a cultivar. The present sequence is a ryegrass or fescue SSR

SQ Sequence 16 BP; 0 A; 1 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGCTGTGTGTGTCT 1809
DB 1 GTCTGTGTGTGTGTCT 16

RESULT 289

ID ABX50034 standard; DNA; 16 BP.

AC ABX50034;

DT 12-FEB-2003 (first entry)

DE Telomere length and/or telomerase activity related polynucleotide #57.

XX Cell proliferation; cell senescence; telomere length;
KW telomerase activity; cell replication; neoplasia; cancer;
KW age-related macular degeneration; Alzheimer's disease; atherosclerosis;
KW telomerase; telomerase inhibitor; immortalised cell; ss.

OS Synthetic.

PN US2002127634-A1.

PD 12-SEP-2002.

PF 05-JUN-1995; 95US-00463404.

PR 13-MAY-1992; 92US-00882438.

PR 24-MAR-1993; 93US-00038766.

PR 13-MAY-1993; 93US-00060952.

XX (WEST/) WEST M D.

PA (SHAY/) SHAY J.

PA (WRIGHT/) WRIGHT W.

PA (BLAC/) BLACKBURN E H.

XX West MD, Shay J, Wright W, Blackburn EH;

XX WPI; 2003-066896/06.

XX Treating condition associated with cell senescence or increased rate of
PT cell proliferation, by administering to cell an agent that derepresses
PT telomerase in the senescing cells of that reduces loss of telomere
PT length.

XX Disclosure; Page 51; 86pp; English.

XX The invention describes a method use for treating increased rate of
XX proliferation of a cell or extending the ability of a cell to replicate,
XX or treating a disease associated with cell senescence. The method
XX comprises administering an agent to reduce loss of telomere length within
XX the cell during proliferation or replication, or to derepress telomerase
XX in the senescing cells. The method is useful for treating a condition
XX associated with an increased rate of proliferation of a cell extending
XX the ability of a cell to replicate, or for treating a disease or
XX condition associated with cell senescence e.g. neoplasia. A second method
XX disclosed in the invention is useful for treating a condition associated
XX with an elevated level of telomerase activity within a cell e.g. cancer.
XX Also disclosed is a method useful for diagnosis of an individual e.g.
XX with an increased rate of proliferation in a cell in an individual e.g.
XX age-related macular degeneration, astrocytes associated with Alzheimer's
XX disease and endothelial cells associated with atherosclerosis. This
XX sequence represents a polynucleotide used in the study of telomere length
XX and telomerase activity described in the invention

XX Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
DB 1 TGGGTGTGTGTGTGTG 16

RESULT 290

ID ADC06894 standard; DNA; 16 BP.

XX ADC06894;

XX 18-DEC-2003 (first entry)

XX Saccharomyces cerevisiae telomere repeat sequence DNA.

XX nanocircle; telomere repeat sequence; cytostatic; ophthalmological;
KW cancer; liver degeneration; macular; skin aging; gene therapy;
KW biomedical research; tissue engineering; transplantation; ds; yeast.

XX Saccharomyces cerevisiae.

XX Key Location/Qualifiers

FT misc_difference 4 /*tag= a
FT /note= "Optionally absent"

FT misc_difference 7.16

FT /*tag= b
FT /note= "Each TG unit may be optionally absent"

XX WO2003057849-A2.

XX 17-JUL-2003.

XX 03-JAN-2003; 2003WO-US000109.

XX 04-JAN-2002; 2002US-0345056P.

XX (STRD) UNIV STANFORD.

XX Kool ET;

XX WPI; 2003-697275/66.

XX Novel nucleic acid nanocircle comprising at least 2 repeats of a telomere
PT repeat sequence, useful for extending length of telomere in vitro or in
PT vivo, and for treating macular degeneration, and cancer in mammals.

XX Disclosure; Page; 81pp; English.

XX The invention relates to a novel nucleic acid nanocircle comprising at
XX least two repeats of a telomere repeat sequence. The nanocircle of the
XX invention demonstrates cytostatic and ophthalmological activities and may
XX be useful during the diagnosis and treatment of cancer, liver
XX degeneration, macular degeneration and skin aging, as well as during gene
XX therapy procedures. Furthermore, the nanocircle may be used to extend the
XX lifespan of non-cancerous cell populations in culture, providing enhanced
XX materials for biomedical research, tissue engineering and
XX transplantation. The current sequence is that of the Saccharomyces
XX cerevisiae telomere repeat sequence DNA of the invention. Note: this
XX sequence is not displayed within the specification per se but was created
XX by the indexer.

XX Sequence 16 BP; 0 A; 0 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
 DB 1 TGGGTGTGTGTGTGTG 16

RESULT 291
 AAQ35687
 ID AAQ35687 standard; DNA; 17 BP.

XX AC AAQ35687;
 XX DT 25-MAR-2003 (revised)
 XX DT 24-FEB-1993 (first entry)
 XX DE 42kd promoter element primer RG286.

XX NYVAC; EHV-1; GB; GC; GP; glycoprotein; homolog; vaccinia virus; ATI;
 KW I3L promoter; H6 promoter; entomopox virus; 42 kd gene promoter; HA;
 KW deletion loci; Copenhagen vaccine; virulence factors; deletion loci;
 KW recipient loci; polymerase chain reaction; PCR; amplify; ss.

XX Synthetic.

XX PN WO9215672-A1.

XX PD 17-SEP-1992.

XX PF 09-MAR-1992; 92WO-US001906.

XX PR 07-MAR-1991; 91US-00666056.

XX PR 11-JUN-1991; 91US-00713967.

XX PR 06-MAR-1992; 92US-00847951.

XX PA (VIRO-) VIROGENETICS CORP.

XX PI Paolletti E, Perkus ME, Taylor J, Tartaglia J, Norton EK;

XX PI Riviere M, De Taisne C, Limbach KJ, Johnson GP, Pincus SZ, Cox WI;

XX PI Francis J, Gettig RR;

XX DR WPI; 1992-331718/40.

XX PT Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating
 PT against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,
 PT mumps etc.

XX PS Disclosure; Page 182; 456pp; English.

XX The sequences given in AAQ35675-90 were used in the construction of NYVAC
 CC -based recombinants expressing the EHV-1 GB, GC and GP glycoprotein
 CC homologs. Expression of the EHV-1 GB glycoprotein was accomplished by
 CC putting the EHV-1 GB homolog gene under the control of the vaccinia virus
 CC I3L promoter. The EHV-1 GC gene was expressed by placing the homolog gene
 CC under the control of the vaccinia virus H6 promoter and the EHV-GP
 CC glycoprotein was expressed by putting the homolog gene under the control
 CC of the entomopox virus 42 KD gene promoter. The homolog genes were
 CC derived by polymerase chain reaction (PCR) and were inserted into the ATI
 CC and HA deletion loci of NYVAC. NYVAC is a Copenhagen vaccine strain of
 CC vaccinia virus which has been modified by deletion of six non-essential
 CC regions of the genome encoding known or potential virulence factors. The
 CC deletion loci were engineered as recipient loci for the insertion of
 CC foreign genes. See also AAQ35501-864. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX SQ Sequence 17 BP; 6 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792

DB 1 TTTATATTGTAATAT 16

RESULT 292
 AAT81558/C
 ID AAT81558 standard; RNA; 17 BP.

XX AC AAT81558;

XX DT 14-DEC-1997 (first entry)

XX DE Human c-myb hammerhead ribozyme target sequence (nt. position 2896).

XX Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
 KW smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;
 KW coronary angioplasty; ss.

XX OS Homo sapiens.

XX PV WO9531541-A2.

XX PD 23-NOV-1995.

XX PF 18-MAY-1995; 95WO-US006368.

XX PR 18-MAY-1994; 94US-00245466.

XX PR 13-JAN-1995; 95US-00373124.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;

XX DR WPI; 1996-010927/01.

XX PT New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,
 PT for treating restenosis or cancer.

XX PS Claim 1; Page 78; 128pp; English.

XX The present sequence represents the preferred target sequence for an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the human c-myb sequence at the base position indicated in the descriptor
 CC line. The c-myb sequence was screened for optimal ribozyme target sites
 CC using a computer folding algorithm, and regions of the mRNA which did not
 CC form secondary folding structures and contained potential ribozyme
 CC cleavage sites were identified. Ribozymes were synthesised and their
 CC activities optimised by either varying the length of the binding arms or
 CC by modification to prevent degradation by nucleases. The ribozymes cleave
 CC the c-myb sequence and can be used to prevent smooth muscle cell
 CC hyperproliferation in restenosis, especially after coronary angioplasty,
 CC and in cancers

XX SQ Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826

DB 17 TGTATATATATATAA 2

RESULT 293

AAK71409
 ID AAK71409 standard; RNA; 17 BP.

XX AC AAK71409;

XX DT 28-JUL-1999 (first entry)

XX DE Human KDR VEGF receptor hammerhead ribozyme substrate #421.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX Homo sapiens.
 XX OS
 XX WO9715662-A2.
 XX 01-MAY-1997.
 XX 25-OCT-1996; 96WO-US017480.
 XX 26-OCT-1995; 95US-0005974P.
 XX 11-JAN-1996; 96US-00584040.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX (CHIR) CHIRON CORP.
 XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX Claim 4; Page 109; 218pp; English.
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;
 Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 2.3e+02;
 Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1749 TGCTCTGTAACAGCCA 1764
 Db :|||:|||||
 2 UGCCUGUACCAAGCCA 17
 RESULT 294
 AAT47175
 ID AAT47175 standard; DNA; 17 BP.
 XX AC
 XX AAT47175;
 XX 27-MAR-1997 (first entry)
 XX Primer RG286 used in pJCA080 construction.
 XX Feline herpes virus type 1; FHV-1; vaccine; poxvirus; ALVAC; vCP243;
 KW canarypox virus; antigen; vector; primer; PCR; polymerase chain reaction;
 KW pJCA109; pJCA080; ss.
 XX OS
 XX Synthetic.
 XX WO9640241-A1.
 XX 19-DEC-1996.
 XX 03-JUN-1996; 96WO-IB000715.
 XX 07-JUN-1995; 95US-00486969.

XX (VIRO-) VIROGENETICS CORP.
 PA Paoletti E, Maki J;
 PI WPI; 1997-051904/05.
 XX Compen. for inducing immunological response, esp. in dogs - comprises
 PT recombinant virus or expression prod., and additional antigen.
 XX Example 18; Page 168; 243pp; English.
 CC PCR primers (AAT47153-78) were used in the construction of plasmid
 CC intermediates used in the generation of donor plasmid pJCA109. This
 CC plasmid is required for the insertion of genes encoding the feline herpes
 CC virus (FHV-1) homologues of gB, gC and gD under control of the I3L, He
 CC and 42k promoters, respectively, into the C6 site of an ALVAC vector.
 CC Recombinant vCP243 is generated. Primers RG286 (AAT47175) and M13F
 CC (AAT47176) were used to synthesise by PCR a 130 bp EcoRI-blunt fragment
 CC contg. the 42k promoter using pJCA038 as template. The amplified fragment
 CC was used in the construction of intermediate plasmid pJCA080
 XX Sequence 17 BP; 6 A; 0 C; 1 G; 10 T; 0 U; 0 Other;
 Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1777 TTTATATTCTGAATAT 1792
 Db :|||:|||||
 1 TTTATATTCTGAATAT 16
 RESULT 295
 AAV91398
 ID AAV91398 standard; RNA; 17 BP.
 XX AC
 XX AAV91398;
 XX 18-FEB-1999 (first entry)
 XX Human C-raf target site nucleotide position 2898.
 DE Human: c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX Homo sapiens.
 XX WO9850530-A2.
 XX 12-NOV-1998.
 XX 05-MAY-1998; 98WO-US009249.
 XX 09-MAY-1997; 97US-0046059P.
 XX 09-JUN-1997; 97US-0049002P.
 XX 03-JUL-1997; 97US-0051718P.
 XX 22-AUG-1997; 97US-0056808P.
 XX 02-OCT-1997; 97US-0061321P.
 XX 02-OCT-1997; 97US-0061324P.
 XX 05-NOV-1997; 97US-0064866P.
 XX 19-DEC-1997; 97US-0068212P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 XX WPI; 1999-009494/01.

XX Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.
 XX
 XX Claim 177; Page 154; 259pp; English.
 XX
 XX A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene
 XX
 SQ Sequence 17 BP; 2 A; 0 C; 2 G; 0 T; 13 U; 0 Other;
 Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 12.5%; Pred. No. 2.3e+02;
 Matches 2; Conservative 13; Mismatches 1; Indels 0; Gaps 0;
 QY 1866 TTTTATTTTCTTTT 1881
 Db 2 UUUUAAUUUGUUUUU 17
 RESULT 296
 AAV91400
 ID AAV91400 standard; RNA; 17 BP.
 XX
 AC AAV91400;
 XX
 XX 18-FEB-1999 (first entry)
 XX Human C-raf target site nucleotide position 2900.
 DE
 DE Human: c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
 KW screening; identification; synthesis; deprotection; purification; cancer;
 KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
 KW restenosis; rheumatoid arthritis; ss.
 XX
 OS Homo sapiens.
 PN WO9850530-A2.
 XX
 PD 12-NOV-1998.
 XX
 XX 05-MAY-1998; 98WO-US009249.
 PF
 XX 09-MAY-1997; 97US-0046039P.
 PR 09-JUN-1997; 97US-0049002P.
 PR 03-JUL-1997; 97US-0051718P.
 PR 22-AUG-1997; 97US-0056808P.
 PR 02-OCT-1997; 97US-0061321P.
 PR 02-OCT-1997; 97US-0061324P.
 PR 05-NOV-1997; 97US-0064866P.
 PR 19-DEC-1997; 97US-0068212P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA

XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
 PI Parry T, Beigelman L, Mcswiggen JA, Karpelsky A, Burgin A;
 PI Thompson J, Workman CT, Beaudry A, Sweedler D;
 DR WPI; 1999-009494/01.
 XX
 XX Identifying new catalytic nucleic acid that modulates selected processes
 PT - especially ribozymes that cleave Raf RNA for treating cancer,
 PT restenosis, and also new ribozymes and modified nucleoside triphosphates
 PT used as antiviral agents and synthons.
 XX
 XX Claim 177; Page 154; 259pp; English.
 XX
 XX A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules with
 CC endonuclease activity and catalytic activity, from the present invention,
 CC are used to modulate gene expression in plant and mammalian cells and to
 CC cleave target nucleic acid, particularly for treating systemic diseases
 CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
 CC ascites and infection. They may also be used to detect genetic drift and
 CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
 CC with RNA-cleaving activity that modulate expression of the Raf gene, are
 CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
 CC generally any condition associated with the level of c-raf. Introduction
 CC of sugar/phosphate modifications increases stability against nuclease and
 CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
 CC method, specifically for modulating the expression of a Raf gene
 XX
 SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;
 Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 18.8%; Pred. No. 2.3e+02;
 Matches 3; Conservative 12; Mismatches 1; Indels 0; Gaps 0;
 QY 1867 TTTTATTTTCTTTT 1882
 Db 1 UUUUAAUUUGUUUUU 16
 RESULT 297
 AAZ43714/C
 ID AAZ43714 standard; DNA; 17 BP.
 XX
 AC AAZ43714;
 XX
 DT 23-FEB-2000 (first entry)
 XX
 DE Mass spectrometric mutation analysis primer 24.
 XX
 KW Primer; mass-spectrometry; genetic mutation; amplification; ss.
 OS Synthetic.
 XX
 PN DE19824280-A1.
 XX
 PD 02-DEC-1999.
 XX
 XX 29-MAY-1998; 98DE-01024280.
 XX
 PR 29-MAY-1998; 98DE-01024280.
 XX (BRUK-) BRUKER DALTONIK GMBH.
 XX
 DR WPI; 2000-073581/07.
 XX
 PT Mass-spectrometric analysis of known gene mutations.
 XX

PS Example; Page 9; 16pp; German.

XX This invention describes a method for mass-spectrometric analysis of

CC known genetic mutations, using modified nucleoside triphosphates to

CC improve the performance. The method comprises: (1) amplifying a DNA

CC sequence by polymerase chain reaction (PCR) using primers selected to

CC amplify a sequence containing the mutation; (2) adding a particular set

CC of modified nucleoside triphosphates (NTPs) to effect limited extension

CC of already present or newly added primers, where: (a) the extension

CC reaction stops at the next occurrence of a particular base in the DNA

CC strand being copied; (b) the extension reaction proceeds up to or past

CC the mutation site, so that wild-type amplification products will have a

CC different molecular weight from mutant amplification products; and (c)

CC the modification of the NTPs results in stabilization of the DNA chains

CC during ionization, a reduction in ion adduct formation, an increase in

CC ionization yields and/or a change in the mass of the DNA chains; (3)

CC performing the limited primer extension using an enzyme that generates

CC the complement of the DNA strand being copied; (4) performing at least

CC partial primer degradation and optionally further modification of the

CC amplification products; and (5) determining the mass of the modified

CC amplification products by mass spectrometry and assigning the masses to

CC wild type or mutant. AA243691-243717 represent primers used in the method

CC of the invention

XX

SQ Sequence 17 BP; 6 A; 2 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1991 ATATTTCAATGTCAGC 1906

DB 16 ATATTTCAATGTCAGC 1

RESULT 298

AAZ47021

ID AAZ47021 standard; DNA; 17 BP.

XX

AC AAZ47021;

XX

DT 29-FEB-2000 (first entry)

XX

DE Primer RG286 for PCR of promoter entomopoxvirus AmEPV 42K.

XX

KW Antibacterial; antiviral; primer; RT-PCR; amplification; haemagglutinin;

KW recombinant; vaccine; viral vector; pathogen; adjuvant; methacrylic acid;

KW maleic anhydride; alkenyl derivative; animal; herpes virus; tetanus;

KW influenza virus; feline leukemia; canine distemper; promoter; ss.

XX

OS Synthetic.

XX

XX WO9944533-A1.

XX

XX 10-SEP-1999.

XX

XX 01-MAR-1999; 99WO-FR000453.

XX

XX 03-MAR-1998; 98FR-00002800.

XX

XX (MERI-) MERIAL.

XX

XX Audonnet JF, Minke JM;

XX

XX WPI; 2000-022918/02.

XX

XX Live recombinant vaccine comprising viral vector and polymeric adjuvant,

XX particularly directed against animal herpes and influenza viruses.

XX

XX Example 7; Page 14; 41pp; French.

XX

XX Primers AAZ47021-247022 were used to PCR amplify the entomopoxvirus AmEPV

CC 42K promoter for generating a plasmid construct in which the feline

CC herpes virus glycoprotein D (gD) gene is expressed under control of the

CC 42K promoter. The gD gene is used to generate a live recombinant vaccine

CC which comprises: (1) a viral vector including, and expressing in vivo, a

CC heterologous nucleotide sequence particularly a gene from a pathogen; and

CC (2) at least one adjuvant, i.e. a (meth)acrylic acid polymer or a

CC copolymer of maleic anhydride and alkenyl derivatives. The vaccines are

CC used particularly to protect against animal herpes or influenza viruses,

CC but also feline leukemia, tetanus and canine distemper

XX

SQ Sequence 17 BP; 6 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792

DB 1 TTTATATTGTAATAT 16

RESULT 299

AAZ25184

ID AAZ25184 standard; DNA; 17 BP.

XX

AC AAZ25184;

XX

DT 19-JUL-2000 (first entry)

XX

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1692.

XX

KW Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;

KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;

KW gene expression modification; cancer; phosphorothioate; endonuclease;

KW anticancer; breast cancer; endometrium cancer; ss.

XX

OS Homo sapiens.

XX

XX WO9954459-A2.

XX

XX 28-OCT-1999.

XX

XX 19-APR-1999; 99WO-US008547.

XX

XX 20-APR-1998; 98US-0082404P.

XX

XX 23-JUN-1998; 98US-00103636.

XX

XX (RIBO-) RIBOZYME PHARM INC.

XX

XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;

XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;

XX Matulic-Adamic J;

XX

XX WPI; 2000-013248/01.

XX

XX New nucleic acids that interact, and optionally cleave, target sequences,

XX used to treat cancer.

XX

XX Claim 77; Page 71; 148pp; English.

XX

XX The present invention describes nucleic acids (A) that interact stably

XX with a target sequence and contain at least one phosphorodithioate

XX link, having endonuclease activity. (A), and more generally any catalytic

XX nucleic acid (A') that modulates expression of the oestrogen receptor

XX gene, are used to treat cancer (particularly of breast or endometrium), or

XX in vivo or by transforming cells ex vivo and implanting treated cells, or

XX for other conditions associated with levels of oestrogen receptor.

XX Because of the high selectivity for targeted RNA, (A) can also be used to

XX correlate inhibition of gene expression with alterations in phenotype,

XX particularly for identification of therapeutic targets, and as research

XX reagents (for RNA, in the same way that restriction endonucleases are

XX used with DNA). The combination of modifications in (A) improves

XX resistance to nucleases, binding affinity and/or activity. AAZ23503 to

XX AAZ24747 represent oestrogen receptor hammerhead ribozyme sequences, and

CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention

SQ Sequence 17 BP; 1 A; 0 C; 3 G; 13 T; 0 U; 0 Other;
 Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1865 TTTTATTTTGTGTTT 1880
 |||||
 Db 2 TTTTATTTTGTGTT 17

RESULT 300
 AAA25185
 ID AAA25185 standard; DNA; 17 BP.
 XX
 AC AAA25185;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1683.
 XX
 KW Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US008547.
 XX
 PR 20-APR-1998; 98US-0082404P.
 XX
 PR 23-JUN-1998; 98US-00103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpelsky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;
 PI Matulic-Adamic J;
 XX
 XX WPI; 2000-013248/01.
 XX
 XX New nucleic acids that interact, and optionally cleave, target sequences,
 XX used to treat cancer.
 XX
 XX Claim 77; Page 71; 148pp; English.
 XX
 XX The present invention describes nucleic acids (A) that interact stably
 XX with a target sequence and contain at least one phosphorodithioate
 XX link, having endonuclease activity. (A), and more generally any catalytic
 XX nucleic acid (A') that modulates expression of the oestrogen receptor
 XX gene, are used to treat cancer (particularly of breast or endometrium),
 XX in vivo or by transforming cells ex vivo and implanting treated cells, or
 XX for other conditions associated with levels of oestrogen receptor.
 XX Because of the high selectivity for targeted RNA, (A) can also be used to
 XX correlate inhibition of gene expression with alterations in phenotype,
 XX particularly for identification of therapeutic targets, and as research
 XX reagents (for RNA, in the same way that restriction endonucleases are
 XX used with DNA). The combination of modifications in (A) improves
 XX resistance to nucleases, binding affinity and/or activity. AAA23503 to
 XX AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 XX AAA24748 to AAA25992 represent their corresponding target sequences.
 XX AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme

CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention

SQ Sequence 17 BP; 2 A; 0 C; 2 G; 13 T; 0 U; 0 Other;
 Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1865 TTTTATTTTGTGTTT 1880
 |||||
 Db 1 TTTTATTTTGTGTT 16

RESULT 301
 ABV82842
 ID ABV82842 standard; DNA; 17 BP.
 XX
 AC ABV82842;
 XX
 DT 03-JAN-2003 (first entry)
 XX
 DE Human HTPc scanning oligonucleotide SEQ ID 4088.
 XX
 KW Human; gene therapy; tumour suppressor; HTPc; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FN EP1229046-A2.
 XX
 PD 07-AUG-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 XX
 PR 30-JAN-2001; 2001WO-US000664.
 XX
 PR 30-JAN-2001; 2001WO-US000665.
 XX
 PR 30-JAN-2001; 2001WO-US000667.
 XX
 PR 30-JAN-2001; 2001WO-US000668.
 XX
 PR 30-JAN-2001; 2001WO-US000669.
 XX
 PR 23-MAY-2001; 2001US-00864761.
 XX
 PR 09-OCT-2001; 2001US-0327898P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhan J;
 XX
 XX WPI; 2002-676582/73.
 XX
 XX Novel isolated human testis expressed Patched like protein (HTPL), useful
 XX for identifying agonist and antagonist and specific binding partners, and
 XX for treating subjects having defects in HTPL.
 XX
 XX Example 2; Page 599; 718pp; English.
 XX
 XX The present invention relates to human testis expressed Patched like
 XX protein (HTPL), see ABV8759 to ABV8762 and ABV8762 to ABV8762. HTPL
 XX has two isoforms, with a few single base pair differences between the
 XX two. One of the single base pair changes introduces a premature stop
 XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 XX shares an overall structure organisation with the Patched protein. The
 XX shared structural features strongly imply that HTPL plays a role similar
 XX to that of Patched, and is a potential tumour suppressor. HTPL is
 XX important in regulating male germ cell development, and the HTPL gene was
 XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 XX useful for diagnosing a disorder caused by mutation in HTPL, and in
 XX therapy and manufacture of a medicament for treatment or prevention of
 XX such disorder associated with decreased expression or activity of human

CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 CC
 CC Sequence 17 BP; 8 A; 3 C; 2 G; 0 T; 4 U; 0 Other;
 SQ

Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1289 TAAATCTGTTTCTA 1304
 Db 17 TAAATCTGTTTCTA 2

RESULT 304
 ACC51306/c
 ID ACC51306 standard; DNA; 17 BP.
 XX
 AC ACC51306;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human tumour suppressor sequence #73.
 XX
 KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
 KW tumour regression; apoptosis; virus resistance; diagnosis;
 KW cellular degeneration.
 OS Homo sapiens.
 XX
 PN FR2826373-A1.
 XX
 PD 27-DEC-2002.
 XX
 PF 20-JUN-2001; 2001FR-00008139.
 XX
 PR 20-JUN-2001; 2001FR-00008139.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB SA.
 XX
 PI Tuijnder M, Telerman A, Amson R;
 XX
 DR WPI; 2003-250498/25.
 XX
 PT New nucleic acid sequences associated with tumor suppression, regression,
 PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.
 XX
 PS Claim 1; Page 57; 798pp; French.
 CC
 CC This sequence represents an isolated nucleic acid sequence associated
 CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 CC
 CC Sequence 17 BP; 10 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTGTTTCTACTTTGAT 2181
 Db 17 TTGTTTCTACTTTGAT 2

RESULT 305
 ABT38195/c
 ID ABT38195 standard; DNA; 17 BP.
 XX
 AC ABT38195;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 3832.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW anticancer; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004208.
 XX
 PR 17-SEP-2001; 2001FR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 482; 720pp; French.
 CC
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumors or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 CC
 CC Sequence 17 BP; 8 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.3e+02;

DT	04-DEC-2003	(first entry)		
XX	Tumour suppression/reversion associated nucleotide #4252.			
XX	cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;			
KW	primer; probe; tumour suppression; tumour reversion; apoptosis;			
KW	virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;			
KW	diagnosis.			
OS	Homo sapiens.			
XX	WO2003040369-A2.			
XX	15-MAY-2003.			
XX	17-SEP-2002; 2002WO-IB004219.			
XX	17-SEP-2001; 2001PR-00011981.			
XX	(MOLE-) MOLECULAR ENGINES LAB.			
XX	Telerman A, Amson R, Tuijnder M;			
PI	WPI; 2003-441574/41.			
DR	XX			
XX	New nucleic acid encoding human prostate membrane-specific antigen,			
PT	useful e.g. for treatment of tumors and viral infection, also related			
PT	polypeptide and antibodies.			
PT	Disclosure; Page 529; 71pp; French.			
PS	XX			
XX	The invention relates to the isolation of 6327 nucleotide sequences,			
CC	fragments of at least 15 consecutive nucleotides of these nucleotides, a			
CC	sequence having at least 80% identity, after optimal alignment, with the			
CC	nucleotides, a sequence that hybridizes under stringent conditions with			
CC	the nucleotides, or the complement, or corresponding RNA, of the			
CC	nucleotides. The nucleotides are used as probes or primers for detecting,			
CC	identifying, quantifying and/or amplifying nucleic acids, as in vitro			
CC	sense and antisense sequences, of nucleotides involved in tumour			
CC	suppression or reversion, apoptosis and or viral resistance, to produce			
CC	recombinant polypeptides, and to prepare transgenic animals, as			
CC	experimental models. The nucleotides (also vectors containing them and			
CC	cells containing the vectors), the encoded polypeptides and antibodies			
CC	(Ab) against the polypeptide are useful for prevention and/or treatment			
CC	of viral infections or diseases characterized by development of tumours			
CC	or cell degeneration (e.g. Alzheimer's disease or schizophrenia).			
CC	Analysis of the expression of the nucleotides can be used for diagnosis			
CC	and/or prognosis of these diseases. The nucleotides and polypeptides can			
CC	also be used to screen for their specific interactive molecules,			
CC	potentially useful for treating diseases associated with abnormal			
CC	expression of the nucleotides.			
XX	XX			
SQ	Sequence 17 BP; 8 A; 2 C; 2 G; 5 T; 0 U; 0 Other;			
Query Match 1.4%; Score 14.4; DB 1; Length 17;				
Best Local Similarity 93.8%; Pred. No. 2.3e+02;				
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Oy	1888 TTGATATTTCATGCTT 1903			
Db	17 TTGATATTTCATGAT 2			
RESULT 308				
ADB44998/C				
ID	ADB44998 standard; DNA; 17 BP.			
XX	AC ADB44998;			
XX	18-DEC-2003 (first entry)			
DE	Tumour suppression/reversion associated nucleotide #5321.			
XX	XX			

KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX diagnosis.
XX Homo sapiens.
XX OS
XX WO2003040369-A2.
XX PD 15-MAY-2003.
XX PF 17-SEP-2002; 2002WO-IB004219.
XX PP 17-SEP-2001; 2001FR-00011981.
XX PR (MOLE-) MOLECULAR ENGINES LAB.
XX PA Telesman A, Anson R, Tuijnder M;
XX PI WPI; 2003-441574/41.
XX DR New nucleic acid encoding human prostate membrane-specific antigen,
XX PT useful e.g. for treatment of tumors and viral infection, also related
XX PT polypeptide and antibodies.
XX PS Disclosure; Page 654; 771pp; French.
XX CC The invention relates to the isolation of 6327 nucleotide sequences,
XX CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX CC sequence having at least 80% identity, after optimal alignment, with the
XX CC nucleotides, a sequence that hybridizes under stringent conditions with
XX CC the nucleotides, or the complement, or corresponding RNA, of the
XX CC nucleotides. The nucleotides are used as probes or primers for detecting,
XX CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX CC sense and antisense sequences, of nucleotides involved in tumour
XX CC suppression or reversion, apoptosis and or viral resistance, to produce
XX CC recombinant polypeptides, and to prepare transgenic animals, as
XX CC experimental models. The nucleotides (also vectors containing them and
XX CC cells containing the vectors), the encoded polypeptides and antibodies
XX CC (Ab) against the polypeptide are useful for prevention and/or treatment
XX CC of viral infections or diseases characterized by development of tumours
XX CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX CC Analysis of the expression of the nucleotides can be used for diagnosis
XX CC and/or prognosis of these diseases. The nucleotides and polypeptides can
XX CC also be used to screen for their specific interactive molecules,
XX CC potentially useful for treating diseases associated with abnormal
XX CC expression of the nucleotides.
XX SQ Sequence 17 BP; 10 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. NO. 2.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2166 TTGTTCTACTTGTAT 2181
DB 17 TTGTTCTCTTGTAT 2
RESULT 309
AAQ20109
ID AAQ20109 standard; DNA; 18 BP.
XX AC AAQ20109;
XX XX
XX 01-APR-1992 (first entry)
XX DE Cross-linking oligomer 943 to target human TNF Receptor mRNA.
XX XX deoxyribonucleic acid; major groove; ethanocino group;
XX KW tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
XX KW cross-linking group; ss.
XX FT

OS Synthetic.
XX Key modified_base 5 Location/Qualifiers
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
XX FT 18
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "N4N4-ethanocytosine"
XX PN WO9118997-A.
XX PD 12-DEC-1991.
XX PF 25-MAY-1990; 90US-00529346.
XX PP 25-MAY-1990; 90US-00529346.
XX PR 14-JAN-1991; 91US-00640654.
XX XX (GILE-) GILEAD SCIE INC.
XX PA Matteucci MD, Krawczyk S;
XX PI WPI; 1992-007480/01.
XX DR New sequence-specific non-photo-activated crosslinking agents - bind to
XX PT the major groove of duplex DNA and are esp. useful for treating latent
XX FT infections e.g. HIV.
XX PS Example 4; Page 27; 42pp; English.
XX CC The oligomer was designed to target human TNF receptor mRNA beginning at
XX CC nucleotide 2354 and to covalently cross-link to the target via the N4N4-
XX CC ethanocytosine group. See also AAQ20108
XX SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 1.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. NO. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1866 TTTTATTTTGTGTTT 1881
DB 1 TTTTATTTTGTGTTT 16
RESULT 310
AAQ30448
ID AAQ30448 standard; DNA; 18 BP.
XX AC AAQ30448;
XX XX
XX 25-MAR-2003 (revised)
XX DT 07-DEC-1992 (first entry)
XX DE Oligomer TNFR943 for forming triplex with HUMNFR target duplex.
XX XX Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
XX KW HPV; malignancy; hepatitis; inflammation; ss.
XX OS Synthetic.
XX Key modified_base 5 Location/Qualifiers
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "N6 methyl-8-oxo-2' deoxyadenine"
XX FT 18
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "OTHER= N4 N4 ethanocytosine"
XX FT

XX WO9209705-A1.
 PN 11-JUN-1992.
 XX 25-NOV-1991; 91WO-US008811.
 XX 23-NOV-1990; 90US-00617907.
 PR 18-JAN-1991; 91US-00643382.
 PR 08-APR-1991; 91US-00683420.
 PR 17-APR-1991; 91US-00685544.
 PR 17-APR-1991; 91US-00686546.
 PR 17-APR-1991; 91US-00686547.
 PR 27-SEP-1991; 91US-00766733.
 XX (GILE-) GILEAD SCI INC.
 XX Froehner B, Krawczyk S, Matteucci MD, Milligan J;
 PI WPI; 1992-217083/26.
 DR New oligomers contg. modified bases - which form a triplex with G-C
 PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
 PT herpes malignancy and inflammation.
 XX Claim 12; Page 72; 77pp; English.
 XX The synthetic oligomer is capable of forming a triplex at physiological
 CC pH with a purine rich target sequence by coupling into the major groove
 CC of the duplex. The specific target sequence of this oligomer is the human
 CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
 CC a purine rich sequence contd. on one strand of the duplex. The oligomer,
 CC and others like it are useful in diagnosis and therapy of diseases
 CC characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
 CC hepatitis B, herpes, malignant tumours and inflammation. The triple
 CC helices form under mild conditions thus assays may be carried out without
 CC subjecting the test specimen to harsh conditions. See also AAQ25452-25501
 CC and AAQ30226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PD field.)
 XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 SQ Query Match 1.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1866 TTTTATTTTGTGTTT 1881
 DB 1 TTTTATTTTGTGTTT 16
 RESULT 311
 ABL56770
 ID ABL56770 standard; DNA; 18 BP.
 XX ABL56770;
 AC ABL56770;
 XX 20-AUG-2002 (first entry)
 DT Sequence of an oligonucleotide used for triple helix construction.
 DE Nucleic acid detection; nucleic acid labelling; gene therapy;
 XX Nucleic acid purification; triple helix; ss.
 KW Synthetic.
 OS WO200077250-A2.
 PN 21-DEC-2000.
 XX 14-JUN-2000; 2000WO-FR001655.
 PF 14-JUN-1999; 99FR-00007503.
 PR

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX Escude C, Garestier T, Helene C, Roulon T;
 PI WPI; 2001-080698/09.
 DR Circularizing oligonucleotide around double-stranded nucleic acid, useful
 XX e.g. for detecting mutations, using target-binding oligonucleotide with
 PT complementary end sequences.
 PS Example 10; Page 41; 91pp; French.
 XX The specification describes a process for circularizing an
 CC oligonucleotide around a double-stranded nucleic acid that contains a
 CC target sequence. The method is used to detect or label nucleic acids,
 CC particularly plasmids, to detect target sequences in the nucleic acid,
 CC and to distinguish between two sequences that differ in only 1 or 2
 CC mutations. It can be used to select, e.g. from degenerate single-stranded
 CC nucleic acids, sequences that can bind to the nucleic acid, or can target
 CC sequences that promote entry of the nucleic acid into cells or can target
 CC the nucleic acid to specific cellular compartments. The method can also
 CC be used to purify nucleic acids, particularly plasmids, and in gene
 CC therapy for specific inhibition of a gene contained in the nucleic acid.
 CC The present sequence represents an oligonucleotide used in the course of
 CC the invention, during construction of a triple helix
 XX Sequence 18 BP; 0 A; 0 C; 10 G; 8 T; 0 U; 0 Other;
 SQ Query Match 1.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1792 TTGCTGTGTGTGTGTGT 1807
 DB 3 TTGCTGTGTGTGTGTGT 18
 RESULT 312
 ABL31526
 ID ABL31526 standard; DNA; 18 BP.
 XX ABL31526;
 AC ABL31526;
 XX 21-MAR-2002 (first entry)
 DT Human HLA genotyping oligonucleotide SEQ ID NO 1015.
 DE Human; human leukocyte antigen; HLA; genotype; polymorphism;
 XX immunogenetic; transplantation; genetic disease; ss.
 KW Homo sapiens.
 OS WO200192572-A1.
 PN 06-DEC-2001.
 PD 01-JUN-2001; 2001WO-JP004662.
 PF 01-JUN-2000; 2000JP-00164798.
 PR (NISN) NISSHINBO IND INC.
 XX (SYST-) SYSTEM RES INC.
 PA Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;
 PI WPI; 2002-122074/16.
 DR Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of
 XX individuals e.g. by determining immunogenetic differences when
 PT transplanting between them.
 XX

PS Claim 10; Page 285; 345pp; Japanese.

XX The invention relates to a typing kit for judging human leukocyte antigen

CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base

CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of

CC genes e.g. belonging to HLA class I antigens on human genome and

CC containing gene polymorphisms as alloantigens have been immobilised as

CC primers for amplification of cleaved nucleic acids relating to gene

CC polymorphisms. The method is useful for judging HLA genotypes of

CC individuals by determining immunogenetic differences before transplanting

CC between them, providing genetic information to decide compatibility of

CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,

CC pancreas, Langerhans islet in pancreas and cornea, susceptibility

CC diagnosis of genetic diseases and identifying individuals

XX

XX Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;

SQ

Query Match 1.4%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 2.4e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1470 GGGTACCACGACAGAG 1485

DB 2 GGGTACCACGACAGAG 17

RESULT 313

AAS21755

ID AAS21755 standard; DNA; 20 BP.

XX

XX AAS21755;

AC

DT 21-NOV-2001 (first entry)

XX

XX Mouse Survivin antisense oligonucleotide #57.

DE

XX

XX Survivin; human; mouse; cytostatic; antisense oligonucleotide;

KW hyperproliferative condition; cancer; apoptosis; cytokinesis; ss.

KW

XX

XX Mus musculus.

OS

OS Synthetic.

OS

XX WO200157059-A1.

PN

XX

XX 09-AUG-2001.

PD

XX

XX 30-JAN-2001; 2001WO-US002939.

PF

XX

XX 02-FEB-2000; 2000US-00496694.

PR

XX

XX (ISIS-) ISIS PHARM INC.

PA

XX

XX Bennett CF, Ackermann EU, Swayze EE, Cowse LM;

PI

XX

XX WPI; 2001-488863/53.

XX

XX Novel antisense compounds for modulating the expression of Survivin and

PT treatment of cancer.

PT

XX

XX Example 18; Page 62; 120pp; English.

PS

XX The invention relates to antisense oligonucleotides targeted to a nucleic

CC acid molecule encoding human Survivin, where the antisense

CC oligonucleotide inhibits the expression of human Survivin. These

CC antisense oligonucleotides are used in the treatment of an animal

CC suffering from a disease or condition associated with Survivin, e.g. a

CC hyperproliferative condition such as cancer, and comprises administering

CC a therapeutically or prophylactically effective amount of the antisense

CC oligonucleotide so that expression of Survivin is inhibited. The

CC oligonucleotides can also be used to treat a human suffering from a

CC disease or condition characterised by a reduction in apoptosis comprising

CC administering the antisense oligonucleotide to a human. In addition, the

CC antisense oligonucleotide and a cytotoxic chemotherapeutic agent e.g.

CC

CC taxol or cisplatin, can be used to modulate apoptosis, cytokinesis or the

CC cell cycle, or inhibit the proliferation in a cancer cell by contacting

CC the cell with the antisense oligonucleotide. AAS21521-AAS21768 represent

CC Survivin nucleic acids, and antisense oligonucleotides targeted to

CC Survivin, used in the method of the invention

XX

XX Sequence 20 BP; 11 A; 2 C; 0 G; 7 T; 0 U; 0 Other;

SQ

Query Match 1.4%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 2.7e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTACA 1832

DB 1 ACATATATATATATACA 19

RESULT 314

AAT66087/C

ID AAT66087 standard; DNA; 14 BP.

XX

XX AAT66087;

AC

XX

XX 25-MAR-2003 (revised)

DT 18-JUN-1997 (first entry)

DT

XX

XX Repeat sequence found in epsilon haemoglobin gene.

DE

XX

XX Polymorphism; repeat sequence; genetic marker; primer; amplification;

KW PCR; polymerase chain reaction; paternity; maternity; human; pedigree;

KW linkage analysis; genetic disease; animal; plant; breeding; locus;

KW hybridisation; chromosome; ds.

KW

XX Homo sapiens.

OS

XX

XX US5582979-A.

FN

XX

XX 10-DEC-1996.

PD

XX

XX 04-APR-1994; 94US-00222177.

XX

XX 21-APR-1989; 89US-00341562.

XX

XX 05-SEP-1991; 91US-00754351.

PR

XX

XX (MARS-) MARSHFIELD CLINIC.

PA

XX

XX Weber JL;

PI

XX

XX WPI; 1997-042299/04.

DR

XX

XX Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n -

PT using novel nucleic acid mols. as primers.

PT

XX

XX Example 9; Col 59-60; 186pp; English.

PS

XX The invention relates to the isolation of polymorphic repeat sequences

CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic

CC markers. Primers based on these sequences can be used to detect these

CC repeats, especially for use in e.g. paternity or maternity testing, human

CC genetic analysis such as linkage analysis of genetic disease, commercial

CC animal or plant breeding or pedigree analysis. The sequences AAT66084-

CC T66107 represent repeat sequences of low informativeness found in

CC specific human genes. This repeat sequence is found in the epsilon

CC haemoglobin gene located at chromosomal position 1p15.5. The sequence is

CC amplified by primers AAT66088-9. (Updated on 25-MAR-2003 to correct PF

CC field.)

XX

XX Sequence 14 BP; 7 A; 7 C; 0 G; 0 T; 0 U; 0 Other;

SQ

Query Match 1.3%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1807
 DB 14 GTGTGTGTGTGT 1

RESULT 315
 AAZ98486/c
 ID AAZ98486 standard; DNA; 14 BP.
 XX
 AC AAZ98486;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE H. discuss derived sequence #4.
 XX
 KW Satellites sequence; DNA fragmentation; microsatellite DNA; DNA marker;
 KW Haliotis discus; ss.
 XX
 OS Haliotis discus.
 XX
 PN WO200011156-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 01-JUL-1999; 99WO-JP003551.
 XX
 PR 18-AUG-1998; 98JP-00232153.
 XX
 PS (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
 PA Takahashi H, Sekino M;
 XX
 PI WPI; 2000-224692/19.
 XX
 DR Isolation of satellite sequences from genomic DNA for use as DNA markers
 PT comprises isolating a library with high homogeneity by DNA fragmentation.
 XX
 PS Example 5; Page 14; 35pp; Japanese.
 XX
 CC The invention provides a novel method for isolation of satellite
 CC sequences from genomic DNA that comprises fragmentation of the DNA by a
 CC method which is not dependent on base sequences, then selection of the
 CC satellite sequences from the obtained genomic library of high
 CC homogeneity. The method is useful for the isolation of microsatellite DNA
 CC sequences which can be used as DNA markers. The new method markedly
 CC improves the efficiency of isolation of satellite sequences in comparison
 CC to prior art methods which are reliant on base sequences. Sequences
 CC AAZ98483-514 represent sequences from Haliotis discus, used in the method
 CC of the invention
 XX
 SQ Sequence 14 BP; 7 A; 7 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1806
 DB 14 TGTGTGTGTGTGT 1

RESULT 316
 AAS13716/c
 ID AAS13716 standard; DNA; 14 BP.
 XX
 AC AAS13716;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Simple sequence repeat, SSR, #13.
 XX
 KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
 KW cereal profiling; grass profiling; seed batch purity testing.

XX
 OS Poeae.
 XX
 PN NZ509193-A.
 XX
 PD 25-MAY-2001.
 XX
 PF 03-JAN-2001; 2001NZ-00509193.
 XX
 PR 24-DEC-1999; 99AU-00004906.
 XX
 PR 04-MAY-2000; 2000AU-00007310.
 XX
 PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
 PA (UYSC-) UNIV SOUTHERN CROSS.
 PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
 PA (UVAD-) UNIV ADELAIDE.
 PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
 XX
 PI Forster JW, Jones ES;
 XX
 XX WPI; 2001-512563/56.
 XX
 CC New simple sequence repeats having 2 or more tandemly repeated nucleotide
 CC core elements isolated from ryegrass and fescue, useful for selecting of
 CC genes in grass or cereal breeding or profiling grass or cereal species
 CC varieties.
 XX
 PS Claim 6; Page 51; 72pp; English.
 XX
 CC The invention relates to a substantially purified or isolated nucleic
 CC acid (I) from ryegrass or fescue species including a simple sequence
 CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
 CC 2-6 nucleotides in length. Also included are a nucleic acid primer
 CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
 CC library of ryegrass or fescue genomic DNA enriched for SSRs and
 CC identifying clones in the library containing SSRs, a library of ryegrass
 CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
 CC a gene in grass or cereal breeding by identifying an SSR that is closely
 CC associated with the gene such that the SSR and the gene are
 CC preferentially co-inherited, and selecting for the SSR in the breeding, a
 CC method for DNA profiling grass or cereal species varieties by assessing
 CC variation between SSR varieties and testing the purity of grass or cereal
 CC seed batches by assessing variation within seed batch of an SSR. The SSRs
 CC may be used in the selection of genes in grass or cereal breeding, for
 CC profiling grass or cereal species varieties, for testing the purity of
 CC grass or cereal seed batches, and for DNA profiling to establish the
 CC distinct identity, uniformity and/or stability of a cultivar. The present
 CC sequence is a ryegrass or fescue SSR
 XX
 SQ Sequence 14 BP; 7 A; 7 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1806
 DB 14 TGTGTGTGTGTGT 1

RESULT 317
 AAH46009
 ID AAH46009 standard; DNA; 14 BP.
 XX
 AC AAH46009;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synthetic oligonucleotide 9.
 XX
 KW Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
 KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
 KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;

XX PS Claim 7; Col 17; 13pp; English.

XX CC The invention relates to detecting (M1) polymorphisms in a uridine

XX CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining

XX CC the presence of five thymidine-adenine (TA) repeats in the promoter,

XX CC where the presence of the five TA repeats correlates with increased

XX CC expression of the gene. The method is used for detecting polymorphisms in

XX CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is

XX CC useful for screening individuals for variation in glucuronidation

XX CC activity, for optimising drug dosages for a patient, where the drugs

XX CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably

XX CC UGT1A1) and the activity of the drug is effected by its level of

XX CC glucuronidation. The method preferably involves obtaining DNA from an

XX CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene

XX CC promoter) contained in the DNA and determining the number of TA repeats

XX CC in the promoter. Thus the DNA being amplified comprises all or part of

XX CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and

XX CC the number of TA repeats is determined by gel electrophoresis or by

XX CC sequencing the amplified DNA. The polymorphism comprises an allele

XX CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA

XX CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,

XX CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or

XX CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's

XX CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably

XX CC UGT1A1) gene product, the method comprising determining the number of TA

XX CC repeats in a UGT gene promoter, where the number of TA repeats correlates

XX CC with expression of the UGT gene, and the individual's sensitivity to

XX CC xenobiotics is effected by glucuronidation activity. The methods

XX CC preferably involve determining the presence of five, six or seven TA

XX CC repeats in the promoter. Defects in glucuronidation is associated with

XX CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The

XX CC present sequence is the UGT1A1 promoter (TA)7 repeat

XX SQ Sequence 14 BP; 7 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826

DB 1 TATATATATATATA 14

RESULT 320

ABK90418/c

ID ABK90418 standard; DNA; 14 BP.

XX AC ABK90418;

XX DT 05-NOV-2002 (first entry)

XX DE Human UGT1A1 promoter polymorphism (TA)7 repeat.

XX KW Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;

XX KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;

XX KW UGT; polymorphism detection; TA repeat; glucuronidation; irinotecan;

XX KW TAS-103; xenobiotic.

XX OS Homo sapiens.

XX PN US6395481-B1.

XX PD 28-MAY-2002.

XX PF 16-FEB-1999; 99US-00251274.

XX PR 16-FEB-1999; 99US-00251274.

XX FA (ARCH-) ARCH DEV CORP.

XX PI Di Rienzo A, Iyer L, Ratain MJ;

XX WPI; 2002-588597/63.

XX PT Detecting polymorphisms in uridine diphosphate glucuronosyltransferase

XX PT gene promoter, useful for optimizing drug dosages for a patient,

XX PT comprises determining the presence of five thymidine-adenine repeats in

XX PT the promoter.

XX PS Claim 7; Col 17; 13pp; English.

XX CC The invention relates to detecting (M1) polymorphisms in a uridine

XX CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining

XX CC the presence of five thymidine-adenine (TA) repeats in the promoter,

XX CC where the presence of the five TA repeats correlates with increased

XX CC expression of the gene. The method is used for detecting polymorphisms in

XX CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is

XX CC useful for screening individuals for variation in glucuronidation

XX CC activity, for optimising drug dosages for a patient, where the drugs

XX CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably

XX CC UGT1A1) and the activity of the drug is effected by its level of

XX CC glucuronidation. The method preferably involves obtaining DNA from an

XX CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene

XX CC promoter) contained in the DNA and determining the number of TA repeats

XX CC in the promoter. Thus the DNA being amplified comprises all or part of

XX CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and

XX CC the number of TA repeats is determined by gel electrophoresis or by

XX CC sequencing the amplified DNA. The polymorphism comprises an allele

XX CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA

XX CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,

XX CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or

XX CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's

XX CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably

XX CC UGT1A1) gene product, the method comprising determining the number of TA

XX CC repeats in a UGT gene promoter, where the number of TA repeats correlates

XX CC with expression of the UGT gene, and the individual's sensitivity to

XX CC xenobiotics is effected by glucuronidation activity. The methods

XX CC preferably involve determining the presence of five, six or seven TA

XX CC repeats in the promoter. Defects in glucuronidation is associated with

XX CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The

XX CC present sequence is the UGT1A1 promoter (TA)7 repeat

XX SQ Sequence 14 BP; 7 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826

DB 14 TATATATATATATA 1

RESULT 321

AAL50676

ID AAL50676 standard; DNA; 14 BP.

XX AC AAL50676;

XX DT 16-JAN-2003 (first entry)

XX DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #10.

XX KW Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;

XX KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;

XX KW drug dosage optimisation; xenobiotic sensitivity.

XX OS Homo sapiens.

XX PN US2002115097-A1.

XX PD 22-AUG-2002.

XX PF 01-FEB-2002; 2002US-00061693.

CC in the promoter. Thus the DNA being amplified comprises all or part of
 CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
 CC the number of TA repeats is determined by gel electrophoresis or by
 CC sequencing the amplified DNA. The polymorphism comprises an allele
 CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
 CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
 CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
 CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's
 CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
 CC UGT1A1) gene product, the method comprising determining the number of TA
 CC repeats in a UGT gene promoter, where the number of TA repeats correlates
 CC with expression of the UGT gene, and the individuals sensitivity to
 CC xenobiotics is effected by glucuronidation activity. The methods
 CC preferably involve determining the presence of five, six or seven TA
 CC repeats in the promoter. Defects in glucuronidation is associated with
 CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
 CC present sequence is the UGT1A1 promoter (TA)6 repeat region
 CC
 CC Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826
 DB 1 TATATATATATATA 14

RESULT 324
 ABK90421/C
 ID ABK90421 standard; DNA; 15 BP.

AC ABK90421;

DT 05-NOV-2002 (first entry)

DE Human UGT1A1 promoter polymorphism (TA)6 repeat region.

XX Human; ds; UGT1A1; promoter; Gilbert's syndrome; hyperbilirubinaemia;
 KW uridine diphosphate glucuronosyltransferase; Crigler-Najjar syndrome;
 KW UGT; polymorphism detection; TA repeat; glucuronidation; Irinotecan;
 KW TAS-103; xenobiotic.

XX Homo sapiens.

XX US6395481-B1.

XX 28-MAY-2002.

XX 16-FEB-1999; 99US-00251274.

XX 16-FEB-1999; 99US-00251274.

XX (ARCH-) ARCH DEV CORP.

XX Di Rienzo A, Iyer L, Ratain MJ;

XX WPI; 2002-588597/63.

XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
 PT gene promoter, useful for optimizing drug dosages for a patient,
 PT comprises determining the presence of five thymidine-adenine repeats in
 PT the promoter.

XX Example 6; Col 11; 13pp; English.

XX The invention relates to detecting (M1) polymorphisms in a uridine
 CC diphosphate glucuronosyltransferase (UGT) gene promoter by determining
 CC the presence of five thymidine-adenine (TA) repeats in the promoter,
 CC where the presence of the five TA repeats correlates with increased
 CC expression of the gene. The method is used for detecting polymorphisms in
 CC a UGT gene promoter, preferably a UGT 1 (UGT1A1) gene promoter. (M1) is

CC useful for screening individuals for variation in glucuronidation
 CC activity, for optimizing drug dosages for a patient, where the drugs
 CC (e.g. Irinotecan or TAS-103) are glucuronidated by UGT (preferably
 CC UGT1A1) and the activity of the drug is effected by its level of
 CC glucuronidation. The method preferably involves obtaining DNA from an
 CC individual, amplifying all or part of a UGT gene promoter (UGT1A1 gene
 CC promoter) contained in the DNA and determining the number of TA repeats
 CC in the promoter. Thus the DNA being amplified comprises all or part of
 CC UGT1A1 promoter. The DNA is amplified by a polymerase chain reaction and
 CC the number of TA repeats is determined by gel electrophoresis or by
 CC sequencing the amplified DNA. The polymorphism comprises an allele
 CC consisting of five TA repeats (TA)5, six TA repeats (TA)6, or seven TA
 CC repeats (TA)7. The promoter has any one of the genotypes (TA)5/(TA)5,
 CC (TA)5/(TA)6, (TA)5/(TA)7, (TA)5/(TA)8, (TA)6/(TA)8, (TA)7/(TA)8 or
 CC (TA)8/(TA)8. (M1) is also useful for predicting an individual's
 CC sensitivity to xenobiotics that are glucuronidated by a UGT (preferably
 CC UGT1A1) gene product, the method comprising determining the number of TA
 CC repeats in a UGT gene promoter, where the number of TA repeats correlates
 CC with expression of the UGT gene, and the individuals sensitivity to
 CC xenobiotics is effected by glucuronidation activity. The methods
 CC preferably involve determining the presence of five, six or seven TA
 CC repeats in the promoter. Defects in glucuronidation is associated with
 CC Gilbert's syndrome (hyperbilirubinaemia) and Crigler-Najjar syndrome. The
 CC present sequence is the UGT1A1 promoter (TA)6 repeat region
 CC
 CC Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826
 DB 14 TATATATATATATA 1

RESULT 325

ID AAL50678

XX AAL50678 standard; DNA; 15 BP.

XX AAL50678;

XX 16-JAN-2003 (first entry)

DE Human uridine diphosphate glucuronosyltransferase gene polymorphism #12.

XX Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
 KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
 KW drug dosage optimisation; xenobiotic sensitivity.

XX Homo sapiens.

XX US2002115097-A1.

XX 22-AUG-2002.

XX 01-FEB-2002; 2002US-00061693.

XX 16-FEB-1999; 99US-00251274.

XX (ARCH-) ARCH DEV CORP.

XX Di Rienzo AD, Iyer L, Ratain MJ;

XX WPI; 2002-740095/80.

XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
 PT gene promoter, useful for optimizing drug dosages for a patient, involves
 PT determining number of thymidine-adenine repeats in the promoter.
 XX Example 6; Page 2; 13pp; English.

XX The invention comprises a method for detecting polymorphisms in a uridine

CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
 CC UGT1A1). The method involves determining the number of thymidine-adenine
 CC (TA) repeats in the promoter - as the number of TA repeats correlates
 CC with expression of the UGT gene. The method of the invention is useful
 CC for detecting polymorphisms in a UGT gene promoter. The method of the
 CC invention is also useful in optimising drug dosages and predicting an
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
 CC TA repeat polymorphism

XX
 XX
 SQ Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826
 DB 1 TATATATATATATA 14

RESULT 326
 AAL50678/c
 ID AAL50678 standard; DNA; 15 BP.
 XX
 XX AAL50678;
 AC
 XX
 XX 16-JAN-2003 (first entry)
 DT
 XX Human uridine diphosphate glucuronosyltransferase gene polymorphism #12.
 DE
 XX Human; polymorphism; TA repeat; ds; UGT; thymidine-adenine repeat;
 KW uridine diphosphate glucuronosyltransferase gene promoter; UGT1A1;
 KW drug dosage optimisation; xenobiotic sensitivity.
 XX
 XX Homo sapiens.
 OS
 XX US2002115097-A1.
 PN
 XX 22-AUG-2002.
 PD
 XX 01-FEB-2002; 2002US-00061693.
 PF
 XX 16-FEB-1999; 99US-00251274.
 PR
 XX (ARCH-) ARCH DEV CORP.
 PA
 XX Rlenzo AD, Iyer L, Ratain MJ;
 PI
 XX WPI; 2002-740095/80.
 DR
 XX Detecting polymorphisms in uridine diphosphate glucuronosyltransferase
 PT gene promoter, useful for optimizing drug dosages for a patient, involves
 PT determining number of thymidine-adenine repeats in the promoter.
 XX
 XX Example 6; Page 2; 13pp; English.

CC The invention comprises a method for detecting polymorphisms in a uridine
 CC diphosphate glucuronosyltransferase (UGT) gene promoter (preferably
 CC UGT1A1). The method involves determining the number of thymidine-adenine
 CC (TA) repeats in the promoter - as the number of TA repeats correlates
 CC with expression of the UGT gene. The method of the invention is useful
 CC for detecting polymorphisms in a UGT gene promoter. The method of the
 CC invention is also useful in optimising drug dosages and predicting an
 CC individual's sensitivity to xenobiotics for drugs and xenobiotics that
 CC are glucuronidated by UGT. The present DNA sequence represents a UGT gene
 CC TA repeat polymorphism

XX
 XX
 SQ Sequence 15 BP; 8 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826
 DB 14 TATATATATATATA 14

RESULT 327
 AAT81559/c
 ID AAT81559 standard; RNA; 17 BP.
 XX
 XX AAT81559;
 AC
 XX 14-DEC-1997 (first entry)
 DT
 XX Human c-myb hammerhead ribozyme target sequence (nt. position 2898).
 DE
 XX Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
 KW smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;
 KW coronary angioplasty; ss.
 KW
 KW Homo sapiens.
 OS
 XX WO9531541-A2.
 FN
 XX 23-NOV-1995.
 PD
 XX 18-MAY-1995; 95WO-US006368.
 PF
 XX 18-MAY-1994; 94US-00245466.
 PR
 XX 13-JAN-1995; 95US-00373124.
 PA
 XX (RIBO-) RIBOZYME PHARM INC.
 PI
 XX Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;
 XX WPI; 1996-010927/01.
 DR
 XX New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,
 PT for treating restenosis or cancer.
 PT
 XX Claim 1; Page 78; 128pp; English.

CC The present sequence represents the preferred target sequence for an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the human c-myb sequence at the base position indicated in the descriptor
 CC line. The c-myb sequence was screened for optimal ribozyme target sites
 CC using a computer folding algorithm, and regions of the mRNA which did not
 CC form secondary folding structures and contained potential ribozyme
 CC cleavage sites were identified. Ribozymes were synthesised and their
 CC activities optimised by either varying the length of the binding arms or
 CC by modification to prevent degradation by nucleases. The ribozymes cleave
 CC the c-myb sequence and can be used to prevent smooth muscle cell
 CC hyperproliferation in restenosis, especially after coronary angioplasty,
 CC and in cancers

XX
 XX Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. NO. 2.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1811 TGTATATATATATA 1824
 DB 15 TGTATATATATATA 2

RESULT 328
 AAT27921/c
 ID AAT27921 standard; DNA; 17 BP.
 XX
 XX AAT27921;
 AC
 XX 28-JAN-1997 (first entry)
 DT

XX DE 5'-anchored simple sequence repeat primer CGG(CA)6.5.
XX KW Detection; polymorphism; perfect compound simple sequence repeat;
XX KW adaptor directed primer; genome; genetic; fingerprinting;
XX KW amplified fragment length polymorphism assay; microsatellite region;
XX KW genetic trait marking; germplasm comparisons; 5'-anchored; ss.
XX OS Synthetic.
XX XX WO9617082-A2.
XX PN
XX PD 06-JUN-1996.
XX PF 21-NOV-1995; 95WO-US015150.
XX PR 28-NOV-1994; 94US-00346456.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Morgante M, Vogel JM;
XX XX WPI; 1996-277795/28.
XX DR Modified amplified fragment length polymorphism assay - for detection of
XX PT polymorphism esp. in micro:satellite regions.
XX XX
XX PS Example 1; Page 77; 173pp; English.
XX CC Detecting polymorphisms between 2 nucleic acid samples, esp. in
XX CC microsatellite regions, comprises digesting the nucleic acid to generate
XX CC fragments, ligating adaptor segments to their ends, amplifying them using
XX CC primer directed amplification and comparing the prods. to detect
XX CC differences. The primers used in the amplification comprise a primer
XX CC consisting of a perfect cpd. simple sequence complementary to an adaptor
XX CC directed primer, comprising a sequence complementary to an adaptor
XX CC segment. The present sequence is an example of a SSR primer. The method
XX CC represents a modified amplified fragment length polymorphism assay, which
XX CC is partic. useful for genome fingerprinting, i.e. for genetic trait
XX CC marking and germplasm comparisons
XX XX
XX SQ Sequence 17 BP; 7 A; 8 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. NO. 2.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
Db 17 TGTGTGTGTGTGTG 4

RESULT 329
AAH74947
ID AAH74947 standard; DNA; 17 BP.
XX AC
XX AC AAH74947;
XX XX
XX DT 29-OCT-2001 (first entry)
XX DE Nucleotide sequence identified using ligation-based DNA sequencing.
XX KW Nucleotide sequence signature; nucleotide sequencing; ss.
XX OS Unidentified.
XX XX WO200161044-A1.
XX PN
XX PD 23-AUG-2001.
XX PF 15-FEB-2001; 2001WO-US005032.
XX XX
XX PR 15-FEB-2000; 2000US-0182454P.

PR 01-SEP-2000; 2000US-0654187P.
XX PA (LYNX-) LYNX THERAPEUTICS INC.
XX PI Corcoran KC, Eletr S;
XX DR WPI; 2001-522608/57.
XX XX
XX PT Determining nucleotide sequence signature, by obtaining optical values
XX PT for each nucleotide position in a group, adjusting them to get ratio of
XX PT final highest values near predetermined factor, generating base call.
XX XX
XX PS Disclosure; Fig 120; 73pp; English.
XX CC The specification describes a method for determining a nucleotide
XX CC sequence signature. The method comprises obtaining optical measurements
XX CC with values indicating each nucleotide in a group of nucleotide
XX CC positions, adjusting the values until the ratio of highest value in the
XX CC set to next highest values in the set is at least a predetermined factor,
XX CC and generating a base call for a position in the group based on results
XX CC after the adjustment of values. The method is used for determining a
XX CC signature of a nucleotide sequence, and for determining a nucleotide
XX CC sequence of a polynucleotide from a series of optical measurements.
XX CC AAH74933-50 represent yeast sequences, identified using the method of the
XX CC invention
XX XX
XX SQ Sequence 17 BP; 7 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. NO. 2.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2245 TCTAGTTGAAATA 2258
Db 3 TCTAGTTGAAATA 16
|||||
RESULT 330
ADB45500
ID ADB45500 standard; DNA; 17 BP.
XX AC
XX AC ADB45500;
XX XX
XX DT 18-DEC-2003 (first entry)
XX XX
XX DE Tumour suppression/reversion associated nucleotide #5823.
XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX KW primer; probe; tumour suppression; tumour reversion; apoptosis;
XX KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX KW diagnosis.
XX OS Homo sapiens.
XX XX
XX PN WO2003040369-A2.
XX PD 15-MAY-2003.
XX XX
XX PF 17-SEP-2002; 2002WO-IB004219.
XX XX
XX PR 17-SEP-2001; 2001FR-00011981.
XX XX
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX XX
XX PI Telerman A, Amson R, Tuijnder M;
XX XX
XX DR WPI; 2003-441574/41.
XX XX
XX PT New nucleic acid encoding human prostate membrane-specific antigen,
XX PT useful e.g. for treatment of tumors and viral infection, also related
XX PT polypeptide and antibodies.
XX XX
XX PS Disclosure; Page 712; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC cell lines containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 SQ Sequence 17 BP; 4 A; 2 C; 2 G; 9 T; 0 U; 0 Other;
 Query Match 1.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1292 ATCTGTTTCTTAA 1305
 DB 2 ATCTGTTTCTTAA 15
 RESULT 331
 ID AAT53762/C
 AC AAT53762 standard; RNA; 17 BP.
 XX AAT53762;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-APR-1997 (first entry)
 XX Rat ICAM hammerhead ribozyme target sequence (nt. position 2911).
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis; HIV;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 ss.
 XX Rattus rattus.
 OS
 XX
 XX WO9523225-A2.
 XX
 XX 31-AUG-1995.
 XX
 XX 23-FEB-1995; 95WO-IB000156.
 XX
 XX 23-FEB-1994; 94US-00201109.
 XX 29-MAR-1994; 94US-00218934.
 XX 04-APR-1994; 94US-00222795.
 XX 07-APR-1994; 94US-00224483.
 XX 15-APR-1994; 94US-00227958.
 XX 18-MAY-1994; 94US-00228041.
 XX 18-MAY-1994; 94US-00245736.
 XX 06-JUL-1994; 94US-00271280.
 XX 15-AUG-1994; 94US-00291932.

PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 18-AUG-1994; 94US-00293520.
 PR 08-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321933.
 PR 14-OCT-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 DR Ribozymes having modified bases and methods for producing them - for use
 XX in inhibiting disease related genes.
 PT Claim 2; Page 204; 407pp; English.
 PS The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 XX Sequence 17 BP; 2 A; 7 C; 0 G; 0 T; 8 U; 0 Other;
 SQ
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1537 GTGTAATTGAGAGGAA 1553
 DB 17 GGGTAATAGAGAGGAA 1
 RESULT 332
 ID AAT81448/C
 XX AAT81448 standard; RNA; 17 BP.
 XX AAT81448;
 XX
 XX 07-DEC-1997 (first entry)
 XX
 XX Human c-myc hammerhead ribozyme target sequence (nt. position 2527).
 DE Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
 XX smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;
 KW coronary angioplasty; ss.
 XX Homo sapiens.
 XX
 XX WO9531541-A2.

XX PD 23-NOV-1995.
 XX PF 18-MAY-1995; 95WO-US006368.
 XX PR 18-MAY-1994; 94US-00245466.
 XX PR 13-JAN-1995; 95US-00373124.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX STinchcomb DT, Draper K, Mcswiggen J, Jarvis T;
 XX WPI; 1996-010927/01.
 XX New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myc,
 XX for treating restenosis or cancer.
 XX Claim 1; Page 75; 128pp; English.
 XX The present sequence represents the preferred target sequence for an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the human c-myc sequence at the base position indicated in the descriptor
 CC line. The c-myc sequence was screened for optimal ribozyme target sites
 CC using a computer folding algorithm, and regions of the mRNA which did not
 CC form secondary folding structures and contained potential ribozyme
 CC cleavage sites were identified. Ribozymes were synthesised and their
 CC activities optimised by either varying the length of the binding arms or
 CC by modification to prevent degradation by nucleases. The ribozymes cleave
 CC the c-myc sequence and can be used to prevent smooth muscle cell
 CC hyperproliferation in restenosis, especially after coronary angioplasty,
 CC and in cancers
 XX Sequence 17 BP; 8 A; 1 C; 0 G; 0 T; 8 U; 0 Other;
 SQ Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1765 GATTTTAAATTTAT 1781
 DB 17 GATTTTAAATATAT 1
 RESULT 333
 AAT27920
 ID AAT27920 standard; DNA; 17 BP.
 AC AAT27920;
 XX 28-JAN-1997 (first entry)
 DE 5'-anchored simple sequence repeat primer VHVH(TG)6.5.
 XX Detection; polymorphism; perfect compound simple sequence repeat;
 KW adaptor directed primer; genome; genetic; fingerprinting;
 KW amplified fragment length polymorphism assay; microsatellite region;
 KW genetic trait marking; germplasm comparisons; 5'-anchored; ss.
 XX Synthetic.
 OS WO9617082-A2.
 XX 06-JUN-1996.
 XX 21-NOV-1995; 95WO-US015150.
 XX 28-NOV-1994; 94US-00346456.
 XX (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX Morgante M, Vogel JM;
 XX WPI; 1996-277795/28.

XX Modified amplified fragment length polymorphism assay - for detection of
 PT polymorphism esp. in micro:satellite regions.
 XX Example 1; Page 77; 173pp; English.
 XX Detecting polymorphisms between 2 nucleic acid samples, esp. in
 CC microsatellite regions, comprises digesting the nucleic acid to generate
 CC fragments, ligating adaptor segments to their ends, amplifying them using
 CC primer directed amplification and comparing the prods. to detect
 CC differences. The primers used in the amplification comprise a primer
 CC consisting of a perfect cpd. simple sequence repeat (SSR), and an adaptor
 CC directed primer, comprising a sequence complementary to an adaptor
 CC segment. The present sequence is an example of a SSR primer, which is
 CC flanked at its 5'-end by degenerate nucleotides. The method represents a
 CC modified amplified fragment length polymorphism assay, which is partic.
 CC useful for genome fingerprinting, i.e. for genetic trait marking and
 CC germplasm comparisons
 XX Sequence 17 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 4 Other;
 SQ Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.8%; Pred. No. 2.7e+02;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1789 ATATTGTGTGTGTGT 1805
 DB 1 VHVHTGTGTGTGTGT 17
 RESULT 334
 AAX69800
 ID AAX69800 standard; RNA; 17 BP.
 XX AAX69800;
 AC AAX69800;
 XX 28-JUL-1999 (first entry)
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX Homo sapiens.
 OS WO9715662-A2.
 XX 01-MAY-1997.
 XX 25-OCT-1996; 96WO-US017480.
 XX 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 PI WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX Claim 4; Page 79; 218pp; English.
 XX The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient

CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 5.9%; Pred. No. 2.7e+02;
 Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

QY 1864 CTTTATTATTTCTGTTT 1880
 Db 1 CUUUUUUUUUUUUUUUU 17

RESULT 335
 AAX73299
 ID AAX73299 standard; RNA; 17 BP.
 XX
 AC AAX73299;
 XX
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #732.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; Kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Mus sp.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX
 DR WPI; 1997-259017/23.
 XX
 CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 CC stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 CC rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 146; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 6 A; 6 C; 1 G; 0 T; 4 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 5.9%; Pred. No. 2.7e+02;
 Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 70.6%; Pred. No. 2.7e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1643 CCTTAAGTCTAGAACACG 1659
 Db 1 CCUUAUUCUAGAACACC 17

RESULT 336
 AAX73297
 ID AAX73297 standard; RNA; 17 BP.
 XX
 AC AAX73297;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #730.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; Kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Mus sp.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX
 DR WPI; 1997-259017/23.
 XX
 CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 CC stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 CC rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 146; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 58.8%; Pred. No. 2.7e+02;
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1639 TGTCTTAAAGTCAGAA 1655
 Db 1 UGUGCCUUAUUCAGAA 17

RESULT 337
 AAV91401
 ID AAV91401 standard; RNA; 17 BP.

CC method comprises preparing a reduced complexity genome (RCG) from the
 CC genomic sample and analysing the RCG for the presence or absence of a SNP
 CC allele. The method can be used to characterise a tumour, to generate a
 CC genomic pattern for an individual genome or to generate a genomic
 CC classification code for a genome. The method can be used to assess
 CC whether a subject is at risk for developing a disease or to identify a
 CC set of SNP alleles associated with a disease. The method can also be used
 CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences
 CC used in the exemplification of the present invention. AAA35948 to
 CC AAA36632 represent nucleotide sequences containing SNPs
 XX
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1379 TGGTTTGAAGAATGTTA 1395
 DB 17 TGGCTTCAAGAATGTTA 1

RESULT 342
 AAA35972/c
 ID AAA35972 standard; DNA; 17 BP.

AC AAA35972;

DT 26-JUL-2000 (first entry)

DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:29.

XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
 KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
 KW genomic classification; identification; DNA fingerprinting;
 KW tumour characterisation; hybridisation; ss.

OS Homo sapiens.

XX WO2000018960-A2.

XX 06-APR-2000.

XX 24-SEP-1999; 99WO-US022283.

XX 25-SEP-1998; 98US-0101757P.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Landers JE, Jordan B, Housman DE, Charest A;

XX WPI; 2000-293181/25.

XX Detection of single nucleotide polymorphisms in genomes by preparation
 PT and analysis of reduced complexity genomes, useful for genotyping,
 PT fingerprinting and determining allele frequency of SNPs.

XX Disclosure; Page 54; 111pp; English.

XX A method has been developed for detecting the presence or absence of a
 CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
 CC method comprises preparing a reduced complexity genome (RCG) from the
 CC genomic sample and analysing the RCG for the presence or absence of a SNP
 CC allele. The method can be used to characterise a tumour, to generate a
 CC genomic pattern for an individual genome or to generate a genomic
 CC classification code for a genome. The method can be used to assess
 CC whether a subject is at risk for developing a disease or to identify a
 CC set of SNP alleles associated with a disease. The method can also be used
 CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences
 CC used in the exemplification of the present invention. AAA35948 to
 CC AAA36632 represent nucleotide sequences containing SNPs

XX Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1379 TGGTTTGAAGAATGTTA 1395
 DB 17 TGGCTTCAAGAATGTTA 1

RESULT 343

AAA25450
 ID AAA25450 standard; DNA; 17 BP.

XX AAA25450;

DT 19-JUL-2000 (first entry)

DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.

XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.

OS Homo sapiens.

XX WO9954459-A2.

XX 28-OCT-1999.

XX 19-APR-1999; 99WO-US008547.

XX 20-APR-1998; 98US-0082404P.

XX 23-JUN-1998; 98US-00103636.

XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;

XX WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.

XX Claim 77; Page 79; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphoro(di)thioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents for RNA, in the same way that restriction endonucleases are
 CC used with DNA. The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention

XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;

QY 1865 TTTTATTGTTTTTTT 1881
| | | | | | | | | |
Db 1 TTTTATTTTTTTTTTTT 17

RESULT 346
AAAS0197
ID ID AAA50197 standard; DNA; 17 BP.
XX
AC AAAS0197;
XX
DT 07-NOV-2000 (first entry)
XX
DE 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.
XX
KW Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..19
FT /*tag= a
FT /note= "2'-methoxyethoxy modified thymidine"
FT modified_base 1..17
FT /*tag= b
FT /note= "phosphorothioate internucleoside linkages"
XX
XX WO200047593-A1.
XX
XX 17-AUG-2000.
XX
XX 11-FEB-2000; 2000WO-US003543.
XX
XX 12-FEB-1999; 99US-00250075.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Maier MA;
XX
XX WPI; 2000-558188/51.
XX
XX Preparation of mixed backbone oligomeric compounds useful as e.g. primers
XX for diagnostic tests, involves oxidation of H-phosphonate internucleoside
XX linkages to phosphodiester internucleoside linkages.
XX
XX Example 12; Page 34; 49pp; English.
XX
XX The present sequence is that of a phosphorothioate oligonucleotide
XX containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its
XX 5' ribosyl sugar moiety. It is an example of an oligomeric compound
XX produced according to the methods of the invention. The invention
XX provides compounds and methods for the preparation of mixed backbone
XX oligomeric, or chimeric, compounds having phosphodiester internucleoside
XX linkages in addition to phosphorothioate and/or phosphoramidate
XX internucleoside linkages. The methods also include incorporation of
XX boranophosphate internucleoside linkages. The methods utilize H-
XX phosphonate intermediates that are coupled together forming contiguous
XX regions of 1 or more H-phosphonate internucleoside linkages. Each
XX phosphorothioate, phosphoramidate or boranophosphate internucleoside
XX contiguous region is subsequently oxidized to phosphodiester,
XX linkages prior to further elongation. Mixed backbone oligomeric compounds
XX are prepared in this manner by oxidizing adjacent regions with different
XX reagents. Oligomeric compounds of the invention are prepared using novel
XX oxidation steps that oxidize a region of 1 or more H-phosphonate
XX internucleoside linkages without degrading existing linkages that have
XX been previously oxidized. The oligonucleotides obtained are useful as
XX primers in PCR, probes, linkers, gene fragments and for other diagnostic
XX tests on e.g. biological tissue, fluid, cells etc., as research reagents,
XX and as antiviral agents
XX
XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTTTTTT 1881
| | | | | | | | | |
Db 1 TTTTATTTTTTTTTTTT 17

RESULT 347
AAF02995
ID ID AAF02995 standard; DNA; 17 BP.
XX
AC AAF02995;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1290.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
XX interferon alpha; ss.
XX
OS Homo sapiens.
XX
XX WO2000061729-A2.
XX
XX 19-OCT-2000.
XX
XX 11-APR-2000; 2000WO-US009721.
XX
XX 12-APR-1999; 99US-0129390P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
XX WPI; 2000-647423/62.
XX
XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
XX useful for producing e.g. granulocyte colony stimulating factor protein,
XX interferon alpha and erythropoietin.
XX
XX Claim 37; Page 85; 164pp; English.
XX
XX The present invention relates to enzymatic and antisense nucleic acid
XX molecules that act as inhibitors of the expression of repressor genes
XX encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
XX factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
XX Inhibition of the repressors removes prevents inhibition (and
XX consequently increases expression of) genes involved in the production of
XX erythropoietin, granulocyte colony stimulating factor protein and
XX interferon alpha
XX
XX Sequence 17 BP; 8 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.3%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.7e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1760 ACCGAGATTTTAAAAA 1776
| | | | | | | | | |
Db 1 ACAGAGATTTTAAAAA 17

RESULT 348
AAF02349
ID ID AAF02349 standard; DNA; 17 BP.
XX
AC AAF02349;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #644.
XX
XX

KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390F.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 37; Page 70; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the T2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the C/EBP Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1772 TAAATTTATATTGTAA 1788
 DB 1 TATTAATTATATTGTAA 17
 RESULT 349
 ABV82841
 ID ABV82841 standard; DNA; 17 BP.
 AC ABV82841;
 XX
 DT 03-JAN-2003 (first entry)
 XX
 DE Human HTPL scanning oligonucleotide SEQ ID 4087.
 XX
 KW Human; Gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1229046-A2.
 XX
 PD 07-AUG-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 XX
 PR 30-JAN-2001; 2001WO-US0000663.
 PR 30-JAN-2001; 2001WO-US0000664.
 PR 30-JAN-2001; 2001WO-US0000665.
 PR 30-JAN-2001; 2001WO-US0000667.
 PR 30-JAN-2001; 2001WO-US0000668.

PR 30-JAN-2001; 2001WO-US0000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX (ABOM-) AEOMICA INC.
 XX Zhan J;
 PI
 XX WPI; 2002-676582/73.
 DR
 XX
 PF Novel isolated human testis expressed patched like protein (HTPL), useful
 PF for identifying agonist and antagonist and specific binding partners, and
 PF for treating subjects having defects in HTPL.
 XX
 PS Example 2; Page 599; 718pp; English.
 XX
 CC The present invention relates to human testis expressed patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and ABV8519 to ABV8520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-8 (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 3 A; 2 C; 3 G; 9 T; 0 U; 0 Other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2160 AAGCATTGTTTCTACT 2176
 DB 1 ATGCATTGTTTCTAGT 17
 RESULT 350
 ABS74863
 ID ABS74863 standard; DNA; 17 BP.
 XX
 AC ABS74863;
 XX
 DT 24-DEC-2002 (first entry)
 XX
 DE Human PAPP-Ea associated 17-mer SEQ ID 389.
 XX
 KW PAPP-E; human; pregnancy associated plasma protein E; abortive;
 KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
 KW dysgenetic pregnancy; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002102252-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 06-APR-2001; 2001US-00827998.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 XX
 PA (GUY/) GU Y.
 PA (SHAN/) SHANNON M E.

XX Gu Y, Shannon ME;
 XX WPI; 2002-697817/75.
 XX New isolated nucleic acid encoding an isoform of human pregnancy
 PT associated plasma protein E, for preventing or aborting pregnancy.
 XX Example 2; Page 126; 353pp; English.
 XX This invention describes a novel isolated nucleic acid that encodes one
 CC of three new isoforms of human pregnancy associated plasma protein E,
 CC hPAPP-E. The products of the invention have abortive and contraceptive
 CC activity and can be used for gene therapy or in a vaccine. The nucleic
 CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
 CC used in pharmaceutical compositions or vaccines for preventing or
 CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
 CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
 CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
 CC antibodies can be used to assess the expression levels of PAPP-E isoform
 CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
 CC antenatally. This sequence represents an oligomer used in scanning the
 CC human PAPP-E genes described in the disclosure of the invention
 XX Sequence 17 BP; 2 A; 0 C; 6 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1799 TGTGTGTGTGTGTGTAT 1815
 DB 1 TGTGTGTGTGTGTAT 17
 RESULT 351
 ABS74859
 ID ABS74859 standard; DNA; 17 BP.
 AC ABS74859;
 XX 24-DEC-2002 (first entry)
 XX Human PAPP-Ea associated 17-mer SEQ ID 385.
 XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
 XX contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
 XX dysgenetic pregnancy; primer; ss.
 XX Homo sapiens.
 OS
 XX US2002102252-A1.
 XX 01-AUG-2002.
 XX 06-APR-2001; 2001US-00827998.
 XX 26-MAY-2000; 2000US-0207456P.
 XX (GUY/) GU Y.
 XX (SHAN/) SHANNON M E.
 XX Gu Y, Shannon ME;
 XX WPI; 2002-697817/75.
 XX New isolated nucleic acid encoding an isoform of human pregnancy
 PT associated plasma protein E, for preventing or aborting pregnancy.
 XX Example 2; Page 125; 353pp; English.
 XX This invention describes a novel isolated nucleic acid that encodes one
 CC of three new isoforms of human pregnancy associated plasma protein E,

CC hPAPP-E. The products of the invention have abortive and contraceptive
 CC activity and can be used for gene therapy or in a vaccine. The nucleic
 CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
 CC used in pharmaceutical compositions or vaccines for preventing or
 CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
 CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
 CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
 CC antibodies can be used to assess the expression levels of PAPP-E isoform
 CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
 CC antenatally. This sequence represents an oligomer used in scanning the
 CC human PAPP-E genes described in the disclosure of the invention
 XX Sequence 17 BP; 1 A; 0 C; 7 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGT 1809
 DB 1 TGTGTGTGTGTGTGT 17
 RESULT 352
 ABS74862
 ID ABS74862 standard; DNA; 17 BP.
 AC ABS74862;
 XX 24-DEC-2002 (first entry)
 XX Human PAPP-Ea associated 17-mer SEQ ID 388.
 XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
 XX contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
 XX dysgenetic pregnancy; primer; ss.
 XX Homo sapiens.
 OS
 XX US2002102252-A1.
 XX 01-AUG-2002.
 XX 06-APR-2001; 2001US-00827998.
 XX 26-MAY-2000; 2000US-0207456P.
 XX (GUY/) GU Y.
 XX (SHAN/) SHANNON M E.
 XX Gu Y, Shannon ME;
 XX WPI; 2002-697817/75.
 XX New isolated nucleic acid encoding an isoform of human pregnancy
 PT associated plasma protein E, for preventing or aborting pregnancy.
 XX Example 2; Page 126; 353pp; English.
 XX This invention describes a novel isolated nucleic acid that encodes one
 CC of three new isoforms of human pregnancy associated plasma protein E,
 CC hPAPP-E. The products of the invention have abortive and contraceptive
 CC activity and can be used for gene therapy or in a vaccine. The nucleic
 CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
 CC used in pharmaceutical compositions or vaccines for preventing or
 CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
 CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
 CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
 CC antibodies can be used to assess the expression levels of PAPP-E isoform
 CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
 CC antenatally. This sequence represents an oligomer used in scanning the
 CC human PAPP-E genes described in the disclosure of the invention
 XX

SQ Sequence 17 BP; 2 A; 0 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1798 GTGTGTGTGTGTGTGTA 1814
DB 1 GTGTGTGTGTGTGTGTA 17
RESULT 353
ABS74861
ID ABS74861 standard; DNA; 17 BP.
XX AC ABS74861;
XX XX
XX XX
XX 24-DEC-2002 (first entry)
XX Human PAPP-Ea associated 17-mer SEQ ID 387.
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX OS Homo sapiens.
XX US2002102252-A1.
XX PN 01-AUG-2002.
XX PD 06-APR-2001; 2001US-00827998.
XX PF 26-MAY-2000; 2000US-0207456P.
XX PR (GUY/) GU Y.
XX PA (SHAN/) SHANNON M E.
XX PI Gu Y, Shannon ME;
XX WPI; 2002-697817/75.
XX New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
XX Example 2; Page 126; 353pp; English.
XX This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX SQ Sequence 17 BP; 1 A; 0 C; 7 G; 9 T; 0 U; 0 Other;
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGT 1809
DB 1 TGTGTGTGTGTGTGTGT 17
RESULT 354

ABS74858
ID ABS74858 standard; DNA; 17 BP.
XX AC ABS74858;
XX XX
XX 24-DEC-2002 (first entry)
XX Human PAPP-Ea associated 17-mer SEQ ID 384.
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX OS Homo sapiens.
XX US2002102252-A1.
XX PN 01-AUG-2002.
XX PD 06-APR-2001; 2001US-00827998.
XX PF 26-MAY-2000; 2000US-0207456P.
XX PR (GUY/) GU Y.
XX PA (SHAN/) SHANNON M E.
XX PI Gu Y, Shannon ME;
XX WPI; 2002-697817/75.
XX New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
XX Example 2; Page 125; 353pp; English.
XX This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX SQ Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTG 1810
DB 1 GTGTGTGTGTGTGTGTG 17
RESULT 355
ABS74860
ID ABS74860 standard; DNA; 17 BP.
XX AC ABS74860;
XX XX
XX 24-DEC-2002 (first entry)
XX Human PAPP-Ea associated 17-mer SEQ ID 386.
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.

XX OS Homo sapiens.
 XX FN US2002102252-A1.
 XX PD 01-AUG-2002.
 XX PF 06-APR-2001; 2001US-00827998.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PA (GUY/) GU Y.
 XX PA (SHAN/) SHANNON M E.
 XX PI Gu Y, Shannon ME;
 XX WI WI; 2002-697817/75.
 XX PT New isolated nucleic acid encoding an isoform of human pregnancy
 PT associated plasma protein E, for preventing or aborting pregnancy.
 XX PS Example 2; Page 126; 353pp; English.
 XX CC This invention describes a novel isolated nucleic acid that encodes one
 CC of three new isoforms of human pregnancy associated plasma protein E,
 CC hPAPP-E. The products of the invention have abortive and contraceptive
 CC activity and can be used for gene therapy or in a vaccine. The nucleic
 CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
 CC used in pharmaceutical compositions or vaccines for preventing or
 CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
 CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
 CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
 CC antibodies can be used to assess the expression levels of PAPP-E isoform
 CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
 CC antenatally. This sequence represents an oligomer used in scanning the
 CC human PAPP-E genes described in the disclosure of the invention
 XX SQ Sequence 17 BP; 1 A; 0 C; 8 G; 8 T; 0 U; 0 Other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTGTGTG 1810
 DB 1 GTGTGTGTGTGTGTGTG 17
 RESULT 356
 ABK55689/c
 ID ABK55689 standard; RNA; 17 BP.
 XX AC ABK55689;
 XX DT 02-JUL-2002 (first entry)
 XX DE Human CLCA1 gene enzymatic nucleic acid #60.
 XX KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.
 XX OS Homo sapiens.
 XX PN WO200211674-A2.
 XX PD 14-FEB-2002.
 XX PF 09-AUG-2001; 2001WO-US024970.
 XX PA 09-AUG-2000; 2000US-0224383P.
 XX PR

XX PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEX USA LLC.
 PA (THOM/) THOMPSON J.
 XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX WI WI; 2002-217145/27.
 XX PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.
 XX PS Claim 4; Page 54; 152pp; English.
 XX CC The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XX SQ Sequence 17 BP; 7 A; 1 C; 1 G; 0 T; 8 U; 0 Other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1821 TATATATGTACAGTTAT 1837
 DB 17 TATATATATACAGATAT 1
 RESULT 357
 ADB04271
 ID ADB04271 standard; DNA; 17 BP.
 XX AC ADB04271;
 XX DT 20-NOV-2003 (first entry)
 XX DE Human MDZ7 scanning oligonucleotide SEQ ID 5257.
 XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MDZ3; MD24; MD27; MD12; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX OS Homo sapiens.
 XX PN EP1281758-A2.
 XX PD 05-FEB-2003.
 XX PF 30-JUL-2002; 2002EP-00016874.
 XX PR 02-AUG-2001; 2001US-00922181.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.
 XX
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 XX Example 8; SEQ ID NO 5257; 103pp; English.
 XX
 XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1864 CTTTATTATTTGTTTT 1880
 DB 1 CTTTTTTTTTTTTTTT 17
 RESULT 358
 AAD56441
 ID AAD56441 standard; DNA; 17 BP.
 AC AAD56441;
 XX
 XX 07-AUG-2003 (first entry)
 DT Antisense oligo #2, to elicit RNase H degradation of target RNA.
 DE Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 KW antisense; ss.
 XX Unidentified.
 XX Key Location/Qualifiers
 FH misc_feature 9..10
 FT /tag= a
 FT /note= "Bases 9 and 10 are linked by a butanediol linker
 FT which is represented as B in page 49 and X in page 59,
 FT Fig 9 and 10 of the specification"
 XX
 XX WO2003037909-A1.
 PN
 XX
 XX 08-MAY-2003.
 PD
 XX 29-OCT-2002; 2002WO-CA001628.
 PF
 XX 29-OCT-2001; 2001US-0330719P.
 PR (UYMC-) UNIV MCGILL.
 PA
 XX Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;
 PI WPI; 2003-421516/39.
 XX
 XX Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a

PT Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.
 XX
 XX Example 2; Page 90; 104pp; English.
 PS
 XX The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1865 TTTTATTATTTGTTTT 1881
 DB 1 TTTTTTTTTTTTTTTT 17
 RESULT 359
 AAD56448
 ID AAD56448 standard; DNA; 17 BP.
 AC AAD56448;
 XX
 XX 07-AUG-2003 (first entry)
 DT 2'-F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.
 DE Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 KW antisense; ss.
 XX Unidentified.
 XX Key Location/Qualifiers
 FH modified_base 1..17
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
 FT misc_feature 9..10
 FT /tag= b
 FT /note= "Bases 9 and 10 are linked by a butanediol linker
 FT which is represented as B in page 49 and Fig 5 and as X
 FT in page 52, 55 and Fig 6 of the specification"
 XX
 XX WO2003037909-A1.
 PN
 XX
 XX 08-MAY-2003.
 PD
 XX 29-OCT-2002; 2002WO-CA001628.
 PF
 XX 29-OCT-2001; 2001US-0330719P.
 PR (UYMC-) UNIV MCGILL.
 PA
 XX Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;
 PI WPI; 2003-421516/39.
 XX
 XX Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a

target RNA in a system, comprises a modified deoxyribonucleotide.

Example 2; Fig 5; 104pp; English.

The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention

Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
DB 1 TTTTATTTTGTGTTTT 17

RESULT 360

AAD56449
ID AAD56449 standard; DNA; 17 BP.

AC AAD56449;

DT 07-AUG-2003 (first entry)

2'F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.

Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H; antisense; ss.

Unidentified.

Key Location/Qualifiers
modified_base 1..17
/tag= a
/mod_base= OTHER
/note= "2'-deoxy-2'-fluoroarabinothymidine"
misc_feature 12..13
/tag= b
/note= "Bases 12 and 13 are linked by a butanediol linker which is represented as B in page 49 and Fig 5 and as X in page 55 and Fig 6 of the specification"

WO2003037909-A1.

08-MAY-2003.

29-OCT-2002; 2002WO-CA001628.

29-OCT-2001; 2001US-0330719P.

(UYMC-) UNIV MCGILL.

Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

WPI; 2003-421516/39.

Novel acyclic linker-containing oligonucleotide useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.

Example 2; Fig 5; 104pp; English.

The invention relates to an acyclic linker-containing oligonucleotide comprising at least one modified deoxyribonucleotide. Oligonucleotides of the invention are useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system. They are useful for selectively preventing gene expression in a sequence-specific manner, for hybridising to complementary RNA such as cellular mRNA or viral RNA, to hybridise to and induce cleavage of complementary RNA. They are also useful therapeutically in formulations or medicaments to prevent or treat a disease characterised by the expression of a particular target RNA. The invention is used in gene therapy. The present sequence is an antisense oligo used to elicit human RNase (ribonuclease) H degradation of target RNA. This sequence is used in the exemplification of the invention

Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
DB 1 TTTTATTTTGTGTTTT 17

RESULT 361

AAD56447
ID AAD56447 standard; DNA; 17 BP.

AC AAD56447;

DT 07-AUG-2003 (first entry)

2'F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.

Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H; antisense; ss.

Unidentified.

Key Location/Qualifiers
modified_base 1..17
/tag= a
/mod_base= OTHER
/note= "2'-deoxy-2'-fluoroarabinothymidine"
misc_feature 4..5
/tag= b
/note= "Bases 4 and 5 are linked by a butanediol linker which is represented as B in page 49 and Fig 5 and as X in page 55 and Fig 6 of the specification"

WO2003037909-A1.

08-MAY-2003.

29-OCT-2002; 2002WO-CA001628.

29-OCT-2001; 2001US-0330719P.

(UYMC-) UNIV MCGILL.

Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

WPI; 2003-421516/39.

Novel acyclic linker-containing oligonucleotide useful for preventing or decreasing translation, reverse transcription and/or replication of a target RNA in a system, comprises a modified deoxyribonucleotide.

Example 2; Fig 5; 104pp; English.

CC The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1865 TTTTATTTCGTTTT 1881
 DB 1 TTTTTCGTTTTTTT 17
 RESULT 362
 AAD56450
 ID AAD56450 standard; DNA; 17 BP.
 XX
 AC AAD56450;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE 2'-F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA.
 XX
 KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 KW antisense; ss.
 OS Unidentified.
 OS
 FH Key Location/Qualifiers
 FT modified_base 1..17
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
 FT 9..10
 FT /tag= b
 FT /note= "Bases 9 and 10 are linked by a secouridine linker
 FT which is represented as S in page 49 and X in page 57 and
 FT Fig 1, 2, 7 and 8 of the specification"
 XX
 PN WO2003037909-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 29-OCT-2002; 2002WO-CA001628.
 XX
 PR 29-OCT-2001; 2001US-0330719P.
 XX
 XX (UTWC-) UNTV MCGILL.
 PA Damha M, Viazovkina E, Mangos MM, Parniak MA, Min K;
 PI WPI; 2003-421516/39.
 XX
 PT Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.
 XX
 PS Example 2; Fig 7; 104pp; English.
 XX
 CC The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of

CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.7e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1865 TTTTATTTCGTTTT 1881
 DB 1 TTTTTCGTTTTTTT 17
 RESULT 363
 ABL45668/c
 ID ABL45668 standard; DNA; 15 BP.
 XX
 AC ABL45668;
 XX
 DT 19-APR-2002 (first entry)
 XX
 DE Human UBE3A gene ASO PCR primer SEQ ID NO: 35.
 XX
 KW Human; ubiquitin protein ligase E3A; UBE3A; haplotype; SNP; gene therapy;
 KW Angelman syndrome; human papilloma virus E6-associated gene;
 KW single nucleotide polymorphism; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200192582-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 01-JUN-2001; 2001WO-US017994.
 XX
 PR 01-JUN-2000; 2000US-0208539P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Duda A, Klien SE, Koshy B, Sausker EA;
 XX
 DR WPI; 2002-130535/17.
 XX
 PT Novel genetic variants of ubiquitin protein ligase E3A gene useful in
 PT studying expression and function of the protein, and for screening drugs
 PT to treat diseases e.g. Angelman syndrome.
 XX
 PS Claim 17; Page 14; 95pp; English.
 XX
 CC The present invention provides the sequences of fragments of the human
 CC ubiquitin protein kinase E3A (human papilloma virus E6-associated
 CC protein) UBE3A coding sequence and protein. Also described are a number
 CC of single nucleotide polymorphisms (SNPs) identified within these
 CC fragments. The fragments can be used in the gene therapy of Angelman
 CC syndrome and to haplotype the UBE3A gene. The present sequence is an
 CC allele specific primer for a coding sequence fragment of the invention
 XX
 SQ Sequence 15 BP; 7 A; 2 C; 3 G; 2 T; 0 U; 1 Other;
 Query Match 1.3%; Score 13.6; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 2.6e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2167 TGTTCCTACTTTGA 2180
 Db :|||||
 14 TGTTCCTACTTTGA 1

RESULT 364
 ABK16961/C
 ID ABK16961 standard; DNA; 15 BP.
 XX
 AC ABK16961;
 XX

DT 26-MAR-2002 (first entry)
 XX

DE Pyridoxal (Pyridoxine, vitamin B6) Kinase (PDXX) PCR primer #22.
 XX

XX Pyridoxal kinase; pyridoxine; vitamin B6;
 KW PDXX autoimmune polyglandular disease type 1; transgenic animal;
 KW gene therapy; allele specific oligonucleotide; ASO; PCR primer; ss.
 OS Homo sapiens.
 XX
 PN WO200190125-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US016909.
 XX
 PR 24-MAY-2000; 2000US-0206664P.
 XX
 PA (GENA-) GENASSANCE PHARM INC.
 XX
 PI Chew A, Duda A, Koshy B;
 XX
 DR WPI; 2002-106169/14.
 XX
 XX Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNTs, useful
 PT for therapeutic purposes, for studying the expression and function of the
 PT polyNT, and for expressing pyridoxal protein.
 XX
 PS Claim 17; Page 13; 135pp; English.
 CC
 CC The invention describes an isolated human pyridoxal (pyridoxine, vitamin
 CC B6) kinase, (PDXX) polynucleotide. The polynucleotide is useful in
 CC studying the expression and function of PDXX, and in expressing PDXX
 CC protein for use in screening for candidate drugs to treat PDXX related
 CC diseases and for therapeutic purposes. A transgenic animal is useful for
 CC studying expression of the PDXX isogenes in vivo, for in vivo screening
 CC and testing of drugs targeted against PDXX protein, and for testing the
 CC efficacy of therapeutic agents and compounds for autoimmune polyglandular
 CC disease type 1. The polypeptide is useful for studying the effect of the
 CC variation on the biological activity of PDXX and the binding affinity of
 CC candidate drugs targeting PDXX for the treatment of autoimmune
 CC polyglandular disease type 1. Genotyping and haplotyping is useful for
 CC improving the efficacy and reliability of several steps in the discovery
 CC and development of drugs for treating diseases associated with PDXX
 CC activity, e.g., autoimmune polyglandular disease type 1, to validate PDXX
 CC as a candidate agent for treating a specific condition or disease
 CC predicted to be associated with PDXX activity, and in the design of
 CC clinical trials of candidate drugs. This sequence is one of 37 (see
 CC ABK16941-ABK16977) allele specific oligonucleotide (ASO) PCR primers used
 CC for detecting PDXX gene polymorphisms, described in the method of the
 CC invention
 XX
 SQ Sequence 15 BP; 7 A; 5 C; 1 G; 1 T; 0 U; 1 Other;

Query Match 1.3%; Score 13.6; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 2.6e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1801 TGTGTGTGTGTGTA 1814
 Db :|||||
 15 TGTGTGTGTGTGTA 2

RESULT 365
 AAT96304
 ID AAT96304 standard; DNA; 15 BP.
 XX
 AC AAT96304;
 XX

DT 25-MAR-2003 (revised)
 DT 08-APR-1998 (first entry)
 XX
 XX Fungal telomeric nucleic acid sequence.

DE Fungal telomeric nucleic acid sequence.
 XX
 XX Detection; eukaryotic pathogen; telomeric nucleic acid sequence;
 KW telomerase activity; diagnosis; fungal infection; fungus; fungi;
 KW malarial infection; malaria; ss.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN US5695932-A.
 XX
 PD 09-DEC-1997.
 XX
 PF 13-MAY-1993; 93US-00060952.
 XX
 PR 13-MAY-1992; 92US-00882438.
 PR 24-MAR-1993; 93US-00038766.
 XX
 PA (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.
 PA (TEXA) UNIV TEXAS SYSTEM;
 XX
 PI Blackburn EH, Shay J, Meeachern MJ, West MD, Wright W;
 XX
 DR WPI; 1998-041292/04.
 XX
 XX Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -
 PT by detecting telomerase activity.
 PT
 XX Claim 5; Col 93-94; 82pp; English.
 PS
 XX The present sequence can be used in a novel method for detecting a
 CC eukaryotic pathogen in a patient. The method comprises obtaining a sample
 CC of somatic tissue or cells from the patient, determining if telomerase
 CC activity is present and correlating this with the presence of the
 CC pathogen. The method is useful for diagnosis of fungal infections,
 CC especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces,
 CC Sporothrix, Coccidioides, Histoplasma, Blastomyces, Paracoccidioides,
 CC Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections,
 CC especially Plasmodium vivax, P. ovale, P. malariae or P. falciparum.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806
 Db :|||||
 1 TGGTGTGTGTGTGTG 15

RESULT 366
 AAF47617/C
 ID AAF47617 standard; DNA; 15 BP.
 XX
 AC AAF47617;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 XX IGFBP3 oligonucleotide #1037.
 DE
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;

KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX

OS Homo sapiens.

PN WO200078341-A1.

XX 28-DEC-2000.

PF 21-JUN-2000; 2000WO-AU000693.

PR 21-JUN-1999; 99US-0140345P.

PA (MURD-) MURDOCH CHILDRENS RES INST.

PI Wright CJ, Werther GA, Edmondson SR;

DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX

PS Example 7; Page 50; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX

SQ Sequence 15 BP; 6 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 2.7e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2045 TGTCCTGGCAGGCT 2059

DB 15 TGTCCTGGCAGTCT 1

RESULT 367

AAF80919

ID AAF80919 standard; DNA; 15 BP.

AC AAF80919;

XX 02-MAY-2001 (first entry)

XX PTGS2 allele specific oligonucleotide probe SEQ ID 25.

XX Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
KW inflammation; probe; ss.
XX

OS Homo sapiens.

PN WO200107662-A1.

XX 01-FEB-2001.

XX 24-JUL-2000; 2000WO-US020114.

XX 22-JUL-1999; 99US-0145170P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;

XX WPI; 2001-182805/18.

XX New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
PT for gene therapy of inflammation and for establishing a genotype or
PT haplotype.
XX

PS Disclosure; Page 21; 118pp; English.

XX This invention relates to a polynucleotide sequence that is a polymorphic
CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
CC protein is represented by AAF872199. The invention includes PCR and
CC sequencing primers, and probes represented in AAF80898 - AAF81151 which
CC are used to isolate and characterise the PTGS2 gene sequence, and to
CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide
CC sequences are used to express variant PTGS2 proteins, for structural
CC analysis or drug-binding studies and also in gene therapy (either
CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
CC useful for diagnosis, prognosis and therapy and analysis of the new, and
CC known, polymorphisms and used to determine PTGS2 haplotype and genotype.
CC especially for determining association between a particular trait, e.g. a
CC clinical response to drugs that target PTGS2 but also disease
CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
CC used for developing diagnostic tests and treatments for immune-related
CC disorders such as arthritis and inflammation. The polymorphisms may also
CC be used to study expression and biological function of PTGS2. Transgenic
CC animals that express PTGS2 are used to study expression of PTGS2
CC isogenes, for in vivo drug screening and testing, and for assessing
CC effects of therapeutic agents
XX

SQ Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 2.7e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1867 TTTATTTTGTGTTTT 1881

DB 1 TTTATTTTGTGTTTT 15

RESULT 368

ABX79758/c

ID ABX79758 standard; cDNA; 15 BP.

AC ABX79758;

XX 17-APR-2003 (first entry)

XX EST polymorphic DNA repeat polynucleotide #83.

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX

OS Homo sapiens.

XX PN US6472154-B1.
 XX PD 29-OCT-2002.
 XX PF 31-DEC-1999; 99US-00475947.
 XX PR 31-DEC-1999; 99US-00475947.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX WPI; 2003-208819/20.
 XX Identifying a candidate polymorphic repeat within a coding sequence, for
 XX understanding or treating genetic disease, comprises detecting tandem
 XX repeats in a target coding sequence and scoring the repeats for
 XX polymorphic probability.
 XX Example; Col 309; 588pp; English.
 XX The invention discloses a method for identifying a candidate polymorphic
 XX repeat within a coding sequence (expressed sequence tag, EST), which
 XX comprises detecting tandem repeats in a target coding sequence, scoring
 XX the repeats for polymorphic probability and generating a dataset
 XX correlating the repeats with polymorphic probability to identify a
 XX candidate polymorphic repeat. The computational methods (polymorphic
 XX marker prediction of ubiquitous simple sequences, POMPUS, and Rep-X) are
 XX useful for identifying and detecting candidate polymorphic repeats in
 XX human genes, which can be used to understand, treat or eliminate genetic
 XX diseases, predispositions or adverse drug-treatment reactions. Examples
 XX of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 XX syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 XX myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 XX spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 XX the polymorphic repeats identified for a search of human ESTs
 XX
 XX SQ Sequence 15 BP; 9 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 1.3%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred.No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1811 TGTATATATATATAT 1825
 Db 15 TTTATATATATATAT 1
 RESULT 369
 ABX94519
 ID ABX94519 standard; DNA; 15 BP.
 AC ABX94519;
 XX 10-JUN-2003 (first entry)
 XX 23S rDNA helix 54 region probe SEQ ID 37.
 XX Diagnostic; Gram-positive bacterium; high G+C content; amplification;
 XX mycobacterial infection; PCR; primer; probe; detection; ss.
 XX Corynebacterium pseudotuberculosis.
 XX Corynebacterium ulcerans.
 XX WO200297126-A2.
 XX 05-DEC-2002.
 XX 09-APR-2002; 2002WO-EP003956.
 XX 03-MAY-2001; 2001DE-01021505.

PA (HAIN-) HAIN LIFESCIENCE GMBH.
 PI Weizenegger M;
 XX WPI; 2003-140491/13.
 XX Detecting and identifying Gram-positive bacteria of high G/C content,
 XX useful particularly for diagnosis of mycobacterial infection, by specific
 XX amplification and hybridization.
 XX Claim 1b; Fig 2B; 34pp; German.
 XX This invention describes a novel method for the diagnostic detection
 XX and/or identification of Gram-positive bacteria that have a high G+C
 XX content, especially Mycobacteria. The method comprises subjecting a
 XX sample to nucleic acid amplification using the PCR primers represented in
 XX ABX94483-ABX94492. The amplification mixture, or part of it, is then
 XX tested for hybridisation to at least one of the probes represented in
 XX ABX94493-ABX94524 which can be immobilised on a solid phase or used in
 XX kit form. The specified primers/probes provide highly specific detection
 XX of particular Gram positive bacteria, which are difficult to
 XX differentiate by morphological or biochemical tests and/or those which
 XX take a long time to test because of their slow growth
 XX
 XX SQ Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 1.3%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred.No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1793 TGTGTGTGTGTGTGT 1807
 Db 1 TGTGTGTGTGTGTGT 15
 RESULT 370
 ABX50028
 ID ABX50028 standard; DNA; 15 BP.
 AC ABX50028;
 XX 12-FEB-2003 (first entry)
 XX Telomere length and/or telomerase activity related polynucleotide #51.
 XX Cell proliferation; cell senescence; telomere length;
 XX telomerase activity; cell replication; neoplasia; cancer;
 XX age-related macular degeneration; Alzheimer's disease; atherosclerosis;
 XX telomerase; telomerase inhibitor; immortalised cell; ss.
 XX Synthetic.
 XX US2002127634-A1.
 XX 12-SEP-2002.
 XX 05-JUN-1995; 95US-00463404.
 XX 13-MAY-1992; 92US-00892438.
 XX 24-MAR-1993; 93US-00038766.
 XX 13-MAY-1993; 93US-00060952.
 XX (WEST/) WEST M D.
 XX (SHAY/) SHAY J.
 XX (WRIGHT/) WRIGHT W.
 XX (BLAC/) BLACKBURN E H.
 XX West MD, Shay J, Wright W, Blackburn EH;
 XX WPI; 2003-066896/06.
 XX Treating condition associated with cell senescence or increased rate of
 XX cell proliferation, by administering to cell an agent that derepresses

PT telomerase in the senescing cells or that reduces loss of telomere
 PT length.
 XX
 PS Disclosure; Page 50; 86pp; English.
 XX
 CC The invention describes a method use for treating increased rate of
 CC proliferation of a cell or extending the ability of a cell to replicate,
 CC or treating a disease associated with cell senescence. The method
 CC comprises administering an agent to reduce loss of telomere length within
 CC the cell during proliferation or replication, or to derepress telomerase
 CC in the senescing cells. The method is useful for treating a condition
 CC associated with an increased rate of proliferation of a cell extending
 CC the ability of a cell to replicate, or for treating a disease or
 CC condition associated with cell senescence e.g. neoplasia. A second method
 CC disclosed in the invention is useful for treating a condition associated
 CC with an elevated level of telomerase activity within a cell e.g. cancer.
 CC Also disclosed is a method useful for diagnosis of a condition associated
 CC with an increased rate of proliferation in a cell in an individual e.g.
 CC age-related macular degeneration, astrocytes associated with Alzheimer's
 CC disease and endothelial cells associated with atherosclerosis. This
 CC sequence represents a polynucleotide used in the study of telomere length
 CC and telomerase activity described in the invention
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.3%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1722 TTGTTGTGTGTGTG 1806
 Db 1 TGGTGTGTGTGTGTG 15

RESULT 371
 AAT81559
 ID AAT81559 standard; RNA; 17 BP.
 XX
 AC AAT81559;
 XX
 DT 14-DEC-1997 (first entry)
 DE Human c-myb hammerhead ribozyme target sequence (nt. position 2898).
 XX
 KW Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
 KW smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;
 XX coronary angioplasty; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9531541-A2.
 XX
 PD 23-NOV-1995.
 XX
 PF 18-MAY-1995; 95WO-US006368.
 XX
 PR 18-MAY-1994; 94US-00245466.
 PR 13-JAN-1995; 95US-00373124.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;
 XX WPI; 1996-010927/01.
 DR
 XX New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,
 XX for treating restenosis or cancer.
 PT
 PS Claim 1; Page 78; 128pp; English.
 XX

CC The present sequence represents the preferred target sequence for an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the human c-myb sequence at the base position indicated in the descriptor

CC line. The c-myb sequence was screened for optimal ribozyme target sites
 CC using a computer folding algorithm, and regions of the mRNA which did not
 CC form secondary folding structures and contained potential ribozyme
 CC cleavage sites were identified. Ribozymes were synthesised and their
 CC activities optimised by either varying the length of the binding arms or
 CC by modification to prevent degradation by nucleases. The ribozymes cleave
 CC the c-myb sequence and can be used to prevent smooth muscle cell
 CC hyperproliferation in restenosis, especially after coronary angioplasty,
 CC and in cancers
 XX

SQ Sequence 17 BP; 7 A; 1 C; 0 G; 0 T; 9 U; 0 Other;

Query Match 1.3%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 46.7%; Pred. No. 2.9e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
 Db 2 UAUUAUAUAUAUACAU 16

RESULT 372
 ABA10358
 ID ABA10358 standard; DNA; 13 BP.
 XX
 AC ABA10358;
 XX
 DT 03-JUL-2000 (first entry)
 DE DNA ligand binding assay competitor oligonucleotide, SEQ ID NO:41.

XX Nucleic acid ligand binding assay; duplex formation; stability;
 KW detectable signal; competition assay; competitor oligonucleotide; ds.
 XX
 OS Synthetic.
 XX
 PN WO200015848-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 10-SEP-1999; 99WO-US020719.
 XX
 PR 11-SEP-1998; 98US-00151890.
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Schroth GP, Bruice TW, Suh YJ;
 XX WPI; 2000-271478/23.
 DR
 XX Determining binding affinity of a ligand to an oligonucleotide sequence
 XX in double stranded form, comprises measuring the effect of adding
 XX increasing amounts of a ligand on a signal generated by two indicator
 XX oligonucleotides of the duplex.
 XX
 PS Example 3; Page 19; 78pp; English.

CC The invention relates to new methods of determining the binding affinity
 CC of a ligand to an oligonucleotide sequence, particularly to a duplex. The
 CC ligand is typically a metal ion, a small organic or inorganic molecule, a
 CC protein or a multi-protein complex. The methods comprise measuring the
 CC effect of adding increasing amounts of a ligand on a signal generated by
 CC two indicator oligonucleotides of the duplex. In the absence of ligand,
 CC conditions are such that the oligonucleotides exist primarily in single-
 CC stranded form; binding of ligand to double-stranded nucleic acids
 CC stabilises the duplexes, such that duplex formation is favoured. One of
 CC the indicator oligonucleotides contains a first group capable of
 CC producing a detectable signal, while the other indicator oligonucleotide
 CC contains a second group that on hybridisation of the two indicator
 CC molecules, will detectably alter the signal produced by the first group.
 CC The signal may be increased or decreased on hybridisation. For example,
 CC the pairs of signalling groups used could be a radioactive group and a
 CC scintillant (where an increase in signal intensity indicates that

CC hybridisation has taken place) or a fluorophore and a fluorescence
 CC quencher (where a reduction in signal intensity indicates that
 CC hybridisation has occurred). Other methods of the invention comprise a
 CC strand displacement assay, where the ability of an unlabelled displacement
 CC strand to displace one of the oligonucleotides in the duplex is
 CC determined in the absence and presence of ligand; and a competition
 CC assay, where an unlabelled single or double-stranded competitor
 CC oligonucleotide is added to the ligand-bound indicator duplex, and the
 CC effect on the signal produced from the indicator duplex determined. The
 CC methods are useful for determining the binding affinity of a ligand to an
 CC oligonucleotide sequence. They are particularly useful for determining
 CC relative binding affinities of various ligands to various oligonucleotide
 CC sequences, particularly double-stranded oligonucleotide sequences. The
 CC assays allow rapid and convenient determination of nucleic acid binding
 CC specificities. Sequences AAA0342-AB0391 represent competitor
 CC oligonucleotides used in competition assays in exemplifications of the
 CC present invention
 CC
 XX Sequence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806

Db 1 GTGTGTGTGTGTG 13

RESULT 373
 ABC88212
 ID ABC88212 standard; DNA, 13 BP.

AC ABC88212;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 88229 for detecting SNP TSC0022170.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.

XX Claim 1; SEQ ID NO 88229; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1769 TTTTAAATTTAT 1781

Db 1 TTTTAAATTTAT 13

RESULT 374
 ABF52648
 ID ABF52648 standard; DNA, 13 BP.

XX AC ABF52648;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 152645 for detecting SNP TSC0038583.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.

XX Claim 1; SEQ ID NO 152645; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1779 TATATTGTAAATA 1791

```

Db      1 TATATGTAATA 13
RESULT 375
ABC98272
ID ABC98272 standard; DNA; 13 BP.
XX
AC ABC98272;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 98289 for detecting SNP TSC0024420.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 98289; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1811 TGTATATATATAT 1823
DB 1 TGTATATATATAT 13
RESULT 376
ABC13481
ID ABC13481 standard; DNA; 13 BP.
XX
AC ABC13481;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 13488 for detecting SNP TSC0003116.
XX

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```

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 13488; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 0 G; 9 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 TTTTAAAAATTT 1779
DB 1 TTTTAAAAATTT 13
RESULT 377
ABC91693/C
ID ABC91693 standard; DNA; 13 BP.
XX
AC ABC91693;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 91710 for detecting SNP TSC0022946.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX

```

```
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 91710; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2259 AAGTGATATTTT 2271
DB 13 AAGTGATATTTT 1
RESULT 378
ABF90382
ID ABF90382 standard; DNA; 13 BP.
XX
AC ABF90382;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 190379 for detecting SNP TSC0046825.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 190379; 29pp + Sequence Listing; German.
XX
```

```
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 1 A; 0 C; 1 G; 11 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1867 TTTATTTTGTGT 1879
DB 1 TTTATTTTGTGT 13
RESULT 379
ABF06851/c
ID ABF06851 standard; DNA; 13 BP.
XX
AC ABF06851;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 106848 for detecting SNP TSC0026750.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 106848; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
```

SQ Sequence 13 BP; 10 A; 1 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1871 TTTTGGTTTAA 1883
 Db 13 TTTTGGTTTAA 1

RESULT 380
 ABC37111/C
 ID ABC37111 standard; DNA; 13 BP.
 XX
 AC ABC37111;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 37128 for detecting SNP TSC0011593.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 37128; 39pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 2 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1810 GTGTATATATATA 1822
 Db 13 GTGTATATATATA 1

RESULT 381
 ABC12933/C

ID ABC12933 standard; DNA; 13 BP.
 XX
 AC ABC12933;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 12940 for detecting SNP TSC0003018.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 12940; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1812 GTATATATATATA 1824
 Db 13 GTATATATATATA 1

RESULT 382
 ABC8037
 ID ABC8037 standard; DNA; 13 BP.
 XX
 AC ABC8037;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 8054 for detecting SNP TSC0022135.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.

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XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 8054; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 4 A; 2 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1252 TTTTTCGTAATA 1264
Db 1 TTTTTCGTAATA 13

RESULT 383
ABF19131/C
ID ABF19131 standard; DNA; 13 BP.
XX AC ABF19131;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 119128 for detecting SNP TSC0023746.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 17789; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1816 ATATATATATATG 1828
Db 13 ATATATATATATG 1

RESULT 384
ABC17782
ID ABC17782 standard; DNA; 13 BP.
XX AC ABC17782;
XX XX
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 17789 for detecting SNP TSC0003802.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 17789; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1816 ATATATATATATG 1828
Db 13 ATATATATATATG 1

```

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 1806 GTGTGTATATA 1818
Db 1 GTGTGTATATA 13

RESULT 385
ABC82324
ID ABC82324 standard; DNA; 13 BP.
XX
AC ABC82324;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 82341 for detecting SNP TSC020792.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 82341; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1778 TTATATTGTAAT 1790
Db 1 TTATATTGTAAT 13

RESULT 386
ABF60103
ID ABF60103 standard; DNA; 13 BP.
XX
AC ABF60103;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 160100 for detecting SNP TSC0040305.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 160100; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 1253 TTTTCCGTAAAAA 1265
Db 1 TTTTCCGTAAAAA 13

RESULT 387
ABF61495/c
ID ABF61495 standard; DNA; 13 BP.
XX
AC ABF61495;
XX
DT 22-FEB-2002 (first entry)

```

XX DE Oligonucleotide SEQ ID NO 161492 for detecting SNP TSC0040647.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 161492; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF00010-ABP9989, ABH00010-ABH9989 and ABIC0010-ABI62073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1865 TTTTATTTCCT 1877
DB 13 TTTTATTTCCT 1

RESULT 388
ABC5255/c
ID ABC5255 standard; DNA; 13 BP.
AC ABC5255;
XX AC ABC5255;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 55272 for detecting SNP TSC0015107.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 55272; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF00010-ABP9989, ABH00010-ABH9989 and ABIC0010-ABI62073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1865 TTTTATTTCCT 1877
DB 13 TTTTATTTCCT 1

RESULT 388
ABC5255/c
ID ABC5255 standard; DNA; 13 BP.
AC ABC5255;
XX AC ABC5255;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 55272 for detecting SNP TSC0015107.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 55272; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF00010-ABP9989, ABH00010-ABH9989 and ABIC0010-ABI62073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 7 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1771 TTTAAATTTAT 1783
DB 13 TTTAAATTTAT 1

RESULT 389
ABC58807/c
ID ABC58807 standard; DNA; 13 BP.
AC ABC58807;
XX AC ABC58807;
XX XX
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 58824 for detecting SNP TSC0015758.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 58824; 29pp + Sequence Listing; German.
XX XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG9989, ABF00010-ABP9989, ABH00010-ABH9989 and ABIC0010-ABI62073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 13 BP; 7 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1771 TTTAAATTTAT 1783
DB 13 TTTAAATTTAT 1

```


XX PS Claim 1; SEQ ID NO 58824; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 5 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1803 TGTGTGTGTGTAT 1815

Db 13 TGTGTGTGTGTAT 1

RESULT 390

ABC37110

ID ABC37110 standard; DNA; 13 BP.

AC ABC37110;

XX 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 37127 for detecting SNP TSC0011593.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 37127; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1810 GTGTATATATATA 1822

Db 1 GTGTATATATATA 13

RESULT 391

ABF60102/c

ID ABF60102 standard; DNA; 13 BP.

XX AC ABF60102;

XX 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 160099 for detecting SNP TSC0040305.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 160099; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1253 TTTTCGGTAAAAA 1265

Db 13 TTTTCGGTAAAAA 1

RESULT 392
 ID ABC17780 standard; DNA; 13 BP.
 XX
 AC ABC17780;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 17787 for detecting SNP TSC0003802.
 XX
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 17787; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 13 BP; 4 A; 0 C; 3 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1808 GTGTGTATATATA 1820
 DB 1 GTGTGTATATATA 13
 RESULT 393
 ID ABC98273 standard; DNA; 13 BP.
 XX
 AC ABC98273;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 98290 for detecting SNP TSC0024420.
 XX
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 PN WO200177384-A2.
 PD 18-OCT-2001.
 PF 06-APR-2001; 2001WO-IB000713.
 PR 07-APR-2000; 2000DE-01019173.
 PA (EPIG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 DR WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 98290; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 PS Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1811 TGTATATATATAT 1823
 DB 13 TGTATATATATAT 1
 RESULT 394
 ID ABC79591/c
 XX
 AC ABC79591;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 79608 for detecting SNP TSC0020218.
 XX
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.

XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 79608; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 6 C; 0 G; 1 T; 0 U; 0 Other;
SQ

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1802 GTGTGTGTGTGTA 1814
DB 13 GTGTGTGTGTGTA 1

RESULT 395
ABC29729/C
ID ABC29729 standard; DNA; 13 BP.
XX
AC ABC29729;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 29746 for detecting SNP TSC0008889.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 29746; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 7 C; 0 G; 0 T; 0 U; 0 Other;
SQ

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTG 1806
DB 13 GTGTGTGTGTG 1

RESULT 396
ABC33895/C
ID ABC33895 standard; DNA; 13 BP.
XX
AC ABC33895;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 33912 for detecting SNP TSC0010852.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 33912; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 10 A; 1 C; 0 G; 2 T; 0 U; 0 Other;
SQ

```

Query Match      1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1870 ATTTTGTGTTTA 1882
Db 13 ATTTTGTGTTTA 1

RESULT 397
ABF48194
ID ABF48194 standard; DNA; 13 BP.
XX
AC ABF48194;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 148191 for detecting SNP TSC0037417.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 148191; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match      1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1766 ATTTTGTGTTTA 1778
Db 1 ATTTTGTGTTTA 13

RESULT 398
ABF52649/c
ID ABF52649 standard; DNA; 13 BP.
XX

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AC ABF52649;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 152646 for detecting SNP TSC0038583.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 152646; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;

Query Match      1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred.No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1779 TATATTGTTAAATA 1791
Db 13 TATATTGTTAAATA 1

RESULT 399
ABCI1783/c
ID ABCI1783 standard; DNA; 13 BP.
XX
AC ABCI1783;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 17790 for detecting SNP TSC0003802.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX

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CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
DB 13 ATATATATATATA 1
|||||
DE Oligonucleotide SEQ ID NO 12939 for detecting SNP TSC0003018.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 12939; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1812 GTATATATATATA 1824
DB 12 GTATATATATATA 1824
|||||
DE Oligonucleotide SEQ ID NO 12937 for detecting SNP TSC00061564.
```

```
Db 1 GTATATATATATA 13
|||||
RESULT 403
ABF38750
ID ABF38750 standard; DNA; 13 BP.
XX
AC ABF38750;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 138747 for detecting SNP TSC00034761.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 138747; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1817 TATATATATATGT 1829
DB 1 TATATATATATGT 13
|||||
DE Oligonucleotide SEQ ID NO 252372 for detecting SNP TSC00061564.
```

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 252372; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 7 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1805 TGTGTGTGTATAT 1817
 DB 13 TGTGTGTGTATAT 1
 RESULT 405
 ABC43064
 ID ABC43064 standard; DNA; 13 BP.
 XX ABC43064;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 43081 for detecting SNP TSC0012784.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX Claim 1; SEQ ID NO 88230; 29pp + Sequence Listing; German.

PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 43081; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 2 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1804 GTGTGTGTATAT 1816
 DB 1 GTGTGTGTATAT 13
 RESULT 406
 ABC8213/C
 ID ABC8213 standard; DNA; 13 BP.
 XX ABC8213;
 XX 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 88230 for detecting SNP TSC0022170.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 88230; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligonucleotides are also used for detecting cell type differentiation. ABC00010 -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1769 TTTTAAATTTAT 1781
|||||
13 TTTTAAATTTAT 1

Db

RESULT 407
ABH52394
ID ABH52394 standard; DNA; 13 BP.
XX AC ABH52394;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 252371 for detecting SNP TSC0061564.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX Claim 1; SEQ ID NO 252371; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 2 A; 0 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1805 TGTGTGTGTATAT 1817
|||||
1 TGTGTGTGTATAT 13

Db

RESULT 408
ABCI7781/C
ID ABCI7781 standard; DNA; 13 BP.
XX AC ABCI7781;
XX DT 20-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 17788 for detecting SNP TSC0003802.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WIPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX Claim 1; SEQ ID NO 17788; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 6 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1808 GTGTGTATATATA 1820
|||||
13 GTGTGTATATATA 1

Db

RESULT 409

XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 86053; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 6 A; 1 C; 2 G; 4 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1252 TTTTTCGTAATA 1264
 Db 13 TTTTTCGTAATA 1
 RESULT 412
 ABF37479/c
 ID ABF37479 standard; DNA; 13 BP.
 AC ABF37479;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 137476 for detecting SNP TSC0034363.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 137476; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1869 TATTTTGTGTTTT 1881
 Db 13 TATTTTGTGTTTT 1
 RESULT 413
 ABC20146
 ID ABC20146 standard; DNA; 13 BP.
 XX ABC20146;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 20163 for detecting SNP TSC0004136.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 20163; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 1 A; 0 C; 1 G; 11 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1868 TTATTTTGTGTTT 1880
 DB 1 TTATTTTGTGTTT 13

RESULT 414
 ABC05127/c
 ID ABC05127 standard; DNA; 13 BP.
 XX AC ABC05127;
 XX AC ABC05127;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 20164 for detecting SNP TSC0004136.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 20164; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation. ABC00010
 XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 XX represent the oligomers described in the invention. NOTE: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences

QY 1868 TTATTTTGTGTTT 1880
 DB 1 TTATTTTGTGTTT 13

RESULT 415
 ABC05127/c
 ID ABC05127 standard; DNA; 13 BP.
 XX AC ABC05127;
 XX AC ABC05127;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 20164 for detecting SNP TSC0004136.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 20164; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation. ABC00010
 XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 XX represent the oligomers described in the invention. NOTE: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences

QY 1868 TTATTTTGTGTTT 1880
 DB 1 TTATTTTGTGTTT 13

RESULT 416
 ABC05414
 ID ABC05414 standard; DNA; 13 BP.
 XX AC ABC05414;
 XX AC ABC05414;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 5405 for detecting SNP TSC0001818.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.

DT 20-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 5118 for detecting SNP TSC0001771.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 5118; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation. ABC00010
 XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 XX represent the oligomers described in the invention. NOTE: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences

QY 1793 TGTGTGTGTGTGT 1805
 DB 13 TGTGTGTGTGTGT 1

RESULT 416
 ABC05414
 ID ABC05414 standard; DNA; 13 BP.
 XX AC ABC05414;
 XX AC ABC05414;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 5405 for detecting SNP TSC0001818.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1805
 DB 13 TGTGTGTGTGTGT 1

RESULT 416
 ABC05414
 ID ABC05414 standard; DNA; 13 BP.
 XX AC ABC05414;
 XX AC ABC05414;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 5405 for detecting SNP TSC0001818.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 5405; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 7 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1814 ATATATATATATA 1826
 Db 1 ATATATATATATA 13
 RESULT 417
 ABC05414/C
 ID ABC05414 standard; DNA; 13 BP.
 XX
 XX ABC05414;
 XX
 XX 20-FEB-2002 (first entry)
 XX
 XX Oligonucleotide SEQ ID NO 5405 for detecting SNP TSC0001818.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 5405; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 13 BP; 7 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1813 TATATATATATAT 1825
 Db 13 TATATATATATAT 1
 RESULT 418
 ABF61048
 ID ABF61048 standard; DNA; 13 BP.
 XX
 XX ABF61048;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 XX Oligonucleotide SEQ ID NO 161045 for detecting SNP TSC0040548.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 161045; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP).
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1774 AAATTATATGT 1786

Db 1 AAATTATATGT 13

RESULT 419

ABF90363

ID ABF90363 standard; DNA; 13 BP.

XX AC

XX AC ABF90363;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 190360 for detecting SNP TSC0046817.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX PS Claim 1; SEQ ID NO 190360; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 3 A; 1 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2266 TATTTTCTATA 2278

Db 1 TATTTTCTATA 13

RESULT 420

ABF90383/c

ID ABF90383 standard; DNA; 13 BP.

XX AC

XX AC ABF90383;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 190380 for detecting SNP TSC0046825.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.

XX PS Claim 1; SEQ ID NO 190380; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 11 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1867 TTATTTTGTGT 1879

Db 13 TTATTTTGTGT 1

RESULT 421

ABC79590

ID ABC79590 standard; DNA; 13 BP.

XX AC

XX AC ABC79590;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 79607 for detecting SNP TSC0020218.

XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX WO200177384-A2.
 FN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 79607; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 0 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1802 GTGTGTGTGTGTGT 1814
 DB 1 GTGTGTGTGTGTGT 13
 RESULT 422
 ABC05126
 ID ABC05126 standard; DNA; 13 BP.
 XX ABC05126;
 AC ABC05126;
 XX 20-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 5117 for detecting SNP TSC0001771.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX WO200177384-A2.
 FN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX This invention describes novel oligonucleotide primers or peptide nucleic

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 5117; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 0 A; 0 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGT 1805
 DB 1 TGTGTGTGTGTGT 13
 RESULT 423
 ABF37478
 ID ABF37478 standard; DNA; 13 BP.
 XX ABF37478;
 AC ABF37478;
 XX 21-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 137475 for detecting SNP TSC0034363.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX WO200177384-A2.
 FN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 137475; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 1 A; 0 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1869 TATTTTGTGTTT 1891

Db 1 TATTTTGTGTTT 13

RESULT 424

ABF96134

ID ABF96134 standard; DNA; 13 BP.

XX ABF96134;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 196131 for detecting SNP TSC0048267.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 196131; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2202 TTATTTGTTGAGA 2214

Db 1 TTATTTGTTGAGA 13

RESULT 425

ABH13186

ID ABH13186 standard; DNA; 13 BP.

XX ABH13186;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 213163 for detecting SNP TSC0010105.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 213163; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 5 A; 0 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1768 TTTTAAATTA 1780

Db 1 TTTTAAATTA 13

RESULT 426

ABF90362/C

ID ABF90362 standard; DNA; 13 BP.

XX ABF90362;
XX
XX 22-FEB-2002 (first entry)
XX
XX
XX Oligonucleotide SEQ ID NO 190359 for detecting SNP TSC0046817.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 190359; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 9 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Cy 2266 TATTTTTCCTATA 2278
XX
XX Db 13 TATTTTTCCTATA 1
XX
XX
XX RESULT 427
XX ABH60366
XX ID ABH60366 standard; DNA; 13 BP.
XX
XX AC ABH60366;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 260343 for detecting SNP TSC0063217.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX

PN WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
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XX Olek A, Piepenbrock C, Berlin K;
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XX WPI; 2001-657177/75.
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XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 260343; 29pp + Sequence Listing; German.
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XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
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XX central nervous system, cardiovascular and metabolic disorders. The
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XX SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 13; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Cy 1765 GATTTTAAAAAT 1777
XX
XX Db 1 GATTTTAAAAAT 13
XX
XX
XX RESULT 428
XX ABC28588
XX ID ABC28588 standard; DNA; 13 BP.
XX
XX AC ABC28588;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 28605 for detecting SNP TSC0008245.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 28605; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1818 ATATATATATGTA 1830
 Db 1 ATATATATATGTA 13
 RESULT 429
 ABC13480/c
 ID ABC13480 standard; DNA; 13 BP.
 AC ABC13480;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 13487 for detecting SNP TSC0003116.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 13487; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
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 XX
 SQ Sequence 13 BP; 9 A; 0 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1767 TTTTAAAAATTT 1779
 Db 13 TTTTAAAAATTT 1
 RESULT 430
 ABF48195/c
 ID ABF48195 standard; DNA; 13 BP.
 AC ABF48195;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 148192 for detecting SNP TSC0037417.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 148192; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 8 A; 0 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 1766 ATTGTTTAAATTT 1778
Db 13 ATTGTTTAAATTT 1
RESULT 431
ABC43065/C
ID ABC43065 standard; DNA, 13 BP.
XX
AC ABC43065;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 43082 for detecting SNP TSC0012784.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 43082; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC29989, ABP00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
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CC -ABC29989, ABP00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
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CC ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1804 GTGTGTGTGTATA 1816
Db 13 GTGTGTGTGTATA 1
RESULT 432
ABC58806
ID ABC58806 standard; DNA, 13 BP.
XX
AC ABC58806;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 119127 for detecting SNP TSC0029745.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 58823; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
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CC -ABC29989, ABP00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
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Sequence 13 BP; 1 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1803 TGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTAT 13
RESULT 433
ABF19130
ID ABF19130 standard; DNA, 13 BP.
XX
AC ABF19130;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 119127 for detecting SNP TSC0029745.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

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DE Oligonucleotide SEQ ID NO 58823 for detecting SNP TSC0015758.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
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PR 07-APR-2000; 2000DE-01019173.
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PI Olek A, Piepenbrock C, Berlin K;
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DR WPI; 2001-657177/75.
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PT methylation status.
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Sequence 13 BP; 1 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1803 TGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTAT 13
RESULT 433
ABF19130
ID ABF19130 standard; DNA, 13 BP.
XX
AC ABF19130;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 119127 for detecting SNP TSC0029745.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.

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CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTG 1806
Db 1 GTGTGTGTGTGTG 13

RESULT 436
ABC91692
ID ABC91692 standard; DNA; 13 BP.
XX
AC ABC91692;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 91709 for detecting SNP TSC0022946.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
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PI Olek A, Piepenbrock C, Berlin K;
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WPI; 2001-657177/75.
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PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 91709; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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CC central nervous system, cardiovascular and metabolic disorders. The
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CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2259 AAGTGATATTTT 2271
Db 1 AAGTGATATTTT 13

RESULT 437
ABF04284
ID ABF04284 standard; DNA; 13 BP.
XX
AC ABF04284;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 104281 for detecting SNP TSC0026066.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
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PD 18-OCT-2001.
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PF 06-APR-2001; 2001WO-IB000713.
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PR 07-APR-2000; 2000DE-01019173.
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PI Olek A, Piepenbrock C, Berlin K;
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WPI; 2001-657177/75.
XX
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PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 104281; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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CC central nervous system, cardiovascular and metabolic disorders. The
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XX
SQ Sequence 13 BP; 3 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1849 TAAAGTTGTTGT 1861
Db 1 TAAAGTTGTTGT 13

RESULT 438
ABC55254
ID ABC55254 standard; DNA; 13 BP.
XX
AC ABC55254;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 55271 for detecting SNP TSC0015107.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
```

XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX PI WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 55271; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
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 CC was obtained in electronic format from WIPO at
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 XX SQ Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1771 TTAATAATTTATAT 1783
 DB 1 TTAATAATTTATAT 13
 RESULT 439
 ABF06850
 ID ABF06850 standard; DNA; 13 BP.
 AC ABF06850;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 106847 for detecting SNP TSC0026750.
 XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX PI WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 5271; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1771 TTAATAATTTATAT 1783
 DB 1 TTAATAATTTATAT 13
 RESULT 439
 ABF06850
 ID ABF06850 standard; DNA; 13 BP.
 AC ABF06850;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 106847 for detecting SNP TSC0026750.
 XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX PI WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 5271; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 6 A; 0 C; 0 G; 7 T; 0 U; 0 Other;

PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 106847; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 2 A; 0 C; 1 G; 10 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1871 TTTTGTGTTTAA 1883
 DB 1 TTTTGTGTTTAA 13
 RESULT 440
 ABC82325/c
 ID ABC82325 standard; DNA; 13 BP.
 AC ABC82325;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 82342 for detecting SNP TSC0020792.
 XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX PI WPI; 2001-657177/75.
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS Claim 1; SEQ ID NO 82342; 29pp + Sequence Listing; German.
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABF99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABH00010-ABH82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 2 A; 0 C; 1 G; 10 T; 0 U; 0 Other;

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
SQ Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1778 TTATATTCTAAAT 1790
DB 13 TTATATTCTAAAT 1
RESULT 441
ABF38751/C
ID ABF38751 standard; DNA; 13 BP.
XX AC ABF38751;
XX DT 21-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 138748 for detecting SNP TSC0034761.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 138748; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
SQ Query Match 1.2%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1817 TATATATATATGT 1829
DB 13 TATATATATATGT 1
RESULT 442
ABF61494
ID ABF61494 standard; DNA; 13 BP.
XX AC ABF61494;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide SEQ ID NO 161491 for detecting SNP TSC0040647.
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 161491; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 1 A; 0 C; 1 G; 11 T; 0 U; 0 Other;
SQ Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGT 1877
DB 1 TTTTATTTTGT 13
RESULT 443
ABH13187/C
ID ABH13187 standard; DNA; 13 BP.
XX AC ABH13187;

PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PS Claim 1; SEQ ID NO 196132; 29pp + Sequence Listing; German.
 XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2202 TTATTGTGACA 2214

Db 13 TTATTGTGACA 1

RESULT 446

ABF61049/C
 ID ABF61049 standard; DNA; 13 BP.

XX AC ABF61049;

XX 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 161046 for detecting SNP TSC0040548.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 161046; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1774 AAATTATATTTGT 1786

Db 13 AAATTATATTTGT 1

RESULT 447

ABK70590
 ID ABK70590 standard; DNA; 13 BP.

XX AC ABK70590;

XX 15-JUL-2002 (first entry)

DE Ligand binding affinity determining oligonucleotide #32.

XX Ligand binding affinity; ss.

XX Synthetic.

XX US6355428-B1.

XX 12-MAR-2002.

XX 10-SEP-1999; 99US-00393783.

XX 11-SEP-1998; 98US-00151890.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Schroth GP, Bruice TW, Suh YJ;

XX WPI; 2002-380936/41.

XX Determining relative affinity of ligands for oligonucleotides, from
 PT ability to separate a duplex of oligonucleotides, one labeled and the
 PT other having a signal modifying group.

PS Disclosure; Col 16; Sipp; English.

CC The invention relates to a method for determining the relative binding
 CC affinities of a ligand to different oligonucleotides. A mixture is formed
 CC from two oligonucleotides, one carrying a label and a second containing a
 CC group that alters the signal from the label, when the sequences
 CC hybridise. In the absence of the ligand, the oligonucleotides exist
 CC mainly in single-stranded form and the signal is recorded in this state.
 CC The ligand is then added and the signal measured again, and the effect
 CC compared with that observed for a different pair of oligos. The relative
 CC binding affinities of the ligands are determined by comparing their
 CC effects. Sequences ABK70559-ABK70529 represent oligonucleotides used for
 CC determining relative binding affinities of ligands

XX Sequence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806

Db 1 GTGTGTGTGTGTG 13

RESULT 448
 AAD45600
 ID AAD45600 standard; DNA; 13 BP.
 XX
 AC AAD45600;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 Competitor oligo used in the invention #1.
 DE
 XX Competitive binding assay; binding affinity; ligand; indicator;
 KW competitor; ss.
 XX
 OS Unidentified.
 XX
 PN US6420109-B1.
 XX
 PD 16-JUL-2002.
 XX
 PF 11-SEP-1998; 98US-00151890.
 XX
 PR 11-SEP-1998; 98US-00151890.
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Schroth GP, Bruce TW, Suh YJ;
 XX
 DR WPI; 2002-626078/67.
 XX
 XX New assay for determining relative binding affinities of a ligand to
 PT different oligonucleotide sequences is useful to determine nucleic acid
 PT binding specificities and base pair determinants of particularly ligands.
 XX
 PS Disclosure; Col 11; 32pp; English.
 XX
 CC The invention relates to methods for determining relative binding
 CC affinities of a ligand to different oligonucleotide sequences, using
 CC indicator oligonucleotide pairs having a signal and a signal-altering
 CC group attached in direct or competitive binding assays. The method is
 CC used to determine nucleic acid binding specificities and base pair
 CC determinants of particular ligands. The present sequence is a competitor
 CC oligonucleotide used to illustrate the method of the invention
 XX
 SQ Sequence 13 BP; 0 A; 0 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1794 GTGTGTGTGTGTG 1806
 DB 1 GTGTGTGTGTGTG 13
 RESULT 449
 ABX79758
 ID ABX79758 standard; cDNA; 15 BP.
 XX
 AC ABX79758;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #83.
 XX
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX

PN US6472154-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 31-DEC-1999; 99US-00475947.
 XX
 PR 31-DEC-1999; 99US-00475947.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX
 DR WPI; 2003-208818/20.
 XX
 XX Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.
 XX
 PS Example; Col 309; 588pp; English.
 XX
 CC The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 SQ Sequence 15 BP; 9 A; 0 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1814 ATATATATATATATA 1826
 DB 1 ATATATATATATA 13
 RESULT 450
 AAT55014/c
 ID AAT55014 standard; RNA; 15 BP.
 XX
 AC AAT55014;
 XX
 DT 25-MAR-2003 (revised)
 XX
 DT 18-APR-1997 (first entry)
 XX
 DE Human relA hammerhead ribozyme target sequence (nt. position 562).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 XX
 OS Homo sapiens.
 XX

PN WO9523225-A2.
 XX 31-AUG-1995.
 XX 23-FEB-1995; 95WO-IB000156.
 XX 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00321993.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX Ribozyms having modified bases and methods for producing them - for use
 in inhibiting disease related genes.
 PS Claim 2; Page 228; 407pp; English.
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the
 CC nucleotide base position indicated in the DE line. The relA gene product
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated
 CC specifically in the induction of inflammatory responses. Regions of the
 CC mRNA that do not form secondary folding structures and that contain
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified
 CC by computer analysis. Ribozymes directed against these mRNA sequences
 CC were designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit relA expression, making them potentially
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well
 CC as for increasing tolerance to transplanted tissues. The potential
 CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means
 CC that uses are limited to local delivery, acute indications or ex vivo
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
 XX Query Match 1.2%; Score 13; DB 1; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 3e+02;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2152 TCACCTGGAAGCA 2164
 DB 15 TCACCTGGAAGCA 3

RESULT 451
 AAT54825/c
 ID AAT54825 standard; RNA; 15 BP.
 XX
 AC AAT54825;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-APR-1997 (first entry)
 XX
 DE Mouse relA hammerhead ribozyme target sequence (nt. position 562).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW myocardial rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 SS.
 XX
 OS Mus musculus.
 XX
 PN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 XX 23-FEB-1995; 95WO-IB000156.
 XX
 PR 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00321993.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 XX Ribozyms having modified bases and methods for producing them - for use
 in inhibiting disease related genes.
 PS Claim 2; Page 225; 407pp; English.

XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the
 CC nucleotide base position indicated in the DE line. The relA gene product
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated
 CC specifically in the induction of inflammatory responses. Regions of the
 CC mRNA that do not form secondary folding structures and that contain
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified
 CC by computer analysis. Ribozymes directed against these mRNA sequences
 CC were designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit relA expression, making them potentially
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well
 CC as for increasing tolerance to transplanted tissues. The potential
 CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means
 CC that uses are limited to local delivery, acute indications or ex vivo
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2152 TCACCTGGAGCA 2164
 Dd 15 TCACCTGGAGCA 3
 RESULT 452
 AAT54971/C
 ID AAT54971 standard; RNA; 15 BP.
 XX
 AC AAT54971;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-APR-1997 (first entry)
 XX
 DE Mouse relA hammerhead ribozyme target sequence (nt. position 1664).
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.
 XX
 OS Mus musculus.
 XX
 PN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-IB000156.
 XX
 PR 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.

PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Chowira B, Dhirenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcawiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX
 DR WPI; 1995-35i090/45.
 XX
 PT Ribozymes having modified bases and methods for producing them - for use
 PT in inhibiting disease related genes.
 XX
 PS Claim 2; Page 226; 407pp; English.
 XX
 CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the
 CC nucleotide base position indicated in the DE line. The relA gene product
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated
 CC specifically in the induction of inflammatory responses. Regions of the
 CC mRNA that do not form secondary folding structures and that contain
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified
 CC by computer analysis. Ribozymes directed against these mRNA sequences
 CC were designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit relA expression, making them potentially
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well
 CC as for increasing tolerance to transplanted tissues. The potential
 CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means
 CC that uses are limited to local delivery, acute indications or ex vivo
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 1.2%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2152 TCACCTGGAGCA 2164
 Dd 15 TCACCTGGAGCA 3
 RESULT 453
 AAZ90176
 ID AAZ90176 standard; cDNA; 15 BP.
 XX
 AC AAZ90176;
 XX
 DT 19-MAY-2000 (first entry)
 XX
 DE 3-nitropyrrole-containing primer.
 XX
 KW Chemokine receptor; interleukin-8 compound inhibitor; chromosome 7p22;
 KW inflammation; wound healing; neutropenia; myeloid leukaemia; tumour;
 KW toxin delivery; hypermegakaryocytopoietic disease; polycythemia vera;
 KW primer; ss.
 XX
 OS Synthetic.

Key modified_base 8 Location/Qualifiers
 FT FT /tag= a
 FT FT /note= "Optionally A, T, G, C or 1-(2-deoxy-D-
 FT FT riburanosyl)-3-nitropyrolole"
 XX XX
 PN WO20000515-A2.
 XX
 PD 06-JAN-2000.
 XX
 XX 29-JUN-1999; 99WO-US012829.
 XX
 XX 29-JUN-1998; 98US-00106900.
 PR 22-JAN-1999; 99US-00236166.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX WPI; 2000-170907/15.
 DR
 XX New nucleic acid encoding chemokine receptor, useful for diagnosis and
 XX treatment of e.g. neutropenia, inflammation and leukemia.
 PT
 XX Example 2; Page 52; 138pp; English.
 PS
 XX This sequence represents a 3-nitropyrolole-containing primer which is used
 CC in the course of the invention. The invention relates to a polynucleotide
 CC sequence which encodes a human chemokine receptor. The nucleotide
 CC sequence (see AA290174) is derived from a human foetal liver-spleen cDNA
 CC library. The chemokine receptor (see AA78856) encoded by the nucleotide
 CC sequence inhibits the activity of interleukin-8-type compounds through
 CC competition for cell binding sites. The chemokine receptor gene is
 CC located on the short arm of chromosome 7 at 7p22. The polynucleotide
 CC encoding the chemokine receptor is useful as a hybridization probe or a
 CC PCR primer, the nucleotide sequence may also be used for chromosome/gene
 CC mapping or in the recombinant production of polypeptides and the
 CC production of antisense or triplex-forming molecules for the control of
 CC gene expression. The chemokine receptor polypeptides are used to raise
 CC specific antibodies, also for purification, detection or modulation of
 CC interleukin-8-type chemokines (for diagnosis or prognosis, or monitoring
 CC chemokine recruitment at a site of infection or inflammation). The
 CC protein sequence can also be used as molecular weight markers or food
 CC supplements, and to screen compound libraries for specific binding
 CC agents, potential agonists or antagonists. Antibodies raised against the
 CC chemokine receptor polypeptide sequence are used to detect or purify the
 CC polypeptide, also for the diagnosis and treatment of activated or
 CC inflamed cells or tissues, and to promote the healing of wounds. The
 CC polypeptide and antibodies are also used to prevent neutropenia
 CC (associated with chemotherapy or radiation treatment to protect myeloid
 CC precursors), inflammation or other immune responses; also conditions
 CC associated with hyperproliferation of progenitor cells (e.g. some
 CC myelogenous leukaemias, polycythaemia vera and hypermegakaryocytopenic
 CC diseases). The antibodies are potentially useful therapeutically; e.g. to
 CC carry toxins to tumour cells
 XX
 SQ Sequence 15 BP; 0 A; 2 C; 2 G; 10 T; 0 U; 1 Other;
 Query Match 1.2%; Score 13; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1863 CCCTTTTATTGTTG 1876
 Db 1 CCCTTTTATTGTTG 14
 RESULT 454
 ABK55502
 ID ABK55502 standard; DNA; 15 BP.
 XX
 AC ABK55502;
 XX
 DT 18-JUN-2002 (first entry)
 XX

DE Selectin L Lymphocyte Adhesion Molecule 1 (SELL) oligonucleotide #38.
 XX
 KW Human; Selectin L Lymphocyte Adhesion Molecule 1; SELL;
 KW neonatal pertussis; whooping cough; haplotyping; primer;
 KW allele-specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200216654-A1.
 XX
 PD 28-FEB-2002.
 XX
 XX 27-AUG-2001; 2001WO-US026675.
 PF
 XX 25-AUG-2000; 2000US-0228262P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Anastasio AE, Bieglecki KM, Kliem SE, Koshy B, Kumar AM;
 XX WPI; 2002-292071/33.
 DR
 XX Novel genetic variants of selectin L lymphocyte adhesion molecule 1
 PT (SELL) gene useful for therapeutic purposes and for expressing SELL
 PT protein useful in identifying drugs to treat whooping cough.
 XX
 PS Claim 17; Page 14; 137pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence which is a polymorphic variant of a reference
 CC sequence for Selectin L Lymphocyte Adhesion Molecule 1 (SELL) gene. SELL
 CC polypeptide is useful for screening for drugs targeting the polypeptide.
 CC Oligonucleotides derived from (I) are used to target SELL and a haplotype
 CC or haplotype pair of SELL gene. These are useful in developing diagnostic
 CC tests and therapeutic treatments for neonatal pertussis (whooping cough).
 CC (I) is useful for studying the expression and function of SELL and
 CC expressing SELL protein for use in screening for candidate drugs to treat
 CC diseases related to SELL activity. The polymorphism and haplotype data
 CC are useful for validating whether SELL is a suitable target for drugs to
 CC treat whooping cough, screening for such drugs and reducing bias in
 CC clinical trials of such drugs. Establishing the SELL haplotype or
 CC haplotype pair of an individual is useful for improving the efficiency
 CC and reliability of several steps in the discovery and development of
 CC drugs for treating diseases associated with SELL activity e.g. neonatal
 CC pertussis (whooping cough). The haplotyping method is useful to validate
 CC SELL as a candidate target for treating a specific condition or disease
 CC in screening for compounds targeting SELL to treat a specific condition
 CC or disease predicted to be associated with SELL activity, e.g. detecting
 CC which of the SELL haplotypes or haplotype pairs present in individual
 CC members of a population with the specific disease of interest enables one
 CC to screen for compounds that display the highest desired agonist or
 CC antagonist activity for each of the most frequent SELL isoforms present
 CC in the disease population. A polymorphic variant of SELL is useful in
 CC studying the effect of the variation on the biological activity of SELL,
 CC on the binding affinity of candidate drugs targeting SELL for the
 CC treatment of neonatal pertussis (whooping cough) and in assays to measure
 CC the binding affinities of one or more candidate drugs targeting the SELL
 CC protein. ABK5545-ABK5559 represent SELL gene allele-specific
 CC oligonucleotides of the invention
 XX
 SQ Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 1 Other;
 Query Match 1.2%; Score 13; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 3e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1584 CCCCAGTGCAGCT 1598
 Db 1 GCCCAGTGCAGT 15
 RESULT 455

```
ACH50832
ID ACH50832 standard; DNA; 15 BP.
XX
AC ACH50832;
XX
DT 13-OCT-2003 (first entry)
XX
DE 3-nitropyrrole containing oligonucleotide #1.
XX
KW Primer; ss; sequencing by hybridisation; SBH; 3-nitropyrrole;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Synthetic.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
PS Example 2; Page 16; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is an example of an oligonucleotide containing a 3-nitropyrrole base
XX analogue which may be used in the SBH technique
XX
SQ Sequence 15 BP; 0 A; 2 C; 2 G; 10 T; 0 U; 1 Other;
Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1863 CCTTTTATTTTG 1876
DB 1 CCTTTTNTTTTG 14
RESULT 456
ACH50832/c
ID ACH50833 standard; DNA; 15 BP.
XX
AC ACH50833;
XX
DT 13-OCT-2003 (first entry)
```

```
XX
DE 3-nitropyrrole containing oligonucleotide #2.
XX
KW Primer; ss; sequencing by hybridisation; SBH; 3-nitropyrrole;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Synthetic.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
PS Example 2; Page 16; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is an example of an oligonucleotide containing a 3-nitropyrrole base
XX analogue which may be used in the SBH technique
XX
SQ Sequence 15 BP; 10 A; 2 C; 2 G; 0 T; 0 U; 1 Other;
Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1863 CCTTTTATTTTG 1876
DB 15 CCTTTTNTTTTG 2
RESULT 457
ACF63345
ID ACF63345 standard; DNA; 16 BP.
XX
AC ACF63345;
XX
DT 09-OCT-2003 (first entry)
XX
DE Human CD40L antisense oligonucleotide SEQ ID NO:67.
XX
KW Human; pharmacological; hypotensive; antilipaemic; vasotropic; laxative;
KW dermatological; antidepressant; tranquiliser; antiinflammatory; eczema;
KW antiulcer; antimigraine; neuroprotective; antiparkinsonian; analgesic;
```

KW gynaecological; virucide; vulnary; antiarthritic; antipsoriatic; cold;
 KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;
 KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
 KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
 KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
 KW constipation; headache; seizure; multiple sclerosis; polymyositis;
 KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;
 KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
 KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;
 KW inflammation; heart burn; infection; colon cancer; malignant melanoma;
 KW skin disorder; antisense oligonucleotide; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2003006478-A1.
 XX 23-JAN-2003.
 XX 10-JUL-2002; 2002WO-US021664.
 XX 10-JUL-2001; 2001US-0303820P.
 XX (OLIG-) OLIGOS ETC INC.
 XX Dale RMK, Arrow A, Thompson T;
 XX WPI; 2003-221709/21.
 XX Composition with a modified oligonucleotide useful for treating a patient
 PT with a pathological disorder such as abnormal appetite, hypertension,
 PT eczema, anxiety, stress, and cancer.
 XX Claim 17; Page 9; 173pp; English.

XX The present invention describes a composition (I) suitable for
 CC administration in a mammal, which comprises a modified oligonucleotide
 CC (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups
 CC linked by achiral 5'-3' internucleoside phosphate linkages, where the
 CC modified oligonucleotide is complementary to a region of a gene
 CC associated with a pathological disorder. Also described: (1) a
 CC nutritional supplement comprising (II); and (2) a cosmetic composition
 CC comprising (II), where the modified oligonucleotide is complementary to a
 CC region of a gene associated with a skin disorder. (I) and (II) can have
 CC hypotensive, antilipemic, vasotropic, dermatological, antidepressant,
 CC tranquiliser, antiinflammatory, antitumor, laxative, antimigraine,
 CC neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,
 CC litholytic activities. (I) can be used for treating a patient with a
 CC pathological disorder selected from abnormal appetite, hypertension,
 CC hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,
 CC depression, anxiety, stress, inflammatory bowel syndrome, ulcerative
 CC colitis, Crohn's disease, renal stones, gall stones, constipation, colds,
 CC migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,
 CC fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
 CC chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,
 CC chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatitis,
 CC inflammation, heart burn, infection, poison ivy, colon cancer, malignant
 CC melanoma, and malignant nasal polyps. The nutritional supplement is
 CC useful for supplementing the diet of an individual, and the cosmetic
 CC composition is useful for improving the appearance of the skin in an
 CC individual with a skin disorder. ACF63279 to ACF63410 represent
 CC nucleotide sequence given in the exemplification of the present invention
 XX Sequence 16 BP; 4 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.2%; Score 13; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1688 TCACACTGTTTCAG 1700
 DB 4 TCACACTGTTTCAG 16

RESULT 458
 AAQ27968
 ID AAQ27968 standard; DNA; 16 BP.

XX AAQ27968;
 AC AAQ27968;
 XX 11-FEB-1993 (first entry)
 DT Primer V810.

XX Polymerase chain reaction; PCR; amplify; Staphylococcus; ss.

XX Synthetic.

XX JP04211370-A.

XX 03-AUG-1992.

XX 19-FEB-1991; 91JP-00024633.

XX 20-FEB-1990; 90JP-00040398.

XX (SHIO) SHIONOGI & CO LTD.

XX WPI; 1992-304938/37.

XX Novel protease prep'd. using Bacillus or Saccharomyces host - capable of
 PT cleaving peptide bond at carboxyl terminus of glutamic acid residues in
 PT polypeptide(s).

XX Disclosure; Page 4; 25pp; Japanese.

XX The sequences given in AAQ27960-86 are primers which were used in the
 CC construction of the DNA encoding a Staphylococcus protease. The protease
 CC (see also AAQ27987) specifically cleaves the peptide bond at the C-
 CC terminus of the glutamic acid residue in polypeptide
 XX Sequence 16 BP; 5 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 1.2%; Score 12.8; DB 1; Length 16;

Best Local Similarity 87.5%; Pred. No. 3.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2200 GTTATTGTTGAG 2215

DB 1 GTTATTGTTAAAG 16

RESULT 459

AAQ07568/C

ID AAQ07568 standard; cDNA; 16 BP.

XX AAQ07568;

XX 21-JUN-1999 (first entry)

XX Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.

XX Secreted protein; fetal kidney; ds.

XX Homo sapiens.

XX WO9900405-A1.

XX 07-JAN-1999.

XX 29-JUN-1998; 98WO-US013530.

XX 30-JUN-1997; 97US-00685610.

XX (GEM) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Evans C, Agostino MJ;
XX WPI; 1999-095671/08.
XX New polynucleotides encoding secreted human proteins - are derived from
PT foetal kidney or adult retina cDNA libraries, used as, e.g. potential
PT vaccines.
XX Disclosure; Page 54; 76pp; English.
XX The sequence is that of the 3' end of a sequence encoding a secreted
CC protein from a human fetal kidney clone AX296. Such a sequence is
CC predicted to have biological activities which would make them suitable
CC for treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity, and thrombolytic activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC invasion suppressor activity, and tumour inhibition activity. It is also
CC stated to be useful for gene therapy
XX
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
DB 16 TTTTATTTTGTGTTT 1
RESULT 460
AAZ98510/c
ID AAZ98510 standard; DNA; 16 BP.
XX
AC AAZ98510;
XX
XT 19-JUN-2000 (first entry)
XX
XX H. discus derived sequence #28.
XX
XX Satellite sequence; DNA fragmentation; microsatellite DNA; DNA marker;
XX Hallotis discus; ss.
XX
XX Hallotis discus.
XX
XX WO200011156-A1.
XX
XX 02-MAR-2000.
XX
XX 01-JUL-1999; 99WO-JP003551.
XX
XX 18-AUG-1998; 98JP-00232153.
XX
XX (NORQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX
XX Takahashi H, Sekino M;
XX
XX WPI; 2000-224692/19.
XX
XX Isolation of satellite sequences from genomic DNA for use as DNA markers
PT comprises isolating a library with high homogeneity by DNA fragmentation.
XX
XX Example 5; Page 15; 35pp; Japanese.
XX
XX The invention provides a novel method for isolation of satellite
CC sequences from genomic DNA that comprises fragmentation of the DNA by a

CC method which is not dependent on base sequences, then selection of the
CC satellite sequences from the obtained genomic library of high
CC homogeneity. The method is useful for the isolation of microsatellite DNA
CC sequences which can be used as DNA markers. The new method markedly
CC improves the efficiency of isolation of satellite sequences in comparison
CC to prior art methods which are reliant on base sequences. Sequences
CC AAZ98483-514 represent sequences from Hallotis discus, used in the method
CC of the invention
XX
SQ Sequence 16 BP; 8 A; 6 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
DB 16 TCTCTGTGTGTGTGTG 1
RESULT 461
AAC66068/c
ID AAC66068 standard; DNA; 16 BP.
XX
AC AAC66068;
XX
XX 22-FEB-2001 (first entry)
XX
XX DNA chip primer #4.
XX
XX DNA chip; primer; nucleoside derivative; photolabile protecting group;
XX photolithographic nucleic acid chip; ss.
XX
XX Synthetic.
XX
XX WO200061594-A2.
XX
XX 19-OCT-2000.
XX
XX 07-APR-2000; 2000WO-DE001148.
XX
XX 08-APR-1999; 99DE-01015867.
XX
XX 28-JAN-2000; 2000DE-01003631.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Beier M, Hoheisel J;
XX
XX WPI; 2000-679457/66.
XX
XX New nucleoside derivatives with photolabile protecting groups, useful in
PT oligonucleotide synthesis, particularly on solid phases, e.g. for
PT hybridization testing.
XX
XX Disclosure; Fig 9; 48pp; German.
XX
XX This invention describes nucleoside derivatives (I) with photolabile
CC protecting groups. (I) are used to synthesize oligonucleotides using the
CC photolithographic nucleic acid chip method, particularly where these are
CC intended for performing enzymatic reactions initiated from a free 3'-
CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,
CC but also reverse transcription, cDNA synthesis etc.), also for
CC hybridization testing, sequencing and in DNA computing. (I) are produced
CC with high selectivity by reaction with a mild acylating agent that has
CC high specificity for the 3'-position, without significant side-reactions
CC (cf. more reactive acylating agents such as chloroformates)
XX
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OS Synthetic.
XX WO200131063-A1.
PN
XX
XX 03-MAY-2001.
PD
XX
XX 26-OCT-2000; 2000WO-US029786.
PF
XX
XX 26-OCT-1999; 99US-00428236.
PR
XX
XX (EPOC-) EPOCH BIOSCIENCES INC.
PA
XX
XX Dempcy RO, Afonina IA, Vermeulen NMJ;
PI
XX
XX WPI; 2001-328656/34.
DR
XX
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT mismatch discrimination.
XX
XX
PS Disclosure; Page 58; 105pp; English.
XX
XX The present sequence is that of the oligonucleotide (ODN) component of an
CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC invention. MGBs bind in a non-intercalating manner to the minor groove of
CC but in an intercalating manner, or lies in the minor groove, or is
CC oriented in some other way to the DNA molecule by MGB, such that it
CC becomes fluorescent for its fluorescent properties change detectably).
CC The conjugates are used as hybridisation probes and amplification primers
CC for fluorescent detection of specifically hybridising sequences, for
CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC mismatch discrimination, target or signal amplification, array-based
CC assays and sequencing, including detection of double-stranded DNA by
CC triplex formation. Many different targets can be detected a single
CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC hybridisation-triggered fluorescence. Upon hybridisation to the
CC complementary target sequence there was an increase in fluorescence
CC yield, measured as the ratio of the fluorescence emitted by the hybrid
CC between the ODN-MGB-LF conjugate and its target sequence to the
CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC of 8.3
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 465
AAH42481
ID AAH42481 standard; DNA; 16 BP.
XX
XX AAH42481;
AC
XX
XX 01-OCT-2001 (first entry)
DT
XX
XX Oligonucleotide used to produce branched chain compounds.
DE
XX
XX Branched chain compound; nucleic acid synthesis; primer extension;
KW reverse transcription; nucleic acid hybridization;
KW nucleic acid amplification; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1
FT
FT
FT

FT
FT misc_feature /note= "COOH attached"
FT 2. .3
FT /*tag= c
FT /note= "branch present"
FT 2
FT modified_base /tag= b
FT /note= "COOH attached"
XX
XX EP1111068-A1.
PN
XX
XX 27-JUN-2001.
PD
XX
XX 21-DEC-1999; 99EP-00125484.
PF
XX
XX 21-DEC-1999; 99EP-00125484.
PR
XX
XX (LION-) LION BIOSCIENCE AG.
PA (VBCG-) VBC GENOMICS GMBH.
XX
XX Schmidt W, Hiller R, Huber M, Mueller M;
PI WPI; 2001-466959/51.
DR
XX
XX Branched compounds useful in e.g. nucleic acid synthesis reaction
PT comprises nucleic acid moieties optionally extended by a polymerase.
XX
XX Example 1; Page 10; 31pp; English.
PS
XX The specification describes branched compounds containing nucleic acid
CC moieties optionally extended by a polymerase. The branched chain
CC compounds of the invention are used in nucleic acid synthesis reaction,
CC primer extension reaction, reverse transcription reaction of RNA into
CC DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC nucleic acid), and nucleic acid amplification experiment (for analysing
CC the expression pattern of genes). The compounds are also used in solid-
CC phase enzymatic reactions. The present sequence was used in the course of
CC the invention to produce branched chain compounds
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 466
ABA97402
ID ABA97402 standard; DNA; 16 BP.
XX
XX ABA97402;
AC
XX
XX 18-JUN-2002 (first entry)
DT
XX
XX Nucleotide sequence of oligomer # 1 used to test thermal stability.
DE
XX
XX Protein nucleic acid molecule; PNA; ds.
KW
XX
XX Synthetic.
OS
XX
XX WO200168673-A1.
PN
XX
XX 20-SEP-2001.
PD
XX
XX 13-MAR-2001; 2001WO-US008111.
PF
XX
XX 14-MAR-2000; 2000US-0189190P.
PR
XX 30-NOV-2000; 2000US-0250334P.
PR
XX
XX (ACTI-) ACTIVE MOTIF.
PA


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XX Bimov V, Fernandez J, Archdeacon D, Archdeacon J;
PI Chakhmakhechev O, Buryakova A, Choob M, Hondorp K;
XX WPI; 2002-041177/05.
XX
XX Oligonucleotides analogs useful in detection, separation and purification
PT of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
XX Example 17; Page 118; 197pp; English.
XX
XX This invention relates to oligonucleotide analogues comprising a protein
CC nucleic acid molecule (PNA) monomer. They are used in the detection and
CC separation of nucleic acid molecules and as probes, primers, linkers,
CC adapters and antisense agents on solid supports. Modifications enhance
CC their use as capture and detection probes e.g. by the incorporation of
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
CC fluorescein and reporter molecules such as alkaline phosphatase. They are
CC also used for enhancing or inhibiting the activity of an enzyme or
CC cellular activity. The compounds are stable to nucleases and proteases,
CC have high affinity, binding specificity and solubility. The polyamide
CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC nucleic acid molecules with greater affinity than DNA or RNA
CC concentration. The compounds are relatively simple to synthesize and are
CC used in a wide variety of applications. This sequence represents a DNA
CC oligomer which is used to represent the thermal stability of the
CC oligomers of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
DB 1 TTTTATTGTTT 16

RESULT 467
AAL56451
ID AAL56451 standard; DNA; 16 BP.
XX
AC AAL56451;
XX
DT 07-AUG-2003 (first entry)
XX
DE 2'-P-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
XX
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..16
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluorocarbinothymidine"
FT misc_feature 8..9
FT /tag= b
FT /note= "Bases 8 and 9 are linked by two secouridine
FT linkers which is represented as S in page 49 and X in
FT page 57 and Fig 7 and 8 of the specification"
XX
PN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
XX 29-OCT-2002; 2002WO-CA001628.
XX
XX 29-OCT-2001; 2001US-0330719P.
XX

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PA (UTWC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX
XX WPI; 2003-421516/39.
XX
XX Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
XX Example 2; Fig 7; 104pp; English.
XX
XX The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations of complementments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
DB 1 TTTTATTGTTT 16

RESULT 468
AAL54078
ID AAL54078 standard; DNA; 16 BP.
XX
AC AAL54078;
XX
DT 06-MAR-2003 (first entry)
XX
DE Oligo-homodeoxyribonucleotide sequence, oligo dT.
XX
KW Detection; single-stranded sensor; detectable fluorescence emission;
KW forensic testing; paternity testing; tissue typing; hereditary disorder;
KW human population genetics; human evolutionary history; cystic fibrosis;
KW human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
XX
OS Unidentified.
XX
PN WO200284271-A2.
XX
PD 24-OCT-2002.
XX
PF 16-APR-2002; 2002WO-US012176.
XX
PR 16-APR-2001; 2001US-00836579.
XX
PA (REGC ) UNIV CALIFORNIA.
PA (CHAJ/) CHA J N.
XX
PI Cha JN, Morse DE, Stucky GD;
XX
XX WPI; 2003-103378/09.
XX
XX Detecting polynucleotides, for pharmacogenetic testing, comprises
PT contacting a target polynucleotide with a complementary single-stranded
PT sensor polynucleotide and an agent that allows the sensor to fluoresce
PT upon excitation.

```


the human c-myc sequence at the base position indicated in the descriptor line. The c-myc sequence was screened for optimal ribozyme target sites using a computer folding algorithm, and regions of the mRNA which did not form secondary folding structures and contained potential ribozyme cleavage sites were identified. Ribozymes were synthesised and their activities optimised by either varying the length of the binding arms or by modification to prevent degradation by nucleases. The ribozymes cleave the c-myc sequence and can be used to prevent smooth muscle cell hyperproliferation in restenosis, especially after coronary angioplasty, and in cancers

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Query Match      1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 43.8%; Pred. No. 3.4e+02;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

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Qy 1811 TGTATATATATATA 1826
: : : : : : : : : :
Db 2 UUUUUUUUUUUUACA 17

RESULT 471
ABK55689
ID ABK55689 standard; RNA; 17 BP.

XX	ABK55689;
AC	
XX	
DT	02-JUL-2002 (first entry)

Human CLCA1 gene enzymatic nucleic acid #60.

Human; chloride channel calcium activated 1; CLCA1; ss; anisasthmatic;
ant inflammatory; chronic obstructive pulmonary disease; COPD; asthma;
chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
acetylcysteine.

xx
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05
Homo sapiens.

XX PN WO200211674-A2.

14-FEB-2002

XX
PF 09-AUG-2001: 2001WO-US024970.XX
PR 09-AUG-2000: 2000US-0224383P.

XX PA (RTBO-) RTBOZYME PHARM INC.

PA (SYNT) SYNTAX USA LLC.
PA (THOM /) THOMPSON J

XX Thompson J, Mcswiggen J, Mckenzie T, Ayers D, Szymkowski DE;
PI Grupe A;

DR WPI; 2002-217145/27.

Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

PS Claim 4: page 54: 152pp: English.

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises

the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

Sequence 17 BP: 7 A; 1 C; 1 G; 0 T; 8 U; 0 Other;

Query Match : 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 3.4e+02;
Matches 6; Conservative 8; Mismatches 2; Indels

1807 TGTGTATATATA 1822

2 IIANCTUGIAUAUAUA 17

RESULT 472

ABC05097/C

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2000

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ID 7002-FEB-02 221126 CAC-1

XX
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic

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2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

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Figure 1

XIX

PT designed to detect single-nucleotide polymorphisms and cytosine

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XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system and gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABCC00010
CC-ABCS9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC www.wipo.int/pub/published pct sequences

Sequence 13 BP: 10 A; 1 C; 0 G; 1 T; 0 U; 1 Other; XX 50

Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12: Conservative 1; Mismatches 0; Indels

XX	Oligonucleotide SEQ ID NO 182712 for detecting SNP TSC0045154.
DE	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
OS	WO200177384-A2.
PN	18-OCT-2001.
PD	06-APR-2001; 2001WO-IB000713.
XX	07-APR-2000; 2000DE-01019173.
XX	(EPIG-) EPIGENOMICS AG.
PA	Olek A, Piepenbrock C, Berlin K,
PI	WPI; 2001-657177/75.
XX	Set of oligonucleotides, useful for diagnosis and cell typing, is
XX	designed to detect sing-e-nucleotide polymorphisms and cytosine
PT	methylation status.
PT	Claim 1; SEQ ID NO 182712; 29pp + Sequence Listing; German.
PS	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligomers are also used for detecting cell type differentiation. ASC00010
CC	-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC	represent the oligomers described in the invention. NOTE: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	Sequence 13 BP; 4 A; 0 C; 0 G; 8 T; 0 U; 1 Other;
SQ	Query Match 1.2%; Score 12.6; DB 1; Length 13;
	Best Local Similarity 92.3%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
	Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1766 ATTTTAAAAATT 1778
Dd	:
Dd	1 RTTTTAAAAATT 13
RESULT 475	
ABF60174	
ID	ABF60174 standard; DNA; 13 BP.
XX	ABF60174;
AC	22-FEB-2002 (first entry)
DT	Oligonucleotide SEQ ID NO 160171 for detecting SNP TSC0040332.
DE	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	Homo sapiens.
OS	WO200177384-A2.
FN	18-OCT-2001.
XX	22-FEB-2002 (first entry)
PD	

PF 06-APR-2001; 2001WO-IB000713.
 XX PR
 XX 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS
 XX Claim 1; SEQ ID NO 160171; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ
 XX Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;
 Query Match 1.2%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
 Matches 12; Conservative 1; Mismatches 0;
 QY 1866 TTTTATTTTGGT 1878
 DB 1 TTTTATTTTGT 13
 RESULT 476
 ABC68366
 ID ABC68366 standard; DNA; 13 BP.
 XX AC ABC68366;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 68383 for detecting SNP TSC0017833.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 68383; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ
 XX Sequence 13 BP; 2 A; 0 C; 2 G; 8 T; 0 U; 1 Other;
 Query Match 1.2%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
 Matches 12; Conservative 1; Mismatches 0;
 QY 2261 GTGTATATTTT 2273
 DB 1 GTGTATATTTT 13
 RESULT 477
 ABC68367/C
 ID ABC68367 standard; DNA; 13 BP.
 XX AC ABC68367;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 68384 for detecting SNP TSC0017833.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PS
 XX Claim 1; SEQ ID NO 68384; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 8 A; 2 C; 0 G; 2 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2261 GTGTATATTTT 2273

Db 13 GTGTATATTTT 1

RESULT 478

ID ABC14215/C

XX ABC14215 standard; DNA; 13 BP.

AC ABC14215;

DT 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 14222 for detecting SNP TSC0003234.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

PN 18-OCT-2001.

PD 06-APR-2001; 2001WO-IB000713.

PF 07-APR-2000; 2000DE-01019173.

PR (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

PI WPI; 2001-657177/75.

DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 14222; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGT 1805

Db 13 TGTGTGTGTGT 1

RESULT 479

ID ABF96635

XX ABF96635 standard; DNA; 13 BP.

AC ABF96635;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 196632 for detecting SNP TSC0048388.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

PN 18-OCT-2001.

PD 06-APR-2001; 2001WO-IB000713.

PF 07-APR-2000; 2000DE-01019173.

PR (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

PI WPI; 2001-657177/75.

DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

PS Claim 1; SEQ ID NO 196632; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 4 A; 1 C; 0 G; 7 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1283 GTTATTTAAATCT 1295

Db 1 RTTATTTAAATCT 13

RESULT 480

ID ABF87882

XX ABF87882 standard; DNA; 13 BP.

AC ABF87882;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 187879 for detecting SNP TSC0046259.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 187879; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 1 Other;
SQ
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1803 TGTGTCGTGTAT 1815
DB 1 TGTGTCGTGTAT 13
RESULT 481
ABCE9602
ID ABC99602 standard; DNA; 13 BP.
XX ABC99602;
XX 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 89619 for detecting SNP TSC0022467.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
PA

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 89619; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 1 Other;
SQ
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1817 TATATATATATGT 1829
DB 1 TATATATATATGY 13
RESULT 482
ABH25451/C
ID ABH25451 standard; DNA; 13 BP.
XX ABH25451;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 225428 for detecting SNP TSC0054949.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 225428; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 1 Other;
SQ
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1805 TGTGTGTGTAT 1817
Db 13 TGTGTGTGTAT 1
RESULT 483
ABF87883/C
ID ABF87883 standard; DNA; 13 BP.
XX AC
XX ABF87883;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 187880 for detecting SNP TSC0046259.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 187880; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 1 Other;

Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1803 TGTGTGTGTAT 1815
Db 13 TGTGTGTGTAT 1
RESULT 484
ABF64975/C
ID ABF64975 standard; DNA; 13 BP.
XX AC
XX ABF64975;
XX 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 164972 for detecting SNP TSC0006375.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 164972; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 10 A; 1 C; 0 G; 1 T; 0 U; 1 Other;
SQ
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1867 TTTATTTTGTGT 1879
Db 13 TTTATTTTGTGT 1
RESULT 485
ABF82714/C
ID ABF82714 standard; DNA; 13 BP.
XX


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AC ABF82714;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 182711 for detecting SNP TSC0045154.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 182711; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 0 C; 0 G; 4 T; 0 U; 1 Other;
XX
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1766 ATTTTAAATTT 1778
DB 13 RTTTTAAATTT 1
XX
RESULT 486
ABC25106
ID ABC25106 standard; DNA; 13 BP.
XX
AC ABC25106;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 25123 for detecting SNP TSC0006116.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX

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XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 25123; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 0 G; 8 T; 0 U; 1 Other;
XX
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1767 TTTTAAATTT 1779
DB 1 TTTTAAATTT 13
XX
RESULT 487
ABH25450
ID ABH25450 standard; DNA; 13 BP.
XX
XX ABH25450;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 225427 for detecting SNP TSC0054949.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX

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PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.

XX Claim 1; SEQ ID NO 225427; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 1 Other;

XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1805 TGTGTGTGTAT 1817

DB 1 TGTGTGTGTAT 13

RESULT 488

ABF64974

ID ABF64974 standard; DNA; 13 BP.

XX AC ABF64974;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 164971 for detecting SNP TSC0006375.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 164971; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 1 Other;

XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1805 TGTGTGTGTAT 1817

XX 1 TGTGTGTGTAT 13

XX RESULT 488

XX ABF64974

XX ID ABF64974 standard; DNA; 13 BP.

XX AC ABF64974;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 164971 for detecting SNP TSC0006375.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;

XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1867 TTTATTTTGT 1879

DB 1 TTTATTTTGT 13

RESULT 489

ABC28716

ID ABC28716 standard; DNA; 13 BP.

XX AC ABC28716;

XX 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 28733 for detecting SNP TSC0008353.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 28733; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 1 Other;

XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02;
XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 1867 TTTATTTTGT 1879

XX 1 TTTATTTTGT 13

XX RESULT 489

XX ABC28716

XX ID ABC28716 standard; DNA; 13 BP.

XX AC ABC28716;

XX 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 28733 for detecting SNP TSC0008353.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 28733; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010

CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 1 Other;


```

PR 07-APR-2000; 2000DE-01019173.
PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 239455; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 0 G; 7 T; 0 U; 1 Other;
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1769 TTTTAAATTTAT 1781
Db 1 TTTTAAATTTAT 13
RESULT 493
ABC47718
ID ABC47718 standard; DNA; 13 BP.
XX
AC ABC47718;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 47735 for detecting SNP TSC0013684.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-1B000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 47735; 29pp + Sequence Listing; German.

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XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1865 TTTTATTTTTCG 1877
Db 1 TTTTATTTTTCG 13
RESULT 494
ABC05096
ID ABC05096 standard; DNA; 13 BP.
XX
AC ABC05096;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 5087 for detecting SNP TSC0001768.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-1B000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 5087; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

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XX SQ Sequence 13 BP; 1 A; 0 C; 1 G; 10 T; 0 U; 1 Other;
XX
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 0;
Qy 1869 TATTTTGTGTTT 1881
Db 1 TATTTTGTGTTT 13

RESULT 495
ABC14214
ID ABC14214 standard; DNA; 13 BP.
XX
AC ABC14214;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 14221 for detecting SNP TSC0003234.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPITG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 14221; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 0 C; 6 G; 6 T; 0 U; 1 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 0 A; 0 C; 6 G; 6 T; 0 U; 1 Other;
XX
XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
XX Matches 12; Conservative 1; Mismatches 0;
XX
XX 1793 TGTGTGTGTGTGT 1805
XX
XX 1 TGTGTGTGTGTGT 13

RESULT 496

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ABF15465
ID ABF15465 standard; DNA; 13 BP.
XX
AC ABF15465;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 115462 for detecting SNP TSC0028934.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPITG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 115462; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 1 Other;
XX
XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
XX Matches 12; Conservative 1; Mismatches 0;
XX
XX 1239 GATTTCATCTCA 1251
XX
XX 1 TATTTCATCTCA 13

RESULT 497
ABF60175/c
ID ABF60175 standard; DNA; 13 BP.
XX
AC ABF60175;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 160172 for detecting SNP TSC0040332.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX

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OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 PF 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 160172; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation. ABC00010
 XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 XX represent the oligomers described in the invention. NOTE: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 10 A; 1 C; 0 G; 1 T; 0 U; 1 Other;
 SQ
 Query Match 1.2%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1866 TTTTATTTTGT 1878
 DB 13 TTTTATTTTGT 1
 RESULT 498
 ABH39479/c
 ID ABH39479 standard; DNA; 13 BP.
 AC ABH39479;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 239456 for detecting SNP TSC0058411.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 239456; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation. ABC00010
 XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 XX represent the oligomers described in the invention. NOTE: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 10 A; 1 C; 0 G; 1 T; 0 U; 1 Other;
 SQ
 Query Match 1.2%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1866 TTTTATTTTGT 1878
 DB 13 TTTTATTTTGT 1
 RESULT 498
 ABH39479/c
 ID ABH39479 standard; DNA; 13 BP.
 AC ABH39479;
 XX 22-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 239456 for detecting SNP TSC0058411.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 239456; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation. ABC00010
 XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 XX represent the oligomers described in the invention. NOTE: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 10 A; 1 C; 0 G; 1 T; 0 U; 1 Other;
 SQ

XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 239456; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation. ABC00010
 XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 XX represent the oligomers described in the invention. NOTE: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 7 A; 0 C; 0 G; 5 T; 0 U; 1 Other;
 SQ
 Query Match 1.2%; Score 12.6; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 3e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1769 TTTTAAATTTAT 1781
 DB 13 TTTTAAATTTAT 1
 RESULT 499
 ABC25107/c
 ID ABC25107 standard; DNA; 13 BP.
 AC ABC25107;
 XX 20-FEB-2002 (first entry)
 DT Oligonucleotide SEQ ID NO 25124 for detecting SNP TSC0006116.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 OS WO200177384-A2.
 PN 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX Claim 1; SEQ ID NO 25124; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation. ABC00010
 XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 XX represent the oligomers described in the invention. NOTE: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 13 BP; 7 A; 0 C; 0 G; 5 T; 0 U; 1 Other;
 SQ

CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 0 C; 0 G; 4 T; 0 U; 1 Other;
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1767 TTTTAAAAATTT 1779
Db 13 TTTTAAAAATTT 1
RESULT 500
ABC59001
ID ABC59001 standard; DNA; 13 BP.
XX
AC ABC59001;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 59018 for detecting SNP TSC0015817.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 59018; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 0 G; 6 T; 0 U; 1 Other;
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1812 GTATATATATATA 1824
Db 13 TATATATATATATA 13
RESULT 501
ABC59001/c
ID ABC59001 standard; DNA; 13 BP.
XX
AC ABC59001;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 59018 for detecting SNP TSC0015817.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 59018; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 0 G; 6 T; 0 U; 1 Other;
Query Match 1.2%; Score 12.6; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 3e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1813 TATATATATATAT 1825
Db 13 TATATATATATAT 1
RESULT 502
ABC89603/c
ID ABC89603 standard; DNA; 13 BP.
XX
AC ABC89603;
XX

DT 21-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 89620 for detecting SNP TSC0022467.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX Claim 1; SEQ ID NO 89620; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 1 C; 0 G; 5 T; 0 U; 1 Other;
XX
XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02; Mismatches 0; Gaps 0;
XX Matches 12; Conservative 1; Indels 0;
XX
QY 1817 TATATATATGCT 1829
DB 13 TATATATATGCT 1
||| ||||| |||||
13 TATATATATGCT 1
RESULT 503
ABC28717/C
ID ABC28717 standard; DNA; 13 BP.
AC
XX ABC28717;
XX
XX 20-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 28734 for detecting SNP TSC0008353.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX

XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX Claim 1; SEQ ID NO 28734; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 1 C; 0 G; 5 T; 0 U; 1 Other;
XX
XX Query Match 1.2%; Score 12.6; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 3e+02; Mismatches 0; Gaps 0;
XX Matches 12; Conservative 1; Indels 0;
XX
QY 1774 AAATTTATATGCT 1786
DB 13 AAATTTATATGCT 1
||| ||||| |||||
13 AAATTTATATGCT 1
RESULT 504
ABC47719/C
ID ABC47719 standard; DNA; 13 BP.
AC
XX ABC47719;
XX
XX 21-FEB-2002 (first entry)
DT
XX Oligonucleotide SEQ ID NO 47736 for detecting SNP TSC0013684.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
PT
PT

methylation status.

CC Claim 1; SEQ ID NO 47736; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 10 A; 1 C; 0 G; 1 T; 0 U; 1 Other;

XX

XX Query Match 1.2%; Score 12.6; DB 1; Length 13;

XX Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;

XX Matches 12; Conservative 1; Mismatches 0;

XX

QY 1865 TTTTATTTTGT 1877

DB 13 TTTTATTTTGY 1

RESULT 505

ABF96634/C

ID ABF96634 standard; DNA; 13 BP.

XX

XX ABF96634;

XX

XX 22-FEB-2002 (first entry)

XX

XX Oligonucleotide SEQ ID NO 196631 for detecting SNP TSC0048388.

XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

XX Homo sapiens.

XX

XX WO200177384-A2.

XX

XX 18-OCT-2001.

XX

XX 06-APR-2001; 2001WO-IB000713.

XX

XX 07-APR-2000; 2000DE-01019173.

XX

XX (EPIG-) EPIGENOMICS AG.

XX

XX Olek A, Piepenbrock C, Berlin K;

XX

XX WPI; 2001-657177/75.

XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX

XX Claim 1; SEQ ID NO 196631; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

XX Sequence 13 BP; 7 A; 0 C; 1 G; 4 T; 0 U; 1 Other;

XX

XX Query Match 1.2%; Score 12.6; DB 1; Length 13;

XX Best Local Similarity 92.3%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;

XX Matches 12; Conservative 1; Mismatches 0;

XX

QY 1283 GTTATTTTAAATCT 1295

DB 13 RTTATTTTAAATCT 1

RESULT 506

AAT96309

ID AAT96309 standard; DNA; 14 BP.

XX

XX AAT96309;

XX

XX 25-MAR-2003 (revised)

XX

XX 08-APR-1998 (first entry)

XX

XX Fungal telomeric nucleic acid sequence.

XX

XX Detection; eukaryotic pathogen; telomeric nucleic acid sequence;

XX telomerase activity; diagnosis; fungal infection; fungus; fungi;

XX malarial infection; malaria; ss.

XX

XX Saccharomyces cerevisiae.

XX

XX US5695932-A.

XX

XX 09-DEC-1997.

XX

XX 13-MAY-1993; 93US-00060952.

XX

XX 13-MAY-1992; 92US-00882438.

XX

XX 24-MAR-1993; 93US-00038766.

XX

XX (UYCA-) UNIV CALIFORNIA SAN FRANCISCO.

XX

XX (TEXA) UNIV TEXAS SYSTEM.

XX

XX Blackburn EH, Shay J, Mceachern MJ, West MD, Wright W;

XX

XX WPI; 1998-041292/04.

XX

XX Detection of eukaryotic pathogens, especially fungal or Plasmodium spp. -

XX by detecting telomerase activity.

XX

XX Claim 5; Col 93-94; 82pp; English.

XX

XX The present sequence can be used in a novel method for detecting a

XX eukaryotic pathogen in a patient. The method comprises obtaining a sample

XX of somatic tissue or cells from the patient, determining if telomerase

XX activity is present and correlating this with the presence of the

XX pathogen. The method is useful for diagnosis of fungal infections,

XX especially a fungus of the genus Candida, Kluyveromyces, Saccharomyces,

XX Sporothrix, Coccioides, Histoplasma Blastomyces, Paracoccidioides,

XX Cryptococcus, Aspergillus, Mucor or Rhizopus, or malarial infections,

XX especially Plasmodium vivax, P. ovale, P. malariae or P. falciparum.

XX (Updated on 25-MAR-2003 to correct PA field.)

XX

XX Sequence 14 BP; 0 A; 0 C; 8 G; 6 T; 0 U; 0 Other;

XX

XX Query Match 1.2%; Score 12.4; DB 1; Length 14;

XX Best Local Similarity 92.3%; Pred. No. 3.3e+02; 0; Indels 0; Gaps 0;

XX Matches 13; Conservative 0; Mismatches 1;

XX

QY 1793 TGTGTGTGTGTGTG 1806

DB 1 TGGGTGTGTGTGTG 14

telomerase activity; cel replication; neoplasia; cancer;
 age-related macular degeneration; Alzheimer's disease; atherosclerosis;
 telomerase; telomerase inhibitor; immortalised cell; ss.
 Synthetic.
 US2002127634-A1.
 12-SEP-2002.
 05-JUN-1995; 95US-00463404.
 13-MAY-1992; 92US-00892438.
 24-MAR-1993; 93US-00038766.
 13-MAY-1993; 93US-00060952.
 (WEST/) WEST M D.
 (SHAY/) SHAY J.
 (WRIGHT/) WRIGHT W.
 (BLAC/) BLACKBURN E H.
 West MD, Shay J, Wright W, Blackburn EH;
 WPI; 2003-066996/06.
 Treating condition associated with cell senescence or increased rate of
 cell proliferation, by administering to cell an agent that derepresses
 telomerase in the senescing cells or that reduces loss of telomere
 length.
 Disclosure; Page 51; 86pp; English.
 The invention describes a method use for treating increased rate of
 proliferation of a cell or extending the ability of a cell to replicate,
 or treating a disease associated with cell senescence. The method
 comprises administering an agent to reduce loss of telomere length within
 the cell during proliferation or replication, or to derepress telomerase
 in the senescing cells. The method is useful for treating a condition
 associated with an increased rate of proliferation of a cell extending
 the ability of a cell to replicate, or for treating a disease or
 condition associated with cell senescence e.g. neoplasia. A second method
 disclosed in the invention is useful for treating a condition associated
 with an elevated level of telomerase activity within a cell e.g. cancer.
 Also disclosed is a method useful for diagnosis of a condition associated
 with an increased rate of proliferation in a cell in an individual e.g.
 age-related macular degeneration, astrocytes associated with Alzheimer's
 disease and endothelial cells associated with atherosclerosis. This
 sequence represents a polynucleotide used in the study of telomere length
 and telomerase activity described in the invention
 Sequence 14 BP; 0 A; 0 C; 8 G; 6 T; 0 U; 0 Other;
 Query Match 1.2%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 3.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTG 1806
 Db 1 TGGGTGTGTGTGTG 14
 RESULT 509
 AAT54694
 ID AAT54694 standard; RNA; 15 BP.
 XX AC AAT54694;
 XX
 25-MAR-2003 (revised)
 22-APR-1997 (first entry)
 DE Mouse IL-5 hammerhead ribozyme target sequence (nt. position 1350).
 XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;

Human c-fos target sequence nucleotide position 756.
 Human; c-fos; hammerhead ribozyme; hairpin ribozyme; target site; cancer;
 oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift; mutation;
 diseased cell; ss.
 Homo sapiens.
 WO9832846-A2.
 30-JUL-1998.
 20-JAN-1998; 98WO-US001017.
 23-JAN-1997; 97US-0037658P.
 24-DEC-1997; 97US-00998099.
 (RIBO-) RIBOZYME PHARM INC.
 Jarvis T, Mcswiggen JA, Stinchcomb DT;
 WPI; 1998-427942/36.
 Enzymatic nucleic acid molecules which specifically cleave RNA derived
 from a c-fos gene - useful for treating conditions related to levels of c
 -fos, especially cancer.
 Claim 5; Page 53; 72pp; English.
 The present invention describes an enzymatic nucleic acid molecule which
 specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540
 and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin
 ribozymes, respectively, which specifically cleave human c-fos. AAV95261
 to AAV95400 and AAV95585 to AAV95628 represent human c-fos target
 sequences. The enzymatic nucleic acid molecules can be used for treating
 cancer associated with elevated levels of c-fos oncogene, especially
 leukaemia, neuroblastomas and lung, breast and colon cancers. The
 ribozymes may also be used as diagnostic tools to examine genetic drift
 and mutations within diseased cells, or to detect the presence of c-fos
 RNA in a cell
 Sequence 14 BP; 2 A; 7 C; 2 G; 0 T; 3 U; 0 Other;
 Query Match 1.2%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 71.4%; Pred. No. 3.3e+02;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1567 TCACTGACTGCT 1580
 Db 1 UCACCGACCGCCU 14
 RESULT 508
 ABX50033
 ID ABX50033 standard; DNA; 14 BP.
 XX AC ABX50033;
 XX
 12-FEB-2003 (first entry)
 DE Telomere length and/or telomerase activity related polynucleotide #56.
 XX Cell proliferation; cell senescence; telomere length;

gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
intercellular adhesion molecule; rel A; tumour necrosis factor;
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
translocation; chronic myelogenous leukaemia; CML; cancer;
Philadelphia chromosome; inflammation; autoimmune disease;
atherosclerosis; myocardial infarction; stroke; restenosis;
transplant rejection; rheumatoid arthritis; psoriasis;
myocardial ischaemia; Kawasaki disease; septic shock; HIV;
human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
ss.
Mus musculus.
WO9523225-A2.
31-AUG-1995.
23-FEB-1995; 95WO-IB000156.
23-FEB-1994; 94US-00201109.
29-MAR-1994; 94US-00218934.
04-APR-1994; 94US-00222795.
07-APR-1994; 94US-00224483.
15-APR-1994; 94US-00227958.
15-APR-1994; 94US-00227958.
15-APR-1994; 94US-00228041.
18-MAY-1994; 94US-00245736.
06-JUL-1994; 94US-00271280.
15-AUG-1994; 94US-00291932.
16-AUG-1994; 94US-00291433.
17-AUG-1994; 94US-00292620.
19-AUG-1994; 94US-00293520.
02-SEP-1994; 94US-00300000.
08-SEP-1994; 94US-00303039.
23-SEP-1994; 94US-00311486.
23-SEP-1994; 94US-00311749.
28-SEP-1994; 94US-00314397.
28-SEP-1994; 94US-00314397.
03-OCT-1994; 94US-00316771.
07-OCT-1994; 94US-00319492.
11-OCT-1994; 94US-00321993.
04-NOV-1994; 94US-00334847.
10-NOV-1994; 94US-00337608.
28-NOV-1994; 94US-00345516.
16-DEC-1994; 94US-00357577.
23-DEC-1994; 94US-00363233.
30-JAN-1995; 95US-00380734.
(RIBO-) RIBOZYME PHARM INC.
Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, Usman N, Wincott FE, Woolf T;
WPI; 1995-351090/45.
Ribozymes having modified bases and methods for producing them - for use
in inhibiting disease related genes.
Claim 2; Page 221; 407pp; English.
The present sequence represents a preferred target sequence for an
enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
5) mRNA at the nucleotide base position indicated in the DE line. Regions
of the mRNA that do not form secondary folding structures and that
contain potential hammerhead and hairpin ribozyme cleavage sites were
identified by computer analysis. Ribozymes directed against these mRNA
sequences were designed and synthesised with modifications that improve
their nuclease resistance. The ribozymes cleave the IL-5 target sequences
and thereby inhibit IL-5 expression, making them useful for treating
chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
and preventing the recruitment and activation of eosinophils. The
ribozymes can also be used to treat eosinophilia (related to parasitic
infection or with pulmonary infiltration) and L-tryptophan-associated

CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
CC field.)
XX
SQ Sequence 15 BP; 8 A; 1 C; 3 G; 0 T; 3 U; 0 Other;
Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 3.5e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1956 AAAGCATGAAATGG 1969
DB 1 AAAGCAUAAAUUGG 14
RESULT 510
AAT56843/C
ID AAT56843 standard; RNA; 15 BP.
XX
AC AAT56843;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 04-APR-1997 (first entry)
XX
DE RSV 1B hammerhead ribozyme target sequence (nt. position 421).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
intercellular adhesion molecule; rel A; tumour necrosis factor;
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
translocation; chronic myelogenous leukaemia; CML; cancer;
Philadelphia chromosome; inflammation; autoimmune disease;
atherosclerosis; myocardial infarction; stroke; restenosis;
transplant rejection; rheumatoid arthritis; psoriasis;
myocardial ischaemia; Kawasaki disease; septic shock; HIV;
human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
ss.
Respiratory syncytial virus.
WO9523225-A2.
31-AUG-1995.
23-FEB-1995; 95WO-IB000156.
23-FEB-1994; 94US-00201109.
29-MAR-1994; 94US-00218934.
04-APR-1994; 94US-00222795.
07-APR-1994; 94US-00224483.
15-APR-1994; 94US-00227958.
15-APR-1994; 94US-00228041.
18-MAY-1994; 94US-00245736.
06-JUL-1994; 94US-00271280.
15-AUG-1994; 94US-00291932.
16-AUG-1994; 94US-00291433.
17-AUG-1994; 94US-00292620.
19-AUG-1994; 94US-00293520.
02-SEP-1994; 94US-00300000.
08-SEP-1994; 94US-00303039.
23-SEP-1994; 94US-00311486.
23-SEP-1994; 94US-00311749.
28-SEP-1994; 94US-00314397.
28-SEP-1994; 94US-00314397.
03-OCT-1994; 94US-00316771.
07-OCT-1994; 94US-00319492.
11-OCT-1994; 94US-00321993.
04-NOV-1994; 94US-00334847.
10-NOV-1994; 94US-00337608.
28-NOV-1994; 94US-00345516.
16-DEC-1994; 94US-00357577.
23-DEC-1994; 94US-00363233.
30-JAN-1995; 95US-00380734.

PA (RIBO-) RIBOZYME PHARM INC.
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, McSwiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 DR Ribozymes having modified bases and methods for producing them - for use
 XX in inhibiting disease related genes.
 PT Claim 2; Page 265; 407pp; English.
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves mRNA coding for a
 CC protein of respiratory syncytial virus (RSV) at the nucleotide base
 CC position indicated in the DE line. Regions of the mRNA that do not form
 CC secondary folding structures and that contain potential hammerhead and
 CC hairpin ribozyme cleavage sites were identified by computer analysis.
 CC Ribozymes directed against these mRNA sequences were designed and
 CC synthesised with modifications that improve their nuclease resistance.
 CC The ribozymes cleave the target sequences and can be used for treatment
 CC and diagnosis of RSV infection. (Updated on 25-MAR-2003 to correct PI
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 15 BP; 7 A; 5 C; 0 G; 0 T; 3 U; 0 Other;
 XX Query Match 1.2%; Score 12.4; DB 1; Length 15;
 XX Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1784 TGTAAATATTGTGT 1797
 DB 14 TGTGAATATTGTGT 1
 RESULT 511
 AAT54631
 ID AAT54631 standard; RNA; 15 BP.
 XX AC AAT54631;
 XX 25-MAR-2003 (revised)
 DT 22-APR-1997 (first entry)
 XX Mouse IL-5 hammerhead ribozyme target sequence (nt. position 1439).
 DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; ber-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.
 XX Mus musculus.
 OS WO9523225-A2.
 XX PN 31-AUG-1995.
 XX 23-FEB-1995; 95WO-IB000156.
 XX 23-FEB-1994; 94US-00201109.
 XX 29-MAR-1994; 94US-00219934.
 XX 04-APR-1994; 94US-00222795.
 XX 07-APR-1994; 94US-00224483.
 XX 15-APR-1994; 94US-00227958.

PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 28-SEP-1994; 94US-00311749.
 PR 03-OCT-1994; 94US-00314397.
 PR 07-OCT-1994; 94US-00316771.
 PR 11-OCT-1994; 94US-00319492.
 PR 04-NOV-1994; 94US-00321993.
 PR 10-NOV-1994; 94US-00334847.
 PR 28-NOV-1994; 94US-00337608.
 PR 16-DEC-1994; 94US-00345516.
 PR 23-DEC-1994; 94US-00357577.
 PR 30-JAN-1995; 94US-00363233.
 XX 95US-00380734.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisch K, Matulic-Adamic J, McSwiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.
 DR Ribozymes having modified bases and methods for producing them - for use
 XX in inhibiting disease related genes.
 PT Claim 2; Page 221; 407pp; English.
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
 CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions
 CC of the mRNA that do not form secondary folding structures and that
 CC contain potential hammerhead and hairpin ribozyme cleavage sites were
 CC identified by computer analysis. Ribozymes directed against these mRNA
 CC sequences were designed and synthesised with modifications that improve
 CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences
 CC and thereby inhibit IL-5 expression, making them useful for treating
 CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
 CC and preventing the recruitment and activation of eosinophils. The
 CC ribozymes can also be used to treat eosinophilia (related to parasitic
 CC infection or with pulmonary infiltration) and L-tryptophan-associated
 CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX Sequence 15 BP; 3 A; 1 C; 1 G; 0 T; 10 U; 0 Other;
 XX Query Match 1.2%; Score 12.4; DB 1; Length 15;
 XX Best Local Similarity 35.7%; Pred. No. 3.5e+02;
 XX Matches 5; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
 QY 1284 TTATTAAATCTGT 1297
 DB 2 UUAUUAUUCUGU 15
 RESULT 512
 AAT52173
 ID AAT52173 standard; RNA; 15 BP.
 XX AC AAT52173;
 XX 25-MAR-2003 (revised)
 DT 25-MAR-1997 (first entry)
 XX Human ICAM hammerhead ribozyme target sequence (nt. position 2744).
 DE

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.

XX Homo sapiens.
 OS
 XX
 XX WO9523225-A2.
 PN
 XX
 XX 31-AUG-1995.
 PD
 XX
 XX 23-FEB-1995; 95WO-18000156.
 PF
 XX
 XX 23-FEB-1994; 94US-00201109.
 PR
 XX 29-MAR-1994; 94US-00218934.
 PR
 XX 04-APR-1994; 94US-00222795.
 PR
 XX 07-APR-1994; 94US-00224483.
 PR
 XX 15-APR-1994; 94US-00227958.
 PR
 XX 18-APR-1994; 94US-00228041.
 PR
 XX 18-MAY-1994; 94US-00245736.
 PR
 XX 06-JUL-1994; 94US-00271280.
 PR
 XX 15-AUG-1994; 94US-00291932.
 PR
 XX 15-AUG-1994; 94US-00291433.
 PR
 XX 17-AUG-1994; 94US-00292620.
 PR
 XX 19-AUG-1994; 94US-00293520.
 PR
 XX 02-SEP-1994; 94US-00300000.
 PR
 XX 08-SEP-1994; 94US-00303039.
 PR
 XX 23-SEP-1994; 94US-00311486.
 PR
 XX 28-SEP-1994; 94US-00314397.
 PR
 XX 07-OCT-1994; 94US-00315771.
 PR
 XX 11-OCT-1994; 94US-00319492.
 PR
 XX 04-NOV-1994; 94US-00334847.
 PR
 XX 10-NOV-1994; 94US-00337608.
 PR
 XX 28-NOV-1994; 94US-00345516.
 PR
 XX 16-DEC-1994; 94US-00357577.
 PR
 XX 23-DEC-1994; 94US-00363233.
 PR
 XX 30-JAN-1995; 94US-00380734.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LM;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX
 XX WPI; 1995-351090/45.
 DR
 XX
 XX Ribozymes having modified bases and methods for producing them - for use
 PT in inhibiting disease related genes.
 XX
 XX Claim 2; Page 175; 407pp; English.
 PS
 XX
 XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to

CC correct PI field.)
 XX
 SQ Sequence 15 BP; 2 A; 0 C; 6 G; 0 T; 7 U; 0 Other;
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 3.5e+02;
 Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
 QY 1801 TCGTGTGCTGCTGA 1814
 Db 1 UGUGUGAUGUGUA 14

RESULT 513
 AAF47616/c
 ID AAF47616 standard; DNA; 15 BP.
 XX
 AC AAF47616;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP3 oligonucleotide #1036.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200078341-A1.
 PN
 XX 28-DEC-2000.
 PD
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 21-JUN-1999; 99US-0140345P.
 PR
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 PA
 XX Wraight CJ, Werther GA, Edmondson SR;
 PI WPI; 2001-041421/05.
 DR
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 7; Page 50; 201pp; English.
 XX
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 6 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2046 GTCCTGGCAGCT 2059
 DB 15 GTCCTGGCAGCTCT 2

RESULT 514
 AAF50118
 ID AAF50118 standard; DNA; 15 BP.
 XX AAF50118;
 AC AAF50118;
 DT 30-MAR-2001 (first entry)
 DE IGF-I oligonucleotide #1078.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 hyperneovascular condition; hyperplasia; kidney disease;
 neovascular condition of the retina; ss.

Homo sapiens.
 WO200078341-A1.
 28-DEC-2000.

21-JUN-2000; 2000WO-AU000693.
 21-JUN-1999; 99US-0140345P.

(MURD-) MURDOCH CHILDRENS RES INST.
 Wright CJ, Werther GA, Edmondson SR;
 WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 inhibits or reduces growth factor mediated cell proliferation and/or
 inflammation.

Example 8; Page 67; 201pp; English.

The present invention relates to a method for ameliorating the effects of
 skin disorders. The method comprises contacting the skin with an
 antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 inhibiting or reducing growth factor mediated cell proliferation,
 inflammation and/or other disorders. The present sequence is an
 oligonucleotide which can be used to design the antisense
 oligonucleotides of the present invention (see AAF45151 and AAF45153-
 F45161). The method is useful for ameliorating the effects of psoriasis,
 ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 hyperneovascular condition such as a neovascular condition of the retina,
 brain or skin, growth factor-mediated malignancies, other sclerotic
 disease, kidney disease, hyperproliferation of the inside of blood
 vessels or any other hyperplasia

Sequence 15 BP; 3 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1983 AATTCTGCTCAGAT 1996
 DB 1 ACTTCTGCTCAGAT 14

RESULT 515
 AAF46653/C
 ID AAF46653 standard; DNA; 15 BP.
 XX AAF46653;
 AC AAF46653;
 DT 30-MAR-2001 (first entry)
 DE IGFBP3 oligonucleotide #73.

Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 hyperneovascular condition; hyperplasia; kidney disease;
 neovascular condition of the retina; ss.

Homo sapiens.
 WO200078341-A1.
 28-DEC-2000.

21-JUN-2000; 2000WO-AU000693.
 21-JUN-1999; 99US-0140345P.

(MURD-) MURDOCH CHILDRENS RES INST.
 Wright CJ, Werther GA, Edmondson SR;
 WPI; 2001-041421/05.

Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 inhibits or reduces growth factor mediated cell proliferation and/or
 inflammation.

Example 7; Page 44; 201pp; English.

The present invention relates to a method for ameliorating the effects of
 skin disorders. The method comprises contacting the skin with an
 antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 inhibiting or reducing growth factor mediated cell proliferation,
 inflammation and/or other disorders. The present sequence is an
 oligonucleotide which can be used to design the antisense
 oligonucleotides of the present invention (see AAF45151 and AAF45153-
 F45161). The method is useful for ameliorating the effects of psoriasis,
 ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 hyperneovascular condition such as a neovascular condition of the retina,
 brain or skin, growth factor-mediated malignancies, other sclerotic
 disease, kidney disease, hyperproliferation of the inside of blood
 vessels or any other hyperplasia

Sequence 15 BP; 4 A; 7 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2047 TCCTTGGCAGCTG 2060
 DB 15 TCCTTGGCAGCTG 2

RESULT 516
 AAF48749/c
 ID AAF48749 standard; DNA; 15 BP.
 XX
 AC AAF48749;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP3 oligonucleotide #2169.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 7; Page 58; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 6 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1495 ATCAGATAGCATCT 1508
 |||||
 Db . 14 ATCATATAGCATCT 1
 RESULT 517
 AAF47618/c
 ID AAF47618 standard; DNA; 15 BP.

XX
 AC AAF47618;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP3 oligonucleotide #1038.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 7; Page 50; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 5 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2045 TGTCCTGGCAGGC 2058
 |||||
 Db 14 TGTCCTGGCAGTC 1
 RESULT 518
 AAF46654/c
 ID AAF46654 standard; DNA; 15 BP.
 XX
 AC AAF46654;
 XX
 DT 30-MAR-2001 (first entry)

XX IGFBP3 oligonucleotide #74.
DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
XX WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AJ000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional), and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX Example 7; Page 44; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX Sequence 15 BP; 4 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
SQ Sequence 15 BP; 4 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2047 TCCTTGCAGGCTG 2060
Db 14 TCCTTGCAGGCTG 1
RESULT 519
AAF50117
ID AAF50117 standard; DNA; 15 BP.
XX AAF50117;
AC AAF50117;
XX 30-MAR-2001 (first entry)
DT IGF-I oligonucleotide #1077.
XX IGF-I oligonucleotide #1077.
DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;

KW cytosatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX Homo sapiens.
XX WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AJ000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.
XX Wright CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional), and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX Example 8; Page 67; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisense
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
XX Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
SQ Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1983 AATTCCTCAGAT 1996
Db 2 ACTTCTCAGAT 15
RESULT 520
AAF53695
ID AAF53695 standard; DNA; 15 BP.
XX AAF53695;
AC AAF53695;
XX 30-MAR-2001 (first entry)
DT IGF-I oligonucleotide #4655.
DE IGF-I oligonucleotide #4655.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;

KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.

OS Homo sapiens.
XX WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional), and an antisenese nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.

XX Example 8; Page 91; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisenese oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisenese
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia

XX Sequence 15 BP; 2 A; 5 C; 1 G; 7 T; 0 U; 0 Other;
XX Query Match 1.2%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.5e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2236 TTGCACCTTTCTAG 2249
DB 2 TTTCACCTTTCTAG 15

RESULT 521
AAF53696
ID AAF53696 standard; DNA; 15 BP.
XX AAF53696;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #4656.

XX Antisenese therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition of the retina; ss.

OS Homo sapiens.
XX WO200078341-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-AU000693.
XX 21-JUN-1999; 99US-0140345P.
XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR;
XX WPI; 2001-041421/05.
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX UV (ultra-violet) treatment (optional), and an antisenese nucleic acid that
XX inhibits or reduces growth factor mediated cell proliferation and/or
XX inflammation.

XX Example 8; Page 91; 201pp; English.
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
XX antisenese oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX inhibiting or reducing growth factor mediated cell proliferation,
XX inflammation and/or other disorders. The present sequence is an
XX oligonucleotide which can be used to design the antisenese
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX F45161). The method is useful for ameliorating the effects of psoriasis,
XX ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX hyperneovascular condition such as a neovascular condition of the retina,
XX brain or skin, growth factor-mediated malignancies, other sclerotic
XX disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia

XX Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
XX Query Match 1.2%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 92.9%; Pred. No. 3.5e+02;
XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2236 TTGCACCTTTCTAG 2249
DB 1 TTTCACCTTTCTAG 14

RESULT 522
AAF48471/C
ID AAF48471 standard; DNA; 15 BP.
XX AAF48471;
XX 30-MAR-2001 (first entry)
XX IGFBP3 oligonucleotide #1891.

XX Antisenese therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition of the retina; ss.

XX Homo sapiens.
XX WO200078341-A1.
XX

PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 21-JUN-1999; 99US-0140345P.
 XX
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antineoplastic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 XX Example 7; Page 56; 201pp; English.
 XX
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antineoplastic oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antineoplastic
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 XX Sequence 15 BP; 2 A; 3 C; 1 G; 9 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2248 AGTTGAATAAAG 2261
 DB 15 AGATGAATAAAG 2
 RESULT 523
 AAF48748/C
 ID AAF48748 standard; DNA; 15 BP.
 XX
 XX AAF48748;
 XX
 XX 30-MAR-2001 (first entry)
 XX
 XX IGFBP3 oligonucleotide #2168.
 XX
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200078341-A1.
 XX
 XX 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX

PR 21-JUN-1999; 99US-0140345P.
 XX
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antineoplastic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 XX Example 7; Page 58; 201pp; English.
 XX
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antineoplastic oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antineoplastic
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 XX Sequence 15 BP; 5 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1495 ATCAGATAGCATCT 1508
 DB 15 ATCATATAGCATCT 2
 RESULT 524
 AAF48472/C
 ID AAF48472 standard; DNA; 15 BP.
 XX
 XX AAF48472;
 XX
 XX 30-MAR-2001 (first entry)
 XX
 XX IGFBP3 oligonucleotide #1892.
 XX
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200078341-A1.
 XX
 XX 28-DEC-2000.
 XX
 XX 21-JUN-2000; 2000WO-AU000693.
 XX
 XX 21-JUN-1999; 99US-0140345P.
 XX
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX

PI Wright CJ, Werther GA, Edmondson SR;
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 XX Example 7; Page 56; 201pp; English.
 PS
 XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 0 G; 9 T; 0 U; 0 Other;
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. NO. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2248 AGTTGAAATAAAG 2261
 DB 14 AGATGAAATAAAG 1
 RESULT 525
 ABX03996/C
 ID ABX03996 standard; DNA; 15 BP.
 AC ABX03996;
 XX
 XX 09-JAN-2003 (first entry)
 DT
 DE Resistance gene carb-4 DNA fragment.
 XX
 KW Detection; probe; diagnosis; oral disease; parodontitis; caries; therapy;
 KW polymorphism; virulence factor; antibiotic resistance gene; prognosis;
 KW oral infection; detection; pathogen; coronary heart disease;
 KW diabetic symptom; ss.
 XX
 OS Unidentified.
 XX
 XX DB20110013-UI.
 XX
 XX 18-OCT-2001.
 XX
 XX 13-MAR-2001; 2001DE-02010013.
 XX
 XX 13-MAR-2001; 2001DE-01012348.
 PR 13-MAR-2001; 2001DE-02010013.
 XX
 XX (ROET/) ROETGER A.
 PA
 XX WPI; 2001-657777/76.
 DR
 XX Oligonucleotide array, useful for diagnosing oral diseases, particularly
 PT parodontitis, carries human or microbial reference sequences.
 PT
 XX Claim 10; Page 27; 58pp; German.
 PS
 XX
 CC This invention describes a novel nucleotide carrier with probes used for
 CC diagnosis of oral diseases, particularly parodontitis, but also carries,
 CC especially to identify genetic predisposition (as indicated by
 CC polymorphisms) to disease and to identify causative microorganisms or
 CC their associated virulence factors and antibiotic resistance genes, e.g.
 CC for selection of therapy and for prognosis. They are also useful for
 CC research into oral infections. The carriers allow simultaneous detection
 CC of both host and pathogen parameters, providing quickly and simply an
 CC individual's parodontitis profile, including detection of pathogens that
 CC are associated with increased risk of coronary heart diseases and/or
 CC aggravation of diabetic symptoms, and of opportunistic pathogens.
 CC ABX03870-ABX04044 represent DNA fragments used to illustrate the method
 CC of the invention
 XX
 SQ Sequence 15 BP; 4 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. NO. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1275 TAGCACAAGTTATT 1288
 DB 15 TAGCACAAGTTATT 2
 RESULT 526
 AAH18788
 ID AAH18788 standard; DNA; 15 BP.
 XX
 AC AAH18788;
 XX
 XX 25-JUN-2001 (first entry)
 DT
 XX Human IL4 allele-specific primer SEQ ID NO: 47.
 DE
 XX Human; interleukin-4; IL4; single nucleotide polymorphism; SNP; atopy;
 KW inflammatory disorder; immune disorder; population diversity;
 KW paternity test; forensic test; cytokine; chromosome 5q31.1; probe;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200123404-A1.
 PN
 XX 05-APR-2001.
 PD
 XX 28-SEP-2000; 2000WO-US026608.
 PF
 XX 30-SEP-1999; 99US-0156825P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;
 PI WPI; 2001-316132/33.
 XX
 XX Polynucleotide comprising novel single nucleotide polymorphisms in human
 PT interleukin-4 gene for use in studying expression, function of
 PT interleukin-4, in developing drugs, diagnosis and treatment of immune
 PT disorders.
 XX
 XX Claim 12; Page 16; 71pp; English.
 PS
 XX The present invention provides the protein, cDNA and gene of human
 CC interleukin-4 (IL4). The coding sequences for this protein contain single
 CC nucleotide polymorphisms (SNPs) which may be associated with differences
 CC in susceptibility to atopy, inflammatory and immune diseases and
 CC different drug responses. They may also be used in applications such as
 CC forensic and paternity testing and studying population diversity and
 CC anthropological lineage. The IL4 gene is found on human chromosome 5q31.1
 CC
 XX Sequence 15 BP; 3 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
 SQ

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2158 GGAAGCATTGTTT 2171
DB 2 GAAGCATTGTTT 15

RESULT 527
ABX79833
ID ABX79833 standard; cDNA; 15 BP.
XX AC ABX79833;
XX DT 17-APR-2003 (first entry)
XX DE EST polymorphic DNA repeat polynucleotide #158.
XX KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX OS Homo sapiens.
XX PN US6472154-B1.
XX PD 29-OCT-2002.
XX PF 31-DEC-1999; 99US-00475947.
XX PR 31-DEC-1999; 99US-00475947.
XX PS (TEXA) UNIV TEXAS SYSTEM.
XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.
XX PT Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX Example; Col 747; 588pp; English.
XX CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
SQ

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 3.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1865 TTTTATTTTGTGTT 1879
DB TTTTATTTTGTGTT 15

Db 1 TTTTATTTTGTGTT 15
RESULT 528
ACD56418/c
ID ACD56418 standard; RNA; 15 BP.
XX AC ACD56418;
XX DT 24-SEP-2003 (first entry)
XX DE HBV enzymatic nucleic acid substrate sequence #143.
XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX Hepatitis B virus.
XX OS WO200281494-A1.
XX PN 17-OCT-2002.
XX PD 26-MAR-2002; 2002WO-US009187.
XX PF 26-MAR-2001; 2001US-00817879.
XX PR 08-JUN-2001; 2001US-00877478.
XX PR 08-JUN-2001; 2001US-0296876P.
XX PR 24-OCT-2001; 2001US-0335059P.
XX PR 05-DEC-2001; 2001US-0337055P.
XX PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT) BLATT L.
PA (MACE) MACEJAK D.
PA (MCSW) MCSWIGGEN J.
PA (MORR) MORRISSEY D.
PA (PAVC) PAVCO P.
PA (LEEP) LEE P.
PA (DRAP) DRAPER K.
PA (ROBE) ROBERTS E.
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
PI WPI; 2003-229207/22.
XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX Example 1; Page 219; 387pp; English.
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HBV

CC enzymatic nucleic acid sequences disclosed in the present invention
 XX Sequence 15 BP; 2 A; 3 C; 4 G; 0 T; 6 U; 0 Other;
 SQ

Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2095 AATGAACAAATGGC 2108
 Db 14 ACTGAACAAATGGC 1

RESULT 529
 ACD56180/c
 ID ACD56180 standard; RNA; 15 BP.

XX AC ACD56180;

DT 23-SEP-2003 (first entry)

DE HBV enzymatic nucleic acid substrate sequence #69.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW viricide; antiinflammatory; substrate; ss.

OS Hepatitis B virus.

XX WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEF/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

PI WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

XX hepatocellular carcinoma, or condition associated with hepatitis C virus

XX infection.

XX Example 1; Page 214; 387pp; English.

CC transcripase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC enzymatic nucleic acid sequences disclosed in the present invention
 XX
 SQ Sequence 15 BP; 2 A; 3 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.5e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2095 AATGAACAAATGGC 2108

Db 15 ACTGAACAAATGGC 2

RESULT 530

ADE13970/c

ID ADE13970 standard; DNA; 15 BP.

XX AC ADE13970;

XX 29-JAN-2004 (first entry)

DE Optineurin promoter motif, repeat element or regulatory region #79.

XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;

KW SNP; glaucoma; progressive ocular hypertensive disorder;

KW glaucoma related disorder; motif; repeat element; regulatory region.

XX Homo sapiens.

OS US2003190617-A1.

XX 09-OCT-2003.

XX 06-MAR-2002; 2002US-00091281.

XX 06-MAR-2002; 2002US-00091281.

XX (SIEE/) SI E.

PA (RAYM/) RAYMOND V.

PA (MORI/) MORISSETTE J.

XX Raymond V, Morissette J, Si E;

XX WPI; 2003-864169/80.

XX New nucleic acid sequences of the optineurin gene are useful to detect

PT polymorphisms particularly single nucleotide polymorphisms in the

PT optineurin promoter to diagnose, prognose and treat glaucoma and related

PT disorders.

XX Claim 11; SEQ ID NO 81; 159pp; English.

XX The invention relates to an isolated nucleic acid (N1) comprising at

XX least 20 but not more than 1500 consecutive nucleotides of the optineurin

XX promoter appearing as ADE13890. Also included are the optineurin promoter

XX operably linked to a heterologous nucleic acid, a nucleic acid capable of

XX detecting a single nucleotide polymorphism (SNP) in the optineurin

XX promoter, a host cell comprising the promoter operably linked to a

XX heterologous sequence, diagnosing or prognosing glaucoma in a sample
 CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
 CC in a promoter region of the optineurin gene, associated with a glaucoma
 CC phenotype), detecting a SNP sequence variation in a sample containing
 CC DNA, detecting the presence of an optineurin promoter sequence variation

CC in a sample containing DNA, determining the presence or increased
 CC susceptibility to glaucoma or to a progressive ocular hypertensive
 CC disorder resulting in loss of visual field in a patient (or the severity
 CC or progression of glaucoma in a patient, comprising providing
 CC an amplification reaction primers that direct amplification of a selected
 CC nucleic acid region containing the variation within the optineurin
 CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
 CC obtaining a sample containing human genomic DNA, providing a nucleic acid
 CC capable of detecting a SNP located within an optineurin promoter, and
 CC detecting the polymorphism). The invention is used to diagnose and
 CC prognose glaucoma, and also to treat glaucoma related disorders. The
 CC present sequence is an optineurin promoter motif, repeat element or
 CC putative regulatory region.

XX SQ Sequence 15 BP; 5 A; 3 C; 0 G; 7 T; 0 U; 0 Other;

Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 3.5e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1535 AAGTGTAAATGAGA 1548

Db 14 AAGTGTAAATGAAA 1

RESULT 531

ABCI2933
 ID ABCI2933 standard; DNA; 13 BP.

XX AC ABCI2933;

XX DT 20-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 12940 for detecting SNP TSC0003018.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PI WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 12940; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ

Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 12; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATA 1824

Db 1 TATATATATATA 12

RESULT 532

ABFI9131
 ID ABFI9131 standard; DNA; 13 BP.

XX AC ABFI9131;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 119128 for detecting SNP TSC0029746.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX PI WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 119128; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 12; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825

Db 2 ATATATATATAT 13

RESULT 533

```
ABCI2932/c
ID ABC12932 standard; DNA; 13 BP.
XX
XX ABC12932;
XX
XX
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 12939 for detecting SNP TSC0003018.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 12939; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 12; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1813 TATATATATATA 1824
XX
XX DB 13 TATATATATATA 2
XX
XX RESULT 534
XX ABF19130/c
XX ID ABF19130 standard; DNA; 13 BP.
XX
XX AC ABF19130;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 119127 for detecting SNP TSC0029746.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
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OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 119127; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 12; DB 1; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 3.5e+02;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1814 ATATATATATAT 1825
XX
XX DB 12 ATATATATATAT 1
XX
XX RESULT 535
XX AAT30426
XX ID AAT30426 standard; DNA; 22 BP.
XX
XX AC AAT30426;
XX
XX 28-JAN-1997 (first entry)
XX
XX Compound simple sequence repeat primer (CA)6.5(TA)4.5.
XX
XX Detection; polymorphism; perfect compound simple sequence repeat;
XX adaptor directed primer; genome; genetic; fingerprinting;
XX amplified fragment length polymorphism assay; microsatellite region;
XX genetic trait marking; germplasm comparisons; compound; ss.
XX
XX Synthetic.
XX
XX WO9617082-A2.
XX
XX 06-JUN-1996.
XX
XX 21-NOV-1995; 95WO-US015150.
XX
XX 28-NOV-1994; 94US-00346456.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
```

PI Morgante M, Vogel JW;
DR WPI; 1996-277795/28.
XX
PT Modified amplified fragment length polymorphism assay - for detection of
PT polymorphism esp. in micro:satellite regions.
XX
PS Disclosure; Fig 1c; 173pp; English.
XX
CC Detecting polymorphisms between 2 nucleic acid samples, esp. in
CC microsatellite regions, comprises digesting the nucleic acid to generate
CC fragments, ligating adaptor segments to their ends, amplifying them using
CC primer directed amplification and comparing the prods. to detect
CC differences. The primers used in the amplification comprise a primer
CC consisting of a perfect cpd, simple sequence repeat (SSR), and an adaptor
CC directed primer, comprising a sequence complementary to an adaptor
CC segment. The present sequence is an example of a compound SSR primer. The
CC method represents a modified amplified fragment length polymorphism
CC assay, which is partic. useful for genome fingerprinting, i.e. for
CC genetic trait marking and germplasm comparisons
XX
SQ Sequence 22 BP; 11 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 12; DB 1; Length 22;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTACA 1832
DB 1 TATATATATACACACACA 20

RESULT 536
AAH91159
ID AAH91159 standard; DNA; 19 BP.
XX
AC AAH91159;
XX
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease associated polymorphic site #234.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 9
FT /*tag= a
FT /note= "SNP, optional deletion at this position"
XX
XX WO200148511-A2.
XX
XX 14-JUN-2001.
XX
XX 11-DEC-2000; 2000WO-US033632.
XX
XX 10-DEC-1999; 99US-0170257P.
XX
XX 10-APR-2000; 2000US-0196046P.
XX
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX WPI; 2001-367874/38.
XX
XX Testing for the presence of polymorphisms associated with inflammatory
XX bowel disease, using a hybridization assay.
XX
XX Claim 1; Page 48; 463pp; English.
PS

XX The present invention describes a method for detecting the presence of
XX polymorphisms associated with inflammatory bowel diseases such as
XX ulcerative colitis and Crohn's disease. The methods can be used to detect
XX the presence of genetic polymorphisms associated with inflammatory bowel
XX disease and correlating their occurrence with disease states. They may be
XX used in this way for phenotypic correlations, forensics, paternity
XX testing, medicine and genetic analysis. The present sequence is a
XX polymorphic site described in the exemplification of the invention
XX
SQ Sequence 19 BP; 9 A; 4 C; 0 G; 5 T; 0 U; 1 Other;

Query Match 1.1%; Score 11.6; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1813 TATATATATATATGTAC 1831
DB 1 TATATATANACACATAC 19

RESULT 537
ABC98272/c
ID ABC98272 standard; DNA; 13 BP.
XX
XX
AC ABC98272;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 98289 for detecting SNP TSC0024420.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 98289; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pt_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.1%; Score 11.4; DB 1; Length 13;

Best Local Similarity 92.3%; Pred. No. 4e+02; Mismatches 0; Indels 1; Gaps 0;

QY 1814 ATATATATATATA 1826
 Db 13 ATATATATATACA 1

RESULT 538
 ABC98273
 ID ABC98273 standard; DNA; 13 BP.
 XX
 AC ABC98273;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 98290 for detecting SNP TSC0024420.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 DT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 98290; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 4e+02;
 Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
 Db 1 ATATATATATACA 13

RESULT 539
 ABF38750/C
 ID ABF38750 standard; DNA; 13 BP.
 XX
 AC ABF38750;

XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 138747 for detecting SNP TSC0034761.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 DT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 138747; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 5 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 1.1%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 4e+02;
 Mismatches 12; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
 Db 13 ATATATATATATA 1

RESULT 540
 ABC28589
 ID ABC28589 standard; DNA; 13 BP.
 XX
 AC ABC28589;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 28606 for detecting SNP TSC0008245.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX

PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 28606; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 1.1%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1813 TATATATATATAT 1825
 Db 1 TACATATATAT 13
 RESULT 541
 ABC28588/C
 ID ABC28588 standard; DNA; 13 BP.
 XX
 AC ABC28588;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 28605 for detecting SNP TSC0008245.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 28606; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 1 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 1.1%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1813 TATATATATATAT 1825
 Db 1 TACATATATAT 13
 RESULT 541
 ABC28588/C
 ID ABC28588 standard; DNA; 13 BP.
 XX
 AC ABC28588;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 28605 for detecting SNP TSC0008245.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 28605; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
 Query Match 1.1%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 4e+02; 1; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1813 TATATATATATAT 1825
 Db 13 TACATATATATAT 1
 RESULT 542
 ABF38751
 ID ABF38751 standard; DNA; 13 BP.
 XX
 AC ABF38751;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 138748 for detecting SNP TSC0034761.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 138748; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073.

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 7 A; 1 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
DB 1 ACATATATATATA 13
|||||

RESULT 543
ABK87132/C
ID ABK87132 standard; DNA; 20 BP.

XX AC ABK87132;

XX DT 07-OCT-2002 (first entry)

XX DE Human connective tissue growth factor, RT-PCR primer #2.

XX OS Homo sapiens.
KW Human; endothelial cell-specific molecule 4; ECSM4; neovasculature;
KW imaging vascular endothelium; proliferative disease; cancer; psoriasis;
KW diabetic retinopathy; atherosclerosis; menorrhagia; endothelial damage;
KW tumour neovasculature; cardiac disease; endometriosis; hypoxic condition;
KW angiogenesis; cytotatic; RT-PCR; connective tissue growth factor;
KW reverse transcription-PCR; primer; ss.

XX PF 06-NOV-2001; 2001WO-CB004906.

XX PR 06-NOV-2000; 2000US-0245566P.

XX PR 07-MAR-2001; 2001US-0273662P.

XX PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX PI Bicknell R, Huminiecki L;

XX DR WPI; 2002-508120/54.

XX CC Novel endothelial cell-specific molecule polypeptide 1 or 4, useful for
PT imaging, diagnosing and treating a condition involving vascular
PT endothelium e.g. cancer, cardiac disease, endometriosis, diabetes.
XX PS Example 1; Page 165; 248pp; English.

XX CC The present invention relates to endothelial cell-specific molecule 4
CC (ECSM4), and the polynucleotide sequences encoding it. The ECSM4 proteins
CC are useful for imaging vascular endothelium in the body of an individual,
CC and for diagnosing and treating a proliferative disease or condition
CC involving the vascular endothelium (preferably, neovasculature) such as
CC cancer, psoriasis, diabetic retinopathy, atherosclerosis or menorrhagia.
CC The ECSM4 proteins are also useful in the manufacture of diagnostic or
CC prognostic agent for such conditions. The proteins are also useful for
CC detecting endothelial damage or activation, detecting a tumour or tumour
CC neovasculature, cardiac disease, or endometriosis by detecting the amount
CC of ECSM4 present in a sample. The polynucleotide sequences encoding ECSM4
CC are useful in gene therapy for treating a hypoxic condition such as
CC cancer, cardiac disease, endometriosis or atherosclerosis and in the
CC manufacture of medicaments for treating the above disease. The sequences
CC are useful for modulating angiogenesis in an individual. The present
CC sequence represents a RT-PCR primer for RNA encoding human connective
CC tissue growth factor

XX SQ Sequence 20 BP; 8 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 11.4; DB 1; Length 20;
Best Local Similarity 92.3%; Pred. No. 4.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1879 TTTAATGCTTTGA 1891
DB 16 TTTCATGCTTTGA 4
|||||

RESULT 544
ABC89602/C
ID ABC89602 standard; DNA; 13 BP.

XX AC ABC89602;

XX DT 21-FEB-2002 (first entry)

XX DE Oligonucleotide SEQ ID NO 89619 for detecting SNP TSC0022467.

XX OS Homo sapiens.
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX CC Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 89619; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI92073
CC data for this patent did not form part of the invention. NOTE: The sequence
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 1 Other;

Query Match 1.0%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATA 1824
DB 11 ATATATATATA 1
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RESULT 545

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 14:35:20 ; Search time 4 Seconds
(without alignments)
2.749 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 296 seqs, 5242 residues

Total number of hits satisfying chosen parameters: 592

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 316 summaries

Database : rge.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	25	2.4	25	1	AR201291
7	23.4	2.2	25	1	BD242742
8	23.4	2.2	25	1	AR201292
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10	23	2.2	24	1	AR074790
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ALIGNMENTS

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LOCUS AR090280 400 from patent US 5994076. linear PAT 07-SEP-2000
DEFINITION Sequence 400 from patent US 5994076.
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ACCESSION E32226
VERSION AR090280.1 GI:10017035
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS Chenchik, A., Jekhade, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 400 30-NOV-1999;
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LOCUS AR197315
DEFINITION Sequence 400 from patent US 6352829.
AUTHORS Chenchik, A., Jekhade, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 400 05-MAR-2002;
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DEFINITION Sequence 400 from patent US 6489455.
AUTHORS Chenchik, A., Jekhade, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 400 03-DEC-2002;
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PF 05-NOV-1999 JP 2000581045

PR 06-NOV-1998 US 09/187478,14-APR-1999 US 09/292036 PI
BRIAN FREDERICK SCHMIDT, MARGARET LEAH ALLEN, FRAN SVERDRUP, PI
DAVID F CARMICHAEL
PC C12N15/09, A61K31/711, A61K48/00, A61P1/16, A61P9/00, A61P9/10, PC
A61P13/12, A61P17/00, A61P19/02, A61P41/00, A61P43/00, C07K14/475, C07K16/22,
PC A61P1/15,
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DEFINITION Sequence 10 from patent US 6358741.
ACCESSION AR201292
VERSION AR201292.1 GI:20252180
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Schmidt,B.Frederick., Allen,M.Leah., Sverdrup,F. and Carmichael,D.F.
TITLE Connective tissue growth factor (CTGF) and methods of use
JOURNAL Patent: US 6358741-A 10 19-MAR-2002;
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DEFINITION Sequence 601 from Patent WO0151627.
ACCESSION AX196894
VERSION AX196894.1 GI:15387100
KEYWORDS
SOURCE Glycine max (soybean)
ORGANISM Glycine max
REFERENCE 1
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1
AUTHORS Hauge,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.

TITLE Nucleic acid molecules and other molecules associated with soybean cyst nematode resistance
JOURNAL Patent: WO 0151627-A 601 19-JUL-2001;
MONSANTO COMPANY (US)
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AR074790/c
LOCUS AR074790 24 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 87 from patent US 5955276.
ACCESSION AR074790
VERSION AR074790.1 GI:10001543
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 87 21-SEP-1999;
FEATURES
source Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.2%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1805 TGTGTGTGTATATATATATAT 1827
|||||
Db 24 TGTGTGTGTATATATATATAT 2

RESULT 11
AX116747/c
LOCUS AX116747 24 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1870 from Patent WO0129262.
ACCESSION AX116747
VERSION AX116747.1 GI:14033689
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1870 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
source Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 2.2%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTGTGTGTGT 1813
Db 23 ATTGTGTGTGTGTGTGTGTGTGT 1

RESULT 12
I31231/c 131231 27 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 143 from patent US 5582979.
DEFINITION I31231
ACCESSION I31231
VERSION I31231.1 GI:1822022
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 143 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 30;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
Db 27 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 13
AX175241 AX175241 27 bp DNA linear PAT 03-JUL-2001
LOCUS Sequence 5 from Patent WO0144465.
DEFINITION AX175241
ACCESSION AX175241
VERSION AX175241.1 GI:14598609
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips, N.C. and Filion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 5 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES Location/Qualifiers
source 1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 30;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTATAT 1819
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 14
AR074791/c AR074791 22 bp DNA linear PAT 28-AUG-2000
LOCUS Sequence 88 from patent US 5955276.
DEFINITION AR074791
ACCESSION AR074791
VERSION AR074791.1 GI:10001544
KEYWORDS

Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 88 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.1%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1801 TGTGTGTGTGTATATATA 1822
Db 22 TGTGTGTGTGTATATATA 1

RESULT 15
I31234/c I31234 25 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 146 from patent US 5582979.
DEFINITION I31234
ACCESSION I31234
VERSION I31234.1 GI:1822025
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 146 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.1%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 30;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTATAT 1817
Db 25 TGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 16
AR051255/c AR051255 27 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 23 from patent US 5830658.
DEFINITION AR051255
ACCESSION AR051255
VERSION AR051255.1 GI:5974619
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Gryaznov, S.M.
TITLE Convergent synthesis of branched and multiply connected macromolecular structures
JOURNAL Patent: US 5830658-A 23 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 33;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 17
AXI127802/c
LOCUS
DEFINITION Sequence 23 from patent US 6180777.
ACCESSION AXI127802
VERSION AXI127802.1 GI:14114397
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 27)
AUTHORS Horn, T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 23 30-JAN-2001;
FEATURES
Location/Qualifiers
1. .27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 18
AXI128384/c
LOCUS
DEFINITION Sequence 23 from patent US 5571677.
ACCESSION AXI128384
VERSION AXI128384.1 GI:1819160
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 27)
AUTHORS Gvaznov, S.M.
TITLE Convergent synthesis of branched and multiply connected
JOURNAL macromolecular structures
FEATURES Patent: US 5571677-A 23 05-NOV-1996;
Location/Qualifiers
1. .27
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 19
AXI175237
LOCUS
DEFINITION Sequence 1 from Patent WO0144465.
ACCESSION AXI175237
VERSION AXI175237.1 GI:14598605
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

artificial sequences.

REFERENCE 1
AUTHORS Phillips, N.C. and Filion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 1 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
Location/Qualifiers
1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 2 TGTGTGTGTGTGTGTGTGTGT 26

RESULT 20
AXI175302
LOCUS
DEFINITION Sequence 66 from Patent WO0144465.
ACCESSION AXI175302
VERSION AXI175302.1 GI:14598670
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Phillips, N.C. and Filion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 66 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
Location/Qualifiers
1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 2 TGTGTGTGTGTGTGTGTGTGT 26

RESULT 21
AXI189457
LOCUS
DEFINITION Sequence 2 from Patent WO0147561.
ACCESSION AXI189457
VERSION AXI189457.1 GI:15142969
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Phillips, N.C. and Filion, M.C.
TITLE Hyaluronic acid in the treatment of cancer
JOURNAL Patent: WO 0147561-A 2 05-JUL-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
Location/Qualifiers
1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
DB 2 TGTGTGTGTGTGTGTGTGTGT 26

RESULT 22
I31542/c
LOCUS I31542 23 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 454 from patent US 5582979.
ACCESSION I31542
VERSION I31542.1 GI:1822333
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 454 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..23
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.0%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 23 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 23
AX116678
LOCUS AX116678 23 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1801 from Patent WO0129262.
ACCESSION AX116678
VERSION AX116678.1 GI:14033620
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1801 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES Location/Qualifiers
source 1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 2.0%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1790 TATTGTGTGTGTGTGTGTG 1812
DB 1 TTTTGTGTGTGTGTGTGTGTG 23

RESULT 24
I31533/c
LOCUS I31533 24 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 445 from patent US 5582979.

ACCESSION I31533
VERSION I31533.1 GI:1822324
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 445 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 24 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 25
AX104876
LOCUS AX104876 24 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1068 from Patent WO0122972.
ACCESSION AX104876
VERSION AX104876.1 GI:13921073
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 1068 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 26
AX175257
LOCUS AX175257 24 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 21 from Patent WO0144465.
ACCESSION AX175257
VERSION AX175257.1 GI:14598625
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Phillips, N.C. and Filion, M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 21 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES Location/Qualifiers
source 1..24

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 2.0%; Score 21.4; DB 1; Length 24;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 27
AX175258
LOCUS AX175258 24 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 22 from Patent WO0144465.
ACCESSION AX175258
VERSION AX175258.1 GI:14598626
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Fillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 22 21-JUN-2001;
Bioniche Life Sciences, Inc. (CA)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 2.0%; Score 21.4; DB 1; Length 24;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 2 TGTGTGTGTGTGTGTGTGTGT 24

RESULT 28
AX547929
LOCUS AX547929 24 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 1068 from Patent WO05053141.
ACCESSION AX547929
VERSION AX547929.1 GI:25813073
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 1068 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match
Best Local Similarity 2.0%; Score 21.4; DB 1; Length 24;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGTGT 23

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RESULT 29
AX115976
LOCUS AX115976 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 1099 from Patent WO0129262.
ACCESSION AX115976
VERSION AX115976.1 GI:14032918
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1099 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 2.0%; Score 21.4; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 2 TGTGTGTGTGTGTGTGTGTGT 24

RESULT 30
AX117836/c
LOCUS AX117836 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2959 from Patent WO0129262.
ACCESSION AX117836
VERSION AX117836.1 GI:14034787
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2959 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 2.0%; Score 21.4; DB 1; Length 25;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTAT 1815
Db 23 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 31
I31248/c
LOCUS I31248 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 160 from patent US 5582979.
ACCESSION I31248
VERSION I31248.1 GI:1822039
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 21)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 160 10-DEC-1996;
FEATURES
    source
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        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 21 TGTGTGTGTGTGTGTGTGT 1

RESULT 32
AX104715 AX104715 21 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 907 from Patent WO0122972.
DEFINITION AX104715
ACCESSION AX104715
VERSION AX104715.1 GI:13920912
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kriegl,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 907 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
    source
        1..21
        Location/Qualifiers
        1..21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 33
AX175255 AX175255 21 bp DNA linear PAT 03-JUL-2001
LOCUS Sequence 19 from Patent WO0144465.
DEFINITION AX175255
ACCESSION AX175255
VERSION AX175255.1 GI:14598623
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Fillion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 19 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
    source
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 29;

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 34
AX547768 AX547768 21 bp DNA linear PAT 01-MAR-2003
LOCUS Sequence 907 from Patent WO02053141.
DEFINITION AX547768
ACCESSION AX547768
VERSION AX547768.1 GI:25812912
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 907 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
    source
        1..21
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic Sequence"
Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 35
I31213/c I31213 22 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 125 from patent US 5582979.
DEFINITION I31213
ACCESSION I31213
VERSION I31213.1 GI:1822004
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 125 10-DEC-1996;
FEATURES
    source
        1..22
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred.No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 21 TGTGTGTGTGTGTGTGTGT 1

RESULT 36
AR127801/c AR127801 23 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 22 from patent US 6180777.
DEFINITION AR127801
ACCESSION AR127801
VERSION AR127801.1 GI:14114396

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Horn, T.
TITLE       Synthesis of branched nucleic acids
JOURNAL     Patent: US 6180777-A 22 30-JAN-2001;
FEATURES    Location/Qualifiers
            source
            1..23
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      2.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 22 TGTGTGTGTGTGTGTGTGT 2

RESULT 37
AX117828/c
LOCUS      AX117828      25 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 2951 from Patent WO0129262.
ACCESSION  AX117828
VERSION     AX117828.1 GI:14034779
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.

REFERENCE   1
AUTHORS     Picault-Newburg, L. and Pohl, M.
TITLE       Genotyping reagents, kits and methods of use thereof
JOURNAL     Patent: WO 0129262-A 2951 26-APR-2001;
            Orchid Biosciences, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..25
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

Query Match      2.0%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 21 TGTGTGTGTGTGTGTGTGT 1

RESULT 38
AX117832/c
LOCUS      AX117832      25 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 2955 from Patent WO0129262.
ACCESSION  AX117832
VERSION     AX117832.1 GI:14034783
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.

REFERENCE   1
AUTHORS     Picault-Newburg, L. and Pohl, M.
TITLE       Genotyping reagents, kits and methods of use thereof
JOURNAL     Patent: WO 0129262-A 2955 26-APR-2001;
            Orchid Biosciences, Inc. (US)
FEATURES    Location/Qualifiers
            source
            1..25
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

/note="Primer"

Query Match      2.0%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
Db 22 TGTGTGTGTGTGTGTGTGT 2

RESULT 39
A63570
LOCUS      A63570      20 bp      DNA      linear      PAT 12-MAR-1998
DEFINITION Sequence 11 from Patent WO9720324.
ACCESSION  A63570
VERSION     A63570.1 GI:3717225
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.

REFERENCE   1
AUTHORS     Scaggiante, B. and Quadrioglio, P.
TITLE       A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMORAL
JOURNAL     Patent: WO 9720924-A 11 12-JUN-1997;
            SAICOM S R L (IT)
COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 40
AR074792/c
LOCUS      AR074792      20 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 89 from patent US 5955276.
ACCESSION  AR074792
VERSION     AR074792.1 GI:10001545
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.

REFERENCE   1 (bases 1 to 20)
AUTHORS     Morgante, M. and Vogel, J. Marie.
TITLE       Compound microsatellite primers for the detection of genetic
            polymorphisms
JOURNAL     Patent: US 5955276-A 89 21-SEP-1999;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTGTATATA 1818
Db 20 TGTGTGTGTGTGTGTATATA 1

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RESULT 41
AR084543/c
LOCUS AR084543 20 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 32 from patent US 5981185.
ACCESSION AR084543
VERSION AR084543.1 GI:10011314
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 32 09-NOV-1999;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 42
AR123339/c
LOCUS AR123339 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6169176.
ACCESSION AR123339
VERSION AR123339.1 GI:14108305
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bruice,T.C. and Dev,A.P.
TITLE Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 5 02-JAN-2001;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 43
AR129684/c
LOCUS AR129684 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 88 from patent US 6187545.
ACCESSION AR129684
VERSION AR129684.1 GI:14117581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Butler,M.M., Wyatt,J. and Cowsett,L.M.
TITLE Antisense modulation of pepck-cytosolic expression
JOURNAL Patent: US 6187545-A 88 13-FEB-2001;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unknown"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1812
Db 20 TGTGTGTGTGTGTGTGTGT 1

RESULT 44
AR179298/c
LOCUS AR179298 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 1 from Patent WO0141813.
ACCESSION AR179298
VERSION AR179298.1 GI:14598969
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnik,M.D. and Mcnealy,P.A.
TITLE Methods of treating lupus based on antibody affinity and screening
JOURNAL Patent: WO 0141813-A 1 14-JUN-2001;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 45
AR179299/c
LOCUS AR179299 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0141813.
ACCESSION AR179299
VERSION AR179299.1 GI:14598970
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnik,M.D. and Mcnealy,P.A.
TITLE Methods of treating lupus based on antibody affinity and screening
JOURNAL Patent: WO 0141813-A 2 14-JUN-2001;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1812
Db 20 TGTGTGTGTGTGTGTGTGT 1
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/mol_type="unassigned DNA"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 44
AR179298/c
LOCUS AR179298 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 1 from Patent WO0141813.
ACCESSION AR179298
VERSION AR179298.1 GI:14598969
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnik,M.D. and Mcnealy,P.A.
TITLE Methods of treating lupus based on antibody affinity and screening
JOURNAL Patent: WO 0141813-A 1 14-JUN-2001;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGT 20

RESULT 45
AR179299/c
LOCUS AR179299 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0141813.
ACCESSION AR179299
VERSION AR179299.1 GI:14598970
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnik,M.D. and Mcnealy,P.A.
TITLE Methods of treating lupus based on antibody affinity and screening
JOURNAL Patent: WO 0141813-A 2 14-JUN-2001;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGT 1812
Db 20 TGTGTGTGTGTGTGTGTGT 1
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1794 GTGTGTGTGTGTGTGTGT 1813
DB      1 GTGTGTGTGTGTGTGTGT 20

RESULT 48
BD105781/c
LOCUS      BD105781          20 bp      DNA          linear          PAT 27-AUG-2002
DEFINITION      conjugates of biologically stable polymers and polynucleotides for
                  treating systemic lupus erythematosus.
ACCESSION      BD105781.1 GI:22651355
KEYWORDS      JP 2001354569-A/6.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
              1 (bases 1 to 20)
REFERENCE      Conrad,M.J. and Coutts,S.
AUTHORS      conjugates of biologically stable polymers and polynucleotides for
TITLE      treating systemic lupus erythematosus
JOURNAL      Patent: JP 2001354569-A 6 25-DEC-2001;
COMMENT      LA JOLLA PHARMACEUTICAL CO
              OS Artificial Sequence
              PN JP 2001354569-A/6
              PD 25-DEC-2001
              PF 04-APR-2001 JP 2001106534
              PR 16-JAN-1990 US 466138,13-MAR-1990 US 454118 PI
              PC A61K31/7098,A61K47/48,A61E37/02,C07K14/00,C12N15/00,C12N15/00
              CC Synthetic Construct
              FH Key
              FT source
              Location/Qualifiers
              1..20
              /organism='Artificial Sequence'.
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1794 GTGTGTGTGTGTGTGTGT 1813
DB      20 GTGTGTGTGTGTGTGTGT 1

RESULT 49
AX175256
LOCUS      AX175256          21 bp      DNA          linear          PAT 03-JUL-2001
DEFINITION      Sequence 20 from Patent WO0144465.
ACCESSION      AX175256
KEYWORDS      AX175256.1 GI:14598624
SOURCE      synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
              1
REFERENCE      Phillips,N.C. and Filion,M.C.
AUTHORS      Therapeutically useful synthetic oligonucleotides
TITLE      Patent: WO 0144465-A 20 21-JUN-2001;
JOURNAL      Sioniche Life Sciences Inc. (CA)
FEATURES      Location/Qualifiers
              1..21
              /organism="synthetic construct"
source

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 50
AX398276/c
LOCUS      AX398276      21 bp      DNA      linear      PAT 27-MAY-2002
DEFINITION Sequence 1 from Patent WO220543.
ACCESSION  AX398276
VERSION     AX398276.1 GI:21261077
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Sinha,N.
TITLE      Synthesis for oligonucleotide synthesis
JOURNAL    Patent: WO 0220543-A 1 14-MAR-2002;
            Avecia Biotechnology, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Sequence prepared in Example 4"

Query Match      1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 51
AX398277
LOCUS      AX398277      21 bp      DNA      linear      PAT 27-MAY-2002
DEFINITION Sequence 2 from Patent WO220543.
ACCESSION  AX398277
VERSION     AX398277.1 GI:21261078
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Sinha,N.
TITLE      Synthesis for oligonucleotide synthesis
JOURNAL    Patent: WO 0220543-A 2 14-MAR-2002;
            Avecia Biotechnology, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Sequence prepared in Example 4"

Query Match      1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 54
AX074777
LOCUS      AR074777      19 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 74 from patent US 5955276.
ACCESSION  AR074777
VERSION     AR074777.1 GI:10001530
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Morcante,M. and Vogel,J. Marie.
TITLE      Compound microsatellite primers for the detection of genetic
```

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RESULT 52
I30547/c
LOCUS      I30547      21 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 10 from patent US 5580969.
ACCESSION  I30547
VERSION     I30547.1 GI:1821338
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 21)
AUTHORS    Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.-H.
TITLE      Antisense oligonucleotides directed against human ICAM-1 RNA
JOURNAL    Patent: US 5580969-A 10 03-DEC-1996;
            Location/Qualifiers
FEATURES   source
            1..21
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TCTGTGTGTGTGTGTGTGTGT 1813
DB 21 TCTGTGTGTGTGTGTGTGTGT 1

RESULT 53
AX117030
LOCUS      AX117030      24 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 2153 from Patent WO0129262.
ACCESSION  AX117030
VERSION     AX117030.1 GI:14033972
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Picoult-Newburg,L. and Pohl,M.
TITLE      Genotyping reagents, kits and methods of use thereof
JOURNAL    Patent: WO 0129262-A 2153 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..24
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

Query Match      1.8%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TCTGTGTGTGTGTGTGTGTGT 1813
DB 1 TCTGTGTGTGTGTGTGTGTGT 21

RESULT 55
AR074777
LOCUS      AR074777      19 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 74 from patent US 5955276.
ACCESSION  AR074777
VERSION     AR074777.1 GI:10001530
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Morcante,M. and Vogel,J. Marie.
TITLE      Compound microsatellite primers for the detection of genetic
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polymorphisms
JOURNAL Patent: US 595276-A 74 21-SEP-1999;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTATAT 1817
|||||
Db 1 TGTGTGTGTGTGTATAT 19

RESULT 55
I31530/c
LOCUS I31530 19 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 442 from patent US 5582979.
ACCESSION I31530
VERSION I31530.1 GI:1822321
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-da).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A.442 10-DEC-1996;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811
|||||
Db 19 TGTGTGTGTGTGTGTGT 1

RESULT 56
AX040467/c
LOCUS AX040467 19 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 7 from Patent WO063365.
ACCESSION AX040467
VERSION AX040467.1 GI:11230259
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Belotserkovskii,B., Reddy,G. and Zarling,D.
TITLE Locked nucleic acid hybrids and methods of use
JOURNAL Patent: WO 0063365-A 7 26-OCT-2000;
FEATURES Location/Qualifiers
source
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Z-DNA"

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811
|||||

Db 19 TGTGTGTGTGTGTGTGT 1

RESULT 57
AX040468
LOCUS AX040468 19 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 8 from Patent WO063365.
ACCESSION AX040468
VERSION AX040468.1 GI:11230260
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Belotserkovskii,B., Reddy,G. and Zarling,D.
TITLE Locked nucleic acid hybrids and methods of use
JOURNAL Patent: WO 0063365-A 8 26-OCT-2000;
FEATURES Location/Qualifiers
source
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Z-DNA"

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811
|||||
Db 1 TGTGTGTGTGTGTGTGT 19

RESULT 58
AR126570
LOCUS AR126570 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6180349.
ACCESSION AR126570
VERSION AR126570.1 GI:14113163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Ginzinger,D.G., Godfrey,T.E., Jensen,R.H. and Gray,J.W.
TITLE Quantitative PCR method to enumerate DNA copy number
JOURNAL Patent: US 6180349-A 1 30-JAN-2001;
FEATURES Location/Qualifiers
source
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTG 1812
|||||
Db 2 GTGTGTGTGTGTGTGTGTG 20

RESULT 59
AR126571
LOCUS AR126571 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6180349.
ACCESSION AR126571
VERSION AR126571.1 GI:14113164
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)

AUTHORS Ginzinger,D.G., Godfrey,T.E., Jensen,R.H. and Gray,J.W.
TITLE Quantitative PCR method to enumerate DNA copy number
JOURNAL Patent: US 6180349-A 2 30-JAN-2001;
FEATURES Location/Qualifiers
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTGTG 1812
DB 2 GTGTGTGTGTGTGTGTGTG 20

RESULT 60
BD089174 21 bp DNA linear PAT 27-AUG-2002
LOCUS A method of arraying genome clone.
DEFINITION BD089174
ACCESSION BD089174
VERSION BD089174.1 GI:22634784
KEYWORDS JP 2001321190-A/1418.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1418 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS

OS Artificial Sequence
PN JP 2001321190-A/1418
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/09,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1. .21
FT Location/Qualifiers
1. .21
/organism="Artificial Sequence".

FEATURES
source
1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGT 1811
DB 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 61
AB068223 21 bp DNA linear SYN 21-MAY-2003
LOCUS Synthetic construct DNA, reverse primer for human STS sts-R12616F
DEFINITION at 1p36.
ACCESSION AB068223
VERSION AB068223.1 GI:15129027
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,

Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.
A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 21)
AUTHORS Horii,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
Location/Qualifiers
1. .21
source
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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sts-R12616F obtained from clones B12616, B156A20,
B141M15, B137L6, B157P23, Human BAC library
RPC1-11"

Query Match 1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGT 1811
DB 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 62
E32219/c 20 bp DNA linear PAT 18-JUN-2001
LOCUS Method for isolating satellite sequence.
DEFINITION E32219
ACCESSION E32219
VERSION E32219.1 GI:13021841
KEYWORDS JP 2000060559-A/21.
SOURCE Haliotis discus discus
ORGANISM Haliotis discus discus
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.

REFERENCE 1 (bases 1 to 20)
AUTHORS Hideaki,T. and Masashi,S.
TITLE Method for isolating satellite sequence
JOURNAL Patent: JP 2000060559-A 21 29-FEB-2000;
NAIL INST OF AGRICULTURAL RESOURCES
COMMENT OS Haliotis discus discus
PN JP 2000060559-A/21
PD 29-FEB-2000
PF 18-AUG-1998 JP 1998232153
PR
PI HIDEAKI TAKAHASHI,MASASHI SEKINO
PC C12N15/09,C12Q1/68,C12N15/00
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Db 20 TGTGTGTGTGTGTGTGTG 1

RESULT 63
LOCUS AR071775/C 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 4 from patent US 5912147.
ACCESSION AR071775
VERSION AR071775.1 GI:7222663
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 4 15-JUN-1999;
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 18 ATTGTGTGTGTGTGTGTG 1

RESULT 64
LOCUS AR071776/C 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 5 from patent US 5912147.
ACCESSION AR071776
VERSION AR071776.1 GI:7222664
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 5 15-JUN-1999;
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Best Local Similarity 100.0%; Pred. No. 52;
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QY 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 ATTGTGTGTGTGTGTGTG 1

RESULT 65
LOCUS AR178165/C 18 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 1 from patent US 6316186.
ACCESSION AR178165
VERSION AR178165.1 GI:17921058
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ekins,R.Philip.

TITLE Binding assay using binding agents with tail groups
JOURNAL Patent: US 6316186-A 1 13-NOV-2001;
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QY 1793 TGTGTGTGTGTGTGTGTG 1810
Db 18 TGTGTGTGTGTGTGTGTG 1

RESULT 66
LOCUS AR178166 18 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 2 from patent US 6316186.
ACCESSION AR178166
VERSION AR178166.1 GI:17921059
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ekins,R.Philip.
TITLE Binding assay using binding agents with tail groups
JOURNAL Patent: US 6316186-A 2 13-NOV-2001;
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Best Local Similarity 100.0%; Pred. No. 52;
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QY 1794 GTGTGTGTGTGTGTGTGT 1811
Db 1 GTGTGTGTGTGTGTGTGT 18

RESULT 67
LOCUS AR182079 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 28 from patent US 6337188.
ACCESSION AR182079
VERSION AR182079.1 GI:20224995
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Head,S.R., Goelet,P., Karn,J. and Boyce-Jacino,M.
TITLE De novo or 'universal' sequencing array
JOURNAL Patent: US 6337188-A 28 08-JAN-2002;
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QY 1793 TGTGTGTGTGTGTGTGTG 1810
Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 68
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AR261503
LOCUS AR261503 18 bp DNA
DEFINITION Sequence 28 from patent US 6322968.
ACCESSION AR261503
VERSION AR261503.1 GI:28072570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Head,S.R., Golet,P., Karn,J. and Boyce-Jacino,M.
TITLE De novo or 'universal' sequencing array
JOURNAL Patent: US 6322968-A 28 27-NOV-2001;
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QY 1793 TGTGTGTGTGTGTGTGTG 1810
Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 69
LOCUS AX175253 18 bp DNA
DEFINITION Sequence 17 from Patent WO0144465.
ACCESSION AX175253
VERSION AX175253.1 GI:14598621
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO-0144465-A 17 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 70
LOCUS AX175254 18 bp DNA
DEFINITION Sequence 18 from Patent WO0144465.
ACCESSION AX175254
VERSION AX175254.1 GI:14598622
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 18 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 71
LOCUS BD087486 18 bp DNA
DEFINITION De novo or universal sequencing array.
ACCESSION BD087486
VERSION BD087486.1 GI:22633096
KEYWORDS JP 2001524319-A/28.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Head,S.R., Golet,P., Karn,J. and Jacino,M.B.
TITLE De novo or universal sequencing array
JOURNAL Patent: JP 2001524319-A 28 04-DEC-2001;
ORCHID BIOSCIENCES INC
COMMENT OS Artificial Sequence
PN JP 2001524319-A/28
PD 04-DEC-2001
PF 20-NOV-1998 JP 2000522278
PR 21-NOV-1997 US 08/976427
PI STEVEN R HEAD,PHILIP GOLET,JONATHAN KARN,MICHAEL BOYCE JACINO
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/50,C12N15/00, PC
C12N15/00
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FH Key
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Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 72
LOCUS E05497 20 bp DNA
DEFINITION PCR primer for detecting polymorphism of Oryza sativa and Zea
maize.
ACCESSION E05497
VERSION E05497.1 GI:12173685
KEYWORDS JP 1993244995-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Komatsu,Y. and Kikuchi,Y.
TITLE NEW PRIMER
JOURNAL Patent: JP 1993244995-A 7 24-SEP-1993;
KYOWA HAKKO KOGYO CO LTD
COMMENT OS Artificial gene
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OC Artificial sequence; Genes.
OS Zea mize
PN JP 1993244995-A/7
PD 24-SEP-1993
PF 24-SEP-1991 JP 1991243122
PI KOMATSU YUKI, KIKUCHI YASUHIRO
PC C12Q1/68, C12N15/11;
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC Location/Qualifiers
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Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 73
LOCUS AR129716 20 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 120 from patent US 6187545.
ACCESSION AR129716
VERSION AR129716.1 GI:14117613
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay, R., Butler, M.M., Wyatt, J., and Cowsert, L.M.
TITLE Antisense modulation of peck-cytosolic expression
JOURNAL Patent: US 6187545-A 120 15-FEB-2001;
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Best Local Similarity 94.7%; Score 17.4; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812
Db 1 GTGTGTGTGTGTGTGTG 19

RESULT 74
LOCUS AR181773/3 20 bp DNA PAT 20-APR-2002
DEFINITION Sequence 235 from patent US 6335194.
ACCESSION AR181773
VERSION AR181773.1 GI:20223987
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.Frank., Ackermann, E.J., Swayze, E.E. and Cowsert, L.M.
TITLE Antisense modulation of survivin expression
JOURNAL Patent: US 6335194-A 235 01-JAN-2002;
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QY 1792 TTGTGTGTGTGTGTGTG 1808
Db 1 TTGTGTGTGTGTGTGTG 17

RESULT 77
LOCUS AX762730 17 bp DNA PAT 25-JUN-2003
DEFINITION Sequence 6051 from Patent WO03040369.

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Query Match
Best Local Similarity 94.7%; Score 17.4; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATGT 1829
Db 19 TGTATATATATATATGT 1

RESULT 75
LOCUS I31536 17 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 448 from patent US 5582979.
ACCESSION I31536
VERSION I31536.1 GI:1822327
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n. (dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 448 10-DEC-1996;
FEATURES
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Query Match
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 17 TGTGTGTGTGTGTGTGT 1

RESULT 76
LOCUS AX239676 17 bp DNA PAT 26-SEP-2001
DEFINITION Sequence 16 from Patent WO0164948.
ACCESSION AX239676
VERSION AX239676.1 GI:15797341
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 16 07-SEP-2001;
        Dr. van Haeringen Laboratorium B.V. (NL)
        Location/Qualifiers
FEATURES
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            /note="primer"

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Db 1 TTGTGTGTGTGTGTGTG 17

RESULT 77
LOCUS AX762730 17 bp DNA PAT 25-JUN-2003
DEFINITION Sequence 6051 from Patent WO03040369.

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ACCESSION AX762730
VERSION AX762730.1 GI:32257346
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tellerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 6051 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 62;
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QY 2141 GATCAGTTTTTCACT 2157
Db 1 GATCAGTTTTTCACT 17
RESULT 78
AR071772/c
LOCUS AR071772 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 1 from patent US 5912147.
ACCESSION AR071772
VERSION AR071772.1 GI:7222660
KEYWORDS Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 1 15-JUN-1999;
FEATURES Location/Qualifiers
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1792 TTGTGTGTGTGTGTGTG 1808
Db 17 TTGTGTGTGTGTGTGTG 1
RESULT 79
AR071774/c
LOCUS AR071774 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 3 from patent US 5912147.
ACCESSION AR071774
VERSION AR071774.1 GI:7222662
KEYWORDS Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 3 15-JUN-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 68;
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Db 17 TTGTGTGTGTGTGTGTG 1
RESULT 80
AR071799/c
LOCUS AR071799 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 28 from patent US 5912147.
ACCESSION AR071799
VERSION AR071799.1 GI:7222687
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 28 15-JUN-1999;
FEATURES Location/Qualifiers
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Db 17 TTGTGTGTGTGTGTGTG 1
RESULT 81
AR071801/c
LOCUS AR071801 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 30 from patent US 5912147.
ACCESSION AR071801
VERSION AR071801.1 GI:7222689
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 30 15-JUN-1999;
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Best Local Similarity 100.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 17 GTGTGTGTGTGTGTGTG 1
RESULT 82
AR071802/c
LOCUS AR071802 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 31 from patent US 5912147.
ACCESSION AR071802

VERSION AR071802.1 GI:7222690
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Stoler,D., Basik,M. and Anderson,G.
 TITLE Rapid means of quantitating genomic instability
 JOURNAL Patent: US 5912147-A 31-15-JUN-1999;
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 Db 17 GTGTGTGTGTGTGTG 1

RESULT 83
 E36173/c
 LOCUS AR071803 18 bp DNA linear PAT 18-FEB-2000
 DEFINITION Sequence 32 from patent US 5912147.
 ACCESSION AR071803
 VERSION AR071803.1 GI:7222691
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Stoler,D., Basik,M. and Anderson,G.
 TITLE Rapid means of quantitating genomic instability
 JOURNAL Patent: US 5912147-A 32-15-JUN-1999;
 FEATURES Location/Qualifiers
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Query Match 1.6%; Score 17; DB 1; Length 18;
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 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1810
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 Db 17 GTGTGTGTGTGTGTG 1

RESULT 84
 E36173
 LOCUS E36173 20 bp DNA linear PAT 31-JAN-2002
 DEFINITION Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof.
 ACCESSION E36173
 VERSION E36173.1 GI:18626400
 KEYWORDS JP 2000166563-A/15.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE Moro,O., Ifuku,O. and Ideta,T.
 JOURNAL Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof
 Patent: JP 2000166563-A 15 20-JUN-2000;
 SHISEIDO CO LTD
 COMMENT OS Homo sapiens (human)
 PN JP 2000166563-A/15
 PD 20-JUN-2000
 PF 04-DEC-1998 JP 1998345881

PR OSAMU MORO,OJI IFUKU,TATSURO IDETA
 PI C12N15/09,C12N5/10,C12Q1/68//C07K14/705,(C12N15/09,
 PC C12R1:91),
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RESULT 85
 E36173/c
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 DEFINITION Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof.
 ACCESSION E36173
 VERSION E36173.1 GI:18626400
 KEYWORDS JP 2000166563-A/15.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE Moro,O., Ifuku,O. and Ideta,T.
 JOURNAL Upstream regulatory sequence of melanocortin-1 receptor gene and utilization thereof
 Patent: JP 2000166563-A 15 20-JUN-2000;
 SHISEIDO CO LTD
 COMMENT OS Homo sapiens (human)
 PN JP 2000166563-A/15
 PD 20-JUN-2000
 PF 04-DEC-1998 JP 1998345881

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 PC C12R1:91),
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Query Match 1.8%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 82;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATGTA 1830
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 Db 20 TATATATATATATATATA 1

RESULT 86
 AR242049/c
 LOCUS AR242049 20 bp DNA linear PAT 20-DEC-2002


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Unclassified.
REFERENCE 1 (bases 1 to 18)
LOCUS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 7 15-JUN-1999;
FEATURES
    source
        1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 ACTGTGTGTGTGTGTGTG 1

RESULT 91
AR071779/c
LOCUS Stoler,D., Basik,M. and Anderson,G.
DEFINITION Sequence 8 from patent US 5912147.
ACCESSION AR071779
VERSION AR071779.1 GI:7222667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 8 15-JUN-1999;
FEATURES
    source
        1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 ACTGTGTGTGTGTGTGTG 1

RESULT 92
AR071800/c
LOCUS Stoler,D., Basik,M. and Anderson,G.
DEFINITION Sequence 29 from patent US 5912147.
ACCESSION AR071800
VERSION AR071800.1 GI:7222688
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 29 15-JUN-1999;
FEATURES
    source
        1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1793 TCTGTGTGTGTGTGTGTG 1810
Db 18 TCTGTGTGTGTGTGTGTG 1

Unclassified.
REFERENCE 1 (bases 1 to 18)
LOCUS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 7 15-JUN-1999;
FEATURES
    source
        1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 ACTGTGTGTGTGTGTGTG 1

RESULT 93
AR071804/c
LOCUS Stoler,D., Basik,M. and Anderson,G.
DEFINITION Sequence 33 from patent US 5912147.
ACCESSION AR071804
VERSION AR071804.1 GI:7222692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 33 15-JUN-1999;
FEATURES
    source
        1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 AATGTGTGTGTGTGTGTG 1

RESULT 94
AR071806/c
LOCUS Stoler,D., Basik,M. and Anderson,G.
DEFINITION Sequence 35 from patent US 5912147.
ACCESSION AR071806
VERSION AR071806.1 GI:7222694
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 35 15-JUN-1999;
FEATURES
    source
        1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 AATGTGTGTGTGTGTGTG 1

RESULT 95
AR071808/c
LOCUS Stoler,D., Basik,M. and Anderson,G.
DEFINITION Sequence 37 from patent US 5912147.
ACCESSION AR071808
VERSION AR071808.1 GI:7222696
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 37 15-JUN-1999;
FEATURES
    source
        1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 AATGTGTGTGTGTGTGTG 1

RESULT 96
AR071809/c
LOCUS Stoler,D., Basik,M. and Anderson,G.
DEFINITION Sequence 39 from patent US 5912147.
ACCESSION AR071809
VERSION AR071809.1 GI:7222698
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 39 15-JUN-1999;
FEATURES
    source
        1..18
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 AATGTGTGTGTGTGTGTG 1
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/mol_type="unassigned DNA"

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
Db 18 AATGTGTGTGTGTGTG 1

RESULT 96
AR071809/c
LOCUS 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 38 from patent US 5912147.
ACCESSION AR071809
VERSION AR071809.1 GI:7222697
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 38 15-JUN-1999;
FEATURES
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
Db 18 AATGTGTGTGTGTGTG 1

RESULT 97
E28534
LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28534
VERSION E28534.1 GI:13025386
KEYWORDS JP 199075880-A/1.
SOURCE Unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 199075880-A 1 23-MAR-1999;
COMMENT CHEMO SERO THERAPEUT RES INST
OS Unidentified
PN JP 199075880-A/1
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR
PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
Db 18 AATGTGTGTGTGTGTG 1

RESULT 97
E28534
LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28534
VERSION E28534.1 GI:13025386
KEYWORDS JP 199075880-A/1.
SOURCE Unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 199075880-A 1 23-MAR-1999;
COMMENT CHEMO SERO THERAPEUT RES INST
OS Unidentified
PN JP 199075880-A/1
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR
PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
Db 1 TATATATATATATATATA 18

RESULT 98
E28534/c
LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION E28534
VERSION E28534.1 GI:13025386
KEYWORDS JP 199075880-A/1.
SOURCE Unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 199075880-A 1 23-MAR-1999;
COMMENT CHEMO SERO THERAPEUT RES INST
OS Unidentified
PN JP 199075880-A/1
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR
PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
Db 18 TATATATATATATATATA 1

RESULT 99
AR241816
LOCUS 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 104 from patent US 6472154.
ACCESSION AR241816
VERSION AR241816.1 GI:27287628
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 104 29-OCT-2002;
FEATURES
source
1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1810 GTGTATATATATATAT 1827
Db 1 GTATATATATATATAT 18

RESULT 100
AR241816/c
LOCUS AR241816 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 104 from patent US 6472154.
ACCESSION AR241816
VERSION AR241816.1 GI:27287628
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 104 29-OCT-2002;
FEATURES
    source
        1..18
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match 1..6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATATAC 1831
Db 18 ATATATATATATATATAC 1

RESULT 101
BD084130/c
LOCUS BD084130 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Polymorphisms and new genes in the region of the human
hemochromatosis gene.
ACCESSION BD084130
VERSION BD084130.1 GI:22629740
KEYWORDS JP 2001525663-A/18.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 20)
AUTHORS Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Polymorphisms and new genes in the region of the human
hemochromatosis gene
JOURNAL Patent: JP 2001525663-A 18 11-DEC-2001;
COMMENT OS Homo sapiens (human)
PN JP 2001525663-A/18
PD 11-DEC-2001
PF 30-SEP-1997 JP 1998516815
PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
C07H21/04,C12Q1/69,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
and new genes in the region of the human CC hemochromatosis gene
PH Key Location/Qualifiers
FT source 1..20
/organism='Homo sapiens (human)'

Query Match 1..6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATATAC 1831
Db 18 ATATATATATATATATAC 1

RESULT 101
BD084130/c
LOCUS BD084130 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Polymorphisms and new genes in the region of the human
hemochromatosis gene.
ACCESSION BD084130
VERSION BD084130.1 GI:22629740
KEYWORDS JP 2001525663-A/18.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 20)
AUTHORS Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Polymorphisms and new genes in the region of the human
hemochromatosis gene
JOURNAL Patent: JP 2001525663-A 18 11-DEC-2001;
COMMENT OS Homo sapiens (human)
PN JP 2001525663-A/18
PD 11-DEC-2001
PF 30-SEP-1997 JP 1998516815
PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
C07H21/04,C12Q1/69,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
and new genes in the region of the human CC hemochromatosis gene
PH Key Location/Qualifiers
FT source 1..20
/organism='Homo sapiens (human)'

Query Match 1..6%; Score 16.4; DB 1; Length 20;

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Best Local Similarity 94.4%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
Db 2 TATATATATATATATATA 19

RESULT 102
BD084130/c
LOCUS BD084130 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Polymorphisms and new genes in the region of the human
hemochromatosis gene.
ACCESSION BD084130
VERSION BD084130.1 GI:22629740
KEYWORDS JP 2001525663-A/18.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 20)
AUTHORS Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Polymorphisms and new genes in the region of the human
hemochromatosis gene
JOURNAL Patent: JP 2001525663-A 18 11-DEC-2001;
COMMENT OS Homo sapiens (human)
PN JP 2001525663-A/18
PD 11-DEC-2001
PF 30-SEP-1997 JP 1998516815
PR 01-OCT-1996 US 08/724394,07-MAY-1997 US 08/852495 PI
JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
C07H21/04,C12Q1/69,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
and new genes in the region of the human CC hemochromatosis gene
PH Key Location/Qualifiers
FT source 1..20
/organism='Homo sapiens (human)'

Query Match 1..6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
Db 19 TATATATATATATATATA 2

RESULT 103
AI2053
LOCUS AI2053 16 bp DNA linear PAT 09-DEC-1993
DEFINITION Oligonucleotide.
ACCESSION AI2053
VERSION AI2053.1 GI:491255
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 16)
AUTHORS Epplen,J.T.
TITLE Process for the detection of restriction fragment length
polymorphisms in eukaryotic genomes
JOURNAL Patent: EP 0266787-A 13 11-MAY-1988;
FEATURES Max-Planck-Gesellschaft zur Foerderung der Wissenschaften
    source 1..16
    /organism='synthetic construct'

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
|||||
DB 1 GGTGTGTGTGTGTGT 16

RESULT 104

LOCUS A12054 16 bp DNA linear PAT 09-DEC-1993
DEFINITION Oligonucleotide.
ACCESSION A12054
VERSION A12054.1 GI:489449
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 16)
AUTHORS Eppien,J.T.
TITLE Process for the detection of restriction fragment length
polymorphisms in eukaryotic genomes
JOURNAL Patent: EP 0266787-A 14 11-MAY-1988;
Max-Planck-Gesellschaft zur Foerderung der Wissenschaften

FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
|||||
DB 16 GTGTGTGTGTGTGTGT 1

RESULT 105

LOCUS E32224/c 16 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION E32224
VERSION E32224.1 GI:13021854
KEYWORDS JP 2000060559-A/26.
SOURCE Haliotis discus discus
ORGANISM Haliotis discus discus
REFERENCE 1 (bases 1 to 16)
AUTHORS Hideaki,T. and Masashi,S.
TITLE Method for isolating satellite sequence
JOURNAL Patent: JP 2000060559-A 26 29-FEB-2000;
NATL INST OF AGROBIOLOGICAL RESOURCES

COMMENT
OS Haliotis discus discus
PN JP 2000060559-A/26
PD 29-FEB-2000
PF 18-AUG-1998 JP 1998232153
PR HIDEAKI TAKAHASHI,MASASHI SEKINO
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..16
/organism="Haliotis discus discus".

FEATURES
source
1..16
Location/Qualifiers
/organism="Haliotis discus discus"

/mol_type="genomic DNA"
/sub_species="discus"
/db_xref="taxon:91233"

Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1808
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DB 16 TGTGTGTGTGTGTGT 1

RESULT 106

LOCUS I31527/c 16 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 439 from patent US 5582979.
ACCESSION I31527
VERSION I31527.1 GI:1822318
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 439 10-DEC-1996;
FEATURES Location/Qualifiers
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source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1808
|||||
DB 16 TGTGTGTGTGTGTGT 1

RESULT 107

LOCUS AR328667 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6069 from patent US 6566127.
ACCESSION AR328667
VERSION AR328667.1 GI:33714475
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6069 20-MAY-2003;
FEATURES Location/Qualifiers
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source
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
|||||
DB 1 GTGTGTGTGTGTGTGT 16

RESULT 108

AX239677

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JOURNAL Patent: WO 0164948-A 19 07-SEP-2001;
          Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1. .17
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="primer"

Query Match      1.5% Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1793 TGTGTGTGTGTGTGTGTG 1808
DB      17 TGTGTGTGTGTGTGTGTG 2

RESULT 111
AX239680/c
LOCUS      AX239680
DEFINITION Sequence 20 from Patent WO0164948.
ACCESSION  AX239680
VERSION     AX239680.1 GI:15797345
KEYWORDS
SOURCE
ORGANISM   synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    van Haeringen, W.A. and van Haeringen, H.
TITLE      Universal variable fragments
JOURNAL    Patent: WO 0164948-A 20 07-SEP-2001;
            Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1. .17
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="primer"

Query Match      1.5% Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1793 TGTGTGTGTGTGTGTGTG 1808
DB      17 TGTGTGTGTGTGTGTGTG 2

RESULT 112
AX239681/c
LOCUS      AX239681
DEFINITION Sequence 21 from Patent WO0164948.
ACCESSION  AX239681
VERSION     AX239681.1 GI:15797346
KEYWORDS
SOURCE
ORGANISM   synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    van Haeringen, W.A. and van Haeringen, H.
TITLE      Universal variable fragments
JOURNAL    Patent: WO 0164948-A 21 07-SEP-2001;
            Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1. .17
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="primer"

Query Match      1.5% Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1793 TGTGTGTGTGTGTGTGTG 1808
DB      17 TGTGTGTGTGTGTGTGTG 2

RESULT 113
AX239682/c
LOCUS      AX239682
DEFINITION Sequence 22 from Patent WO0164948.
ACCESSION  AX239682
VERSION     AX239682.1 GI:15797347
KEYWORDS
SOURCE
ORGANISM   synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    van Haeringen, W.A. and van Haeringen, H.
TITLE      Universal variable fragments
JOURNAL    Patent: WO 0164948-A 22 07-SEP-2001;
            Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1. .17
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="primer"

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 113
LOCUS AR071773 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 2 from patent US 5912147.
ACCESSION AR071773
VERSION AR071773.1 GI:7222661
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 2 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTGTG 1

RESULT 114
LOCUS AR071777 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 6 from patent US 5912147.
ACCESSION AR071777
VERSION AR071777.1 GI:7222665
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 6 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTGTG 1

RESULT 115
LOCUS AR071805 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 34 from patent US 5912147.
ACCESSION AR071805
VERSION AR071805.1 GI:7222693
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 34 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTGTG 1

RESULT 116
LOCUS AR071807 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 36 from patent US 5912147.
ACCESSION AR071807
VERSION AR071807.1 GI:7222695
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 36 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTGTG 1

RESULT 117
LOCUS AX115187 18 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 310 from Patent WO0123262.
ACCESSION AX115187
VERSION AX115187.1 GI:14032129
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0123262-A 310 26-APR-2001;
FEATURES Location/Qualifiers
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTG 1810
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REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 34 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTGTG 1

RESULT 116
LOCUS AR071807/c 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 36 from patent US 5912147.
ACCESSION AR071807
VERSION AR071807.1 GI:7222695
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 36 15-JUN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 16 TGTGTGTGTGTGTGTG 1

RESULT 117
LOCUS AX115187 18 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 310 from Patent WO0123262.
ACCESSION AX115187
VERSION AX115187.1 GI:14032129
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0123262-A 310 26-APR-2001;
FEATURES Location/Qualifiers
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTG 1810
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Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
Db 2 TATATATATATAT 16

RESULT 128
LOCUS I38642 16 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 2 from patent US 5614617.
ACCESSION I38642
VERSION I38642.1 GI:2084696
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook, P.D. and Sanghvi, Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that
detect and modulate gene expression
JOURNAL Patent: US 5614617-A 2 25-MAR-1997;
FEATURES
source
Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
Db 15 TATATATATATAT 1

RESULT 129
LOCUS AR328666 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6068 from patent US 5566127.
ACCESSION AR328666
VERSION AR328666.1 GI:33714474
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 5566127-A 6068 20-MAY-2003;
FEATURES
source
Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGT 1807
Db 2 TGTGTGTGTGTGTGT 16

RESULT 130
LOCUS AR328668 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6070 from patent US 5566127.
ACCESSION AR328668
VERSION AR328668.1 GI:33714476
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 5566127-A 6070 20-MAY-2003;
FEATURES
source
Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1808
Db 1 GTGTGTGTGTGTGTG 15

RESULT 131
LOCUS AX599310 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 650 from Patent WO02077272.
ACCESSION AX599310
VERSION AX599310.1 GI:28399452
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J.,
Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E.,
Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T.,
Pelet, C. and Ziebarth, H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL Patent: WO 02077272-A 650 03-OCT-2002;
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for ELK1"

Query Match 1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1867 TTTATTTTGTGTGT 1881
Db 1 TTTATTTTGTGTGT 15

RESULT 132
LOCUS AX599902 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 1242 from Patent WO02077272.
ACCESSION AX599902
VERSION AX599902.1 GI:28400052
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J.,
Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E.,
Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T.,
Pelet, C. and Ziebarth, H.
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TITLE      Methods and nucleic acids for the analysis of hematopoietic cell
JOURNAL    proliferative disorders
            Patent: WO 0307272-A 1242 03-OCT-2002;
FEATURES    Epigenomics AG (DE)
            Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Detection oligonucleotide for ELK1"

Query Match      1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1867 TTTATTTTGTGTTT 1881
DB      1 TTTATTTTGTGTTT 15

RESULT 133
LOCUS    AX767726                18 bp      DNA      linear      PAT 02-JUL-2003
DEFINITION
Sequence 374 from Patent WO03044226.
ACCESSION AX767726
VERSION   AX767726.1 GI:32436331
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1
AUTHORS   Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
Nimmrich,I.
TITLE     Method and nucleic acids for the analysis of a lymphoid cell
JOURNAL   proliferative disorder
            Patent: WO 03044226-A 374 30-MAY-2003;
            Epigenomics AG (DE)
FEATURES   Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Detection oligonucleotide for ELK1"

Query Match      1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1867 TTTATTTTGTGTTT 1881
DB      1 TTTATTTTGTGTTT 15

RESULT 134
LOCUS    AX796164                18 bp      DNA      linear      PAT 04-OCT-2003
DEFINITION
Sequence 507 from Patent WO03052135.
ACCESSION AX796164
VERSION   AX796164.1 GI:37516830
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE 1
AUTHORS   Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
and Nimmrich,I.
TITLE     Method and nucleic acids for the analysis of a lung cell
JOURNAL   proliferative disorder
            Patent: WO 03052135-A 507 26-JUN-2003;
            Epigenomics AG (DE)
FEATURES   Location/Qualifiers
            1..18
            /organism="synthetic construct"

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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Detection oligonucleotide for ELK1"

Query Match      1.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1867 TTTATTTTGTGTTT 1881
DB      1 TTTATTTTGTGTTT 15

RESULT 135
LOCUS    AR090280                32 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION
Sequence 400 from patent US 5994076.
ACCESSION AR090280
VERSION   AR090280.1 GI:10017035
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE     Methods of assaying differential expression
JOURNAL   Patent: US 5994076-A 400 30-NOV-1999;
FEATURES   Location/Qualifiers
            1..32
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1731 GCTTGTGGCAAGTGAATTCCTGTAAACAAG 1761
DB      2 GCTTGTACAGGCAATTCACCTGCCACAAG 32

RESULT 136
LOCUS    AR197315                32 bp      DNA      linear      PAT 20-APR-2002
DEFINITION
Sequence 400 from patent US 6352829.
ACCESSION AR197315
VERSION   AR197315.1 GI:20247164
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE     Methods of assaying differential expression
JOURNAL   Patent: US 6352829-A 400 05-MAR-2002;
FEATURES   Location/Qualifiers
            1..32
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1731 GCTTGTGGCAAGTGAATTCCTGTAAACAAG 1761
DB      2 GCTTGTACAGGCAATTCACCTGCCACAAG 32

RESULT 137
LOCUS    AR259469                32 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION
Sequence 400 from patent US 6489455.

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source      1..16  

/organism="unknown"  

/mol_type="unassigned DNA"

Query Match          1.4%; Score 14.4; DB 1; Length 16;  

Best Local Similarity 93.8%; Pred. No. 1.1e+02;  

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   1793 TGTGTTGTGTGTGTG 1808  

     |||||||  

Db    1 TGCGTGTGTGTGTG 16

RESULT 140
ISL1790                                     16 bp       DNA         linear PAT 07-OCT-1997
LOCUS Sequence 58 from patent US 5645986.  

DEFINITION ISL1790  

ACCESSION ISL1790.1 GI:2472991  

VERSION .  

KEYWORDS Unknown.  

SOURCE Unknown.  

ORGANISM Unclassified.  

REFERENCE 1 (bases 1 to 16)  

AUTHORS West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,  

Wright,W.E., Blackburn,E.H. and Vaziri,H.  

TITLE Therapy and diagnosis of conditions related to telomere length  

and/or telomerase activity  

JOURNAL Patent: US 5645986-A 58 08-JUL-1997;  

FEATURES Location/Qualifiers  

             source      1..16  

                        /organism="unknown"  

                        /mol_type="unassigned DNA"

Query Match          1.4%; Score 14.4; DB 1; Length 16;  

Best Local Similarity 93.8%; Pred. No. 1.1e+02;  

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   1793 TGTGTTGTGTGTGTG 1808  

     |||||||  

Db    1 TGCGTGTGTGTGTG 16

RESULT 141
ISL4399                                     16 bp       DNA         linear PAT 04-APR-1998
LOCUS Sequence 57 from patent US 5695932..  

DEFINITION ISL4399  

ACCESSION ISL4399.1 GI:3021919  

VERSION .  

KEYWORDS Unknown.  

SOURCE Unknown.  

ORGANISM Unclassified.  

REFERENCE 1 (bases 1 to 16)  

AUTHORS West,M.D., Shay,J., Wright,W., Blackburn,E.H. and McEachern,M.J.  

TITLE Telomerase activity assays for diagnosing pathogenic infections  

JOURNAL Patent: US 5695932-A 57 09-DEC-1997;  

FEATURES Location/Qualifiers  

             source      1..16  

                        /organism="unknown"  

                        /mol_type="unassigned DNA"

Query Match          1.4%; Score 14.4; DB 1; Length 16;  

Best Local Similarity 93.8%; Pred. No. 1.1e+02;  

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   1793 TGTGTTGTGTGTGTG 1808  

     |||||||  

Db    1 TGCGTGTGTGTGTG 16

RESULT 142
AR204607

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LOCUS AR204607 16 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 57 from patent US 6368789.
ACCESSION AR204607
VERSION AR204607.1 GI:21501976
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J., Wright,W. and Blackburn,E.H.
TITLE Screening methods to identify inhibitors of telomerase activity
JOURNAL Patent: US 6368789-A 57 09-APR-2002;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 143
LOCUS AR307317 16 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 80 from patent US 6551774.
ACCESSION AR307317
VERSION AR307317.1 GI:31697844
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
Shay,J., Wright,W.E., Blackburn,E.H., Kim,N.W. and Vaziri,H.
TITLE Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
JOURNAL Patent: US 6551774-A 80 22-APR-2003;
FEATURES
    source
        /organism="unknown"
        /mol_type="genomic DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 144
LOCUS AR328669 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6071 from patent US 6566127.
ACCESSION AR328669
VERSION AR328669.1 GI:33714477
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Bacabedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6071 20-MAY-2003;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 145
LOCUS AR011362 17 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 235 from patent US 5762938.
ACCESSION AR011362
VERSION AR011362.1 GI:3969352
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Paolletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
Cox,W.I., Audonnet,J.-C.Francis. and Gettig,R.Robert.
TITLE Modified recombinant vaccinia virus and expression vectors thereof
JOURNAL Patent: US 5762938-A 235 03-JUN-1998;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTCTGAATAT 1792
Db 1 TTTATATTCTGAATAT 16

RESULT 146
LOCUS AR046265 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1058 from patent US 5817796.
ACCESSION AR046265
VERSION AR046265.1 GI:5967730
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myc ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 1058 06-OCT-1998;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATA 1826
Db 17 TGTATATATATATAA 2

RESULT 147
LOCUS AR061027 17 bp DNA linear PAT 29-SEP-1999
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LOCUS AR204607 16 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 57 from patent US 6368789.
ACCESSION AR204607
VERSION AR204607.1 GI:21501976
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J., Wright,W. and Blackburn,E.H.
TITLE Screening methods to identify inhibitors of telomerase activity
JOURNAL Patent: US 6368789-A 57 09-APR-2002;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned RNA"
Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
Db 1 GTGTGTGTGTGTGTGTG 16

RESULT 145
LOCUS AR011362 17 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 235 from patent US 5762938.
ACCESSION AR011362
VERSION AR011362.1 GI:3969352
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Paolletti,E., Perkus,M.E., Taylor,J., Tartaglia,J., Norton,E.K.,
Riviere,M., de Taisne,C., Limbach,K.J., Johnson,G.P., Pincus,S.E.,
Cox,W.I., Audonnet,J.-C.Francis. and Gettig,R.Robert.
TITLE Modified recombinant vaccinia virus and expression vectors thereof
JOURNAL Patent: US 5762938-A 235 03-JUN-1998;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTCTGAATAT 1792
Db 1 TTTATATTCTGAATAT 16

RESULT 146
LOCUS AR046265 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1058 from patent US 5817796.
ACCESSION AR046265
VERSION AR046265.1 GI:5967730
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myc ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 1058 06-OCT-1998;
FEATURES
    source
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATA 1826
Db 17 TGTATATATATATAA 2

RESULT 147
LOCUS AR061027 17 bp DNA linear PAT 29-SEP-1999
```

DEFINITION Sequence 52 from patent US 5843456.
ACCESSION AR061027
VERSION AR061027.1 GI:5988718
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Paoletti, E. and Maki, J.
JOURNAL Alvac poxvirus-rabies compositions and combination compositions and uses
FEATURES Patent: US 5843456-A 52 01-DEC-1998;
LOCATION/Qualifiers
source 1. 17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792
DB 1 TTTATATTGTAATAT 16

RESULT 148
LOCUS I18000 17 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 235 from patent US 5494807.
ACCESSION I18000
VERSION I18000.1 GI:1598355
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Paoletti, E., Perkus, M.E., Taylor, J., Tartaglia, J., Norton, E.K.,
Riviere, M., de Taisne, C., Limbach, K.J., Johnson, G.P., Pincus, S.E.,
Cox, W.I., Audonnet, J.-C.F. and Gettig, R.R.
JOURNAL NVVAC vaccinia virus recombinants comprising heterologous inserts
FEATURES Patent: US 5494807-A 235 27-FEB-1996;
LOCATION/Qualifiers
source 1. 17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792
DB 1 TTTATATTGTAATAT 16

RESULT 149
LOCUS I53317/c 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1058 from patent US 5646042.
ACCESSION I53317
VERSION I53317.1 GI:2474520
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
JOURNAL C-myb targeted ribozymes
FEATURES Patent: US 5646042-A 1058 08-JUL-1997;
LOCATION/Qualifiers
source 1. 17
/organism="unknown"

/mol_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826
DB 17 TGTATATATATATAA 2

RESULT 150
LOCUS AR188671 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4159 from patent US 6346398.
ACCESSION AR188671
VERSION AR188671.1 GI:20234636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
JOURNAL Method and reagent for the treatment of diseases or conditions
FEATURES related to levels of vascular endothelial growth factor receptor
Patent: US 6346398-A 4159 12-FEB-2002;
LOCATION/Qualifiers
source 1. 17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1749 TGCCTGTACCAAGCCA 1764
DB 2 TGCCTGTACCAAGCCA 17

RESULT 151
LOCUS AR271518/c 17 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 13 from patent US 6503710.
ACCESSION AR271518
VERSION AR271518.1 GI:29702938
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Gut, I.G., Berlin, K., Lechner, D. and Lehrach, H.
JOURNAL Mutation analysis using mass spectrometry
FEATURES Patent: US 6503710-A 13 07-JAN-2003;
LOCATION/Qualifiers
source 1. 17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1891 ATATTTCATGTTAGC 1906
DB 16 ATATTTCATGTCAGC 1

RESULT 152
LOCUS AR324524 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1926 from patent US 6566127.
ACCESSION AR324524

```
VERSION AR324524.1 GI:33710332
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6566127-A 1926 20-MAY-2003;
Location/Qualifiers
source
1. .17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1749 TGCGTGTACCAAGCCA 1764
Db 2 TGCGTGTACCAAGCCA 17

RESULT 153
LOCUS AR329254 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6556 from patent US 6566127.
ACCESSION AR329254
VERSION AR329254.1 GI:33715062
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6566127-A 6556 20-MAY-2003;
Location/Qualifiers
source
1. .17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1750 GCCTGTACCAAGCCAG 1765
Db 1 GCCTGTACCAAGCCAG 16

RESULT 154
LOCUS AX018733 17 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 22 from Patent WO9944633.
ACCESSION AX018733
VERSION AX018733.1 GI:10042955
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Minke,J.M. and Audonnet,J.C.
TITLE Live recombinant vaccines injected with adjuvant
JOURNAL Patent: WO 9944633-A 22 10-SEP-1999;
MINKE JULES MAARTEN (FR); MERIAL SAS (FR); AUDONNET JEAN CHRISTOPHE
FRANC (FR)
Location/Qualifiers
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned DNA"
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```
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792
Db 1 TTTATATTGTAATAT 16

RESULT 155
LOCUS AX422370 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 706 from Patent WO018124.
ACCESSION AX422370
VERSION AX422370.1 GI:21525752
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., McSwiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 018124-A 706 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1289 TAAATCTGTTTCTA 1304
Db 17 TAAATCTGTTTCTA 2

RESULT 156
LOCUS AX502781 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 4088 from Patent EP1229046.
ACCESSION AX502781
VERSION AX502781.1 GI:23385074
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhan,J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 4088 07-AUG-2002;
Aeonica, Inc. (US)
FEATURES Location/Qualifiers
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 GCATTGTTTCTACTT 2177
Db 2 GCATTGTTTCTACTT 17
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reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 Patent: WO 03025177-A 2133 27-MAR-2003;
 Molecular Engines Laboratories (FR)
 FEATURES
 source

Query Match
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

QY 1877 TTTTAAATGCTTTGAT 1892
 |||||
 Db 17 TTTTAAATGCTTTGAT 2

RESULT 162
 LOCUS AX760931/c 17 bp DNA linear PAT 25-JUN-2003
 DEFINITION Sequence 4252 from Patent WO03040369.
 ACCESSION AX760931
 VERSION AX760931.1 GI:32255547
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM
 HOMO SAPIENS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Telesman,A., Anson,R. and Tuijnder,M.
 Apoptosis involved in tumoral suppression, tumoral reversion,
 sequences and/or viral resistance phenomena and their use as
 medicines
 JOURNAL Patent: WO 03040369-A 4252 15-MAY-2003;
 Molecular Engines Laboratories (FR)
 FEATURES
 source

Query Match
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

QY 1888 TTGATATTTCAATGTT 1903
 |||||
 Db 17 TTGATATTTCAATGAT 2

RESULT 163
 LOCUS AX762000/c 17 bp DNA linear PAT 25-JUN-2003
 DEFINITION Sequence 5321 from Patent WO03040369.
 ACCESSION AX762000
 VERSION AX762000.1 GI:32256616
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM
 HOMO SAPIENS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Telesman,A., Anson,R. and Tuijnder,M.
 Sequences involved in tumoral suppression, tumoral reversion,
 apoptosis and/or viral resistance phenomena and their use as
 medicines
 JOURNAL Patent: WO 03040369-A 5321 15-MAY-2003;
 Molecular Engines Laboratories (FR)
 FEATURES
 source

Query Match
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

/mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

QY 2166 TTGTTTCTACTTTGAT 2181
 |||||
 Db 17 TTGTTTCTCTCTTTGAT 2

RESULT 164
 LOCUS AX058584 18 bp DNA linear PAT 17-JAN-2001
 DEFINITION Sequence 36 from Patent WO0077250.
 ACCESSION AX058584
 VERSION AX058584.1 GI:12310926
 KEYWORDS synthetic construct
 SOURCE
 ORGANISM
 SYNTHETIC CONSTRUCT
 Artificial sequences.
 REFERENCE
 1 Escude,C., Garestier,T., Helene,C. and Roulon,T.
 Method for circularizing oligonucleotides around a double stranded
 nucleic acid, resulting structures and uses thereof
 Patent: WO 0077250-A 36 21-DEC-2000;
 INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
 (FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
 FEATURES
 source

Query Match
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 18;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /notes="Oligonucleotide"

QY 1792 TTGTGTGTGTGTGTGT 1807
 |||||
 Db 3 TTGTGTGTGTGTGTGGT 18

RESULT 165
 LOCUS BD104911 18 bp DNA linear PAT 27-AUG-2002
 DEFINITION Kit and method for determining HLA type.
 ACCESSION BD104911
 VERSION BD104911.1 GI:22650485
 KEYWORDS WO 0192572-A/1015.
 SOURCE
 ORGANISM
 SYNTHETIC CONSTRUCT
 Artificial sequences.
 REFERENCE
 1 (bases 1 to 18)
 Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
 Nishida,M.
 Kit and method for determining HLA type
 Patent: WO 0192572-A 1015 08-DEC-2001;
 NISSHINBO INDUSTRIES INC.,SYSTEM RESEARCH INC.,HIDETOSHI INOKO, TAEKO
 KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
 NISHIDA
 OS Artificial Sequence
 PN WO 0192572-A/1015
 PD 06-DEC-2001
 PP 01-JUN-2001 WO 2001JP004662
 PR 01-JUN-2000 JP 00P 164798
 PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
 MATSUMURA,
 PI SHOGO MORIYA,MICHIO NISHIDA
 PC C1201/69,C12M1/00,C12N15/09,G01N33/53
 CC Description of Artificial Sequence:capture

Query Match
 Best Local Similarity 1.4%; Score 14.4; DB 1; Length 18;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /notes="Oligonucleotide"

QY 1792 TTGTGTGTGTGTGTGT 1807
 |||||
 Db 3 TTGTGTGTGTGTGTGGT 18

RESULT 165
 LOCUS BD104911 18 bp DNA linear PAT 27-AUG-2002
 DEFINITION Kit and method for determining HLA type.
 ACCESSION BD104911
 VERSION BD104911.1 GI:22650485
 KEYWORDS WO 0192572-A/1015.
 SOURCE
 ORGANISM
 SYNTHETIC CONSTRUCT
 Artificial sequences.
 REFERENCE
 1 (bases 1 to 18)
 Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
 Nishida,M.
 Kit and method for determining HLA type
 Patent: WO 0192572-A 1015 08-DEC-2001;
 NISSHINBO INDUSTRIES INC.,SYSTEM RESEARCH INC.,HIDETOSHI INOKO, TAEKO
 KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
 NISHIDA
 OS Artificial Sequence
 PN WO 0192572-A/1015
 PD 06-DEC-2001
 PP 01-JUN-2001 WO 2001JP004662
 PR 01-JUN-2000 JP 00P 164798
 PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
 MATSUMURA,
 PI SHOGO MORIYA,MICHIO NISHIDA
 PC C1201/69,C12M1/00,C12N15/09,G01N33/53
 CC Description of Artificial Sequence:capture

FEATURES source

Query Match

Best Local Similarity 1.4%; Score 14.4; DB 1; Length 18;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1470 GGGTACCGACGAGG 1485

Db 2 GGGTACCGACGACG 17

RESULT 166

LOCUS ARI181773 20 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 235 from patent US 6335194.

ACCESSION ARI181773

VERSION ARI181773.1 GI:20223987

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bennett,C.Frank., Ackermann,E.J., Swayze,E.B. and Cowser,L.M.

TITLE Antisense modulation of survivin expression

JOURNAL Patent: US 6335194-A 235 01-JAN-2002;

FEATURES

Location/Qualifiers

1. .20

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity 1.4%; Score 14.2; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1814 ATATATATATATATATGACA 1832

Db 1 ACATATATATATATAACA 19

RESULT 167

LOCUS E32202/c 14 bp DNA linear PAT 18-JUN-2001

DEFINITION Method for isolating satellite sequence.

ACCESSION E32202

VERSION E32202.1 GI:13021735

KEYWORDS JP 2000060559-A/4

SOURCE Haliotis discus discus

ORGANISM Haliotis discus discus

REFERENCE Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Vetigastropoda; Haliotidae; Haliotidae; Haliotis.

AUTHORS Hideaki,T. and Masashi,S.

TITLE Method for isolating satellite sequence

JOURNAL Patent: JP 2000060559-A 4 29-FEB-2000;

COMMENT NATL INST OF AGRICULTURAL RESOURCES

OS Haliotis discus discus

FN JP 2000060559-A/4

PD 29-FEB-2000

PF 18-AUG-1998 JP 1998232153

PR

PI HIDEAKI TAKAHASHI,MASASHI SEKINO

PC C12N15/09,C12Q1/68,C12N15/00

CC

PH Key

FT source

Location/Qualifiers

1. .14

/organism='Haliotis discus discus'.

FEATURES source

Location/Qualifiers

1. .14

/organism="Haliotis discus discus"

/mol_type="genomic DNA"

/sub_species="discus"

/db_xref="taxon:91233"

Query Match

Best Local Similarity 1.3%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806

Db 14 TGTGTGTGTGTGTG 1

RESULT 168

LOCUS I31524/c 14 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 436 from patent US 5582979.

ACCESSION I31524

VERSION I31524.1 GI:1822315

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 14)

AUTHORS Weber,J.L.

TITLE Length polymorphisms in (dc-da).sub.n.(dg-dr).sub.n sequences and method of using the same

JOURNAL Patent: US 5582979-A 436 10-DEC-1996;

FEATURES

Location/Qualifiers

1. .14

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity 1.3%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGT 1807

Db 14 GTGTGTGTGTGTGT 1

RESULT 169

LOCUS AR431517 14 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 27 from patent US 6653069.

ACCESSION AR431517

VERSION AR431517.1 GI:40193621

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 14)

AUTHORS Goni,I., Sunamachi,H., Takahashi,M. and Yamanishi,K.

TITLE Method for quality control of an attenuated vericella live vaccine

JOURNAL Patent: US 6653069-A 27 25-NOV-2003;

FEATURES

Location/Qualifiers

1. .14

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 1.3%; Score 14; DB 1; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826

Db 1 TATATATATATATA 14

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RESULT 170
AR431517/c
LOCUS       14 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION  Sequence 27 from patent US 6653069.
ACCESSION  AR431517
VERSION    AR431517.1  GI:40193621
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Gomi, Y., Sunamachi, H., Takahashi, M. and Yamanishi, K.
TITLE     Method for quality control of an attenuated varicella live vaccine
JOURNAL   Patent: US 6653069-A 27 25-NOV-2003;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="genomic DNA"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1813 TATATATATATATA 1826
Db  14 TATATATATATATA 1

RESULT 171
AX175251
LOCUS       14 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION  Sequence 15 from Patent WO0144465.
ACCESSION  AX175251
VERSION    AX175251.1  GI:14598619
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM   1
            Phillips, N.C. and Filion, M.C.
REFERENCE  1
AUTHORS   Therapeutically useful synthetic oligonucleotides
TITLE     Patent: WO 0144465-A 15 21-JUN-2001;
JOURNAL   Bioniche Life Sciences Inc. (CA)
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1793 TGTGTGTGTGTGTG 1806
Db  1 TGTGTGTGTGTGTG 14

RESULT 172
BD084125
LOCUS       14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION  BD084125
VERSION    BD084125.1  GI:22629735
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Feder, J.N., Kronmal, G.S., Lauer, P.M., Ruddy, D.A., Thomas, W.J.,
            Tsuchihashi, Z. and Wolff, R.K.
            Polymorphisms and new genes in the region of the human
            hemochromatosis gene
            Patent: JP 2001525663-A 13 11-DEC-2001;
            PROGENITOR INC
            OS Homo sapiens (human)
            PN JP 2001525663-A/13
            PD 11-DEC-2001
            PF 30-SEP-1997 JP 1998516815
            PR 01-OCT-1996 US 08/724394, 07-MAY-1997 US 08/852495 PI
            JOHN N FEDER, GREGORY S KRONMAL, PETER M LAUER, DAVID A RUDDY, PI
            WINSTON J THOMAS, ZENTA TSUCHIHASHI, ROGER K WOLFF PC
            C07H21/04, C12Q1/68, C12N15/63, C12N15/85, C12P21/02 CC Polymorphisms
            and new genes in the region of the human CC hemochromatosis gene
            and new genes in the region of the human CC hemochromatosis gene
            FH Key
            FT source
            1..14
            Location/Qualifiers
            1. .14
            /organism="Homo sapiens (human)"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1813 TATATATATATATA 1826
Db  1 TATATATATATATA 14

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TITLE      Polymorphisms and new genes in the region of the human
            hemochromatosis gene
JOURNAL    Patent: JP 2001525663-A 13 11-DEC-2001;
            PROGENITOR INC
COMMENT    OS Homo sapiens (human)
            PN JP 2001525663-A/13
            PD 11-DEC-2001
            PF 30-SEP-1997 JP 1998516815
            PR 01-OCT-1996 US 08/724394, 07-MAY-1997 US 08/852495 PI
            JOHN N FEDER, GREGORY S KRONMAL, PETER M LAUER, DAVID A RUDDY, PI
            WINSTON J THOMAS, ZENTA TSUCHIHASHI, ROGER K WOLFF PC
            C07H21/04, C12Q1/68, C12N15/63, C12N15/85, C12P21/02 CC Polymorphisms
            and new genes in the region of the human CC hemochromatosis gene
            and new genes in the region of the human CC hemochromatosis gene
            FH Key
            FT source
            1..14
            Location/Qualifiers
            1. .14
            /organism="Homo sapiens (human)"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1813 TATATATATATATA 1826
Db  1 TATATATATATATA 14

RESULT 173
BD084125/c
LOCUS       14 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION  Polymorphisms and new genes in the region of the human
            hemochromatosis gene.
ACCESSION  BD084125
VERSION    BD084125.1  GI:22629735
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Feder, J.N., Kronmal, G.S., Lauer, P.M., Ruddy, D.A., Thomas, W.J.,
            Tsuchihashi, Z. and Wolff, R.K.
            Polymorphisms and new genes in the region of the human
            hemochromatosis gene
            Patent: JP 2001525663-A 13 11-DEC-2001;
            PROGENITOR INC
            OS Homo sapiens (human)
            PN JP 2001525663-A/13
            PD 11-DEC-2001
            PF 30-SEP-1997 JP 1998516815
            PR 01-OCT-1996 US 08/724394, 07-MAY-1997 US 08/852495 PI
            JOHN N FEDER, GREGORY S KRONMAL, PETER M LAUER, DAVID A RUDDY, PI
            WINSTON J THOMAS, ZENTA TSUCHIHASHI, ROGER K WOLFF PC
            C07H21/04, C12Q1/68, C12N15/63, C12N15/85, C12P21/02 CC Polymorphisms
            and new genes in the region of the human CC hemochromatosis gene
            and new genes in the region of the human CC hemochromatosis gene
            FH Key
            FT source
            1..14
            Location/Qualifiers
            1. .14
            /organism="Homo sapiens (human)"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            Query Match      1.3%; Score 14; DB 1; Length 14;
            Best Local Similarity 100.0%; Pred. No. 1.1e+02;
            Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1813 TATATATATATATA 1826
Db  1 TATATATATATATA 14

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Db      14 TATATATATATATA 1
RESULT 174
AR436077 LOCUS          16 bp      RNA          linear          PAT 18-DEC-2003
DEFINITION Sequence 336 from patent US 6656731.
ACCESSION AR436077
VERSION   AR436077.1 GI:40199161
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS  Eckstein, F., Ludwig, J. and Beigelman, L.
TITLE    Nucleic acid catalysts with endonuclease activity
JOURNAL  Patent: US 6656731-A 336 02-DEC-2003;
FEATURES Location/Qualifiers
          source
          1..16
          /organism="unknown"
          /mol_type="unassigned RNA"
Query Match      1.3%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1392 GTTAAGACTTGACA 1405
Db      1 GTTAAGACTTGACA 14
RESULT 175
AR46267/C LOCUS          17 bp      DNA          linear          PAT 29-SEP-1999
DEFINITION Sequence 1060 from patent US 5817796.
ACCESSION AR46267
VERSION   AR46267.1 GI:5967732
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE    C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL  Patent: US 5817796-A 1060 06-OCT-1998;
FEATURES Location/Qualifiers
          source
          1..17
          /organism="unknown"
          /mol_type="unassigned DNA"
Query Match      1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1811 TGTATATATATATA 1824
Db      15 TGTATATATATATA 2
RESULT 176
AR47062 LOCUS          17 bp      DNA          linear          PAT 29-SEP-1999
DEFINITION Sequence 1855 from patent US 5817796.
ACCESSION AR47062
VERSION   AR47062.1 GI:5968527
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE    C-myb ribozymes having 2'-5'-linked adenylate residues
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JOURNAL Patent: US 5817796-A 1855 06-OCT-1998;
FEATURES Location/Qualifiers
          source
          1..17
          /organism="unknown"
          /mol_type="unassigned DNA"
Query Match      1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1763 CAGATTTTAAAAA 1776
Db      4 CAGATTTTAAAAA 17
RESULT 177
AR47064 LOCUS          17 bp      DNA          linear          PAT 29-SEP-1999
DEFINITION Sequence 1857 from patent US 5817796.
ACCESSION AR47064
VERSION   AR47064.1 GI:5968529
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE    C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL  Patent: US 5817796-A 1857 06-OCT-1998;
FEATURES Location/Qualifiers
          source
          1..17
          /organism="unknown"
          /mol_type="unassigned DNA"
Query Match      1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1763 CAGATTTTAAAAA 1776
Db      3 CAGATTTTAAAAA 16
RESULT 178
AR47066 LOCUS          17 bp      DNA          linear          PAT 29-SEP-1999
DEFINITION Sequence 1859 from patent US 5817796.
ACCESSION AR47066
VERSION   AR47066.1 GI:5968531
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE    C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL  Patent: US 5817796-A 1859 06-OCT-1998;
FEATURES Location/Qualifiers
          source
          1..17
          /organism="unknown"
          /mol_type="unassigned DNA"
Query Match      1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1763 CAGATTTTAAAAA 1776
Db      2 CAGATTTTAAAAA 15
RESULT 179
AR47068
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Query Match	1.3%	Score 14	DB 1	Length 17
Best Local Similarity	100.0%	Pred. No. 1.4e+02		
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1811	TGTATATATATATA	1824	
DB	15	TGTATATATATATA	2	
RESULT 182				
LOCUS	IS4114	17 bp	DNA	linear
DEFINITION	Sequence 1855 from patent US 5646042.			
ACCESSION	IS4114			
VERSION	IS4114.1	GI:2475317		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 17)			
AUTHORS	Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.			
TITLE	C-myb targeted ribozymes			
JOURNAL	Patent: US 5646042-A 1855 08-JUL-1997;			
FEATURES	Location/Qualifiers			
source	1..17			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	1.3%	Score 14	DB 1	Length 17
Best Local Similarity	100.0%	Pred. No. 1.4e+02		
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1763	CAGATTTTTTAAAA	1776	
DB	4	CAGATTTTTTAAAA	17	
RESULT 183				
LOCUS	IS4116	17 bp	DNA	linear
DEFINITION	Sequence 1857 from patent US 5646042.			
ACCESSION	IS4116			
VERSION	IS4116.1	GI:2475319		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 17)			
AUTHORS	Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.			
TITLE	C-myb targeted ribozymes			
JOURNAL	Patent: US 5646042-A 1857 08-JUL-1997;			
FEATURES	Location/Qualifiers			
source	1..17			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
Query Match	1.3%	Score 14	DB 1	Length 17
Best Local Similarity	100.0%	Pred. No. 1.4e+02		
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1763	CAGATTTTTTAAAA	1776	
DB	3	CAGATTTTTTAAAA	16	
RESULT 184				
LOCUS	IS4118	17 bp	DNA	linear
DEFINITION	Sequence 1859 from patent US 5646042.			
ACCESSION	IS4118			
VERSION	IS4118.1	GI:2475321		
KEYWORDS	Unknown.			

SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1989 08-JUL-1997;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776
Db 2 CAGATTTTAAAA 15

RESULT 195
LOCUS I54120 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1861 from patent US 5646042.
ACCESSION I54120
VERSION I54120.1 GI:2475323
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1989 08-JUL-1997;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776
Db 1 CAGATTTTAAAA 14

RESULT 186
AX762502
LOCUS AX762502 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5823 from Patent WO03040369.
ACCESSION AX762502
VERSION AX762502.1 GI:32257118
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Teitelman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 5823 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1292 ATCTGTTTCTAA 1305
Db 2 ATCTGTTTCTAA 15

RESULT 187
A28997
LOCUS A28997 17 bp DNA linear PAT 30-JUN-1995
DEFINITION primer sequence 4 from patent EP0522880.
ACCESSION A28997
VERSION A28997.1 GI:1248848
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses therefor
JOURNAL Patent: EP 0522880-A 16 13-JAN-1993;
FEATURES INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
Location/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881
Db 1 TTTTATTTTGTGTTT 17

RESULT 188
AR046081/c
LOCUS AR046081 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 874 from patent US 5817796.
ACCESSION AR046081
VERSION AR046081.1 GI:5967546
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 874 06-OCT-1998;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1765 GATTTTAAAAATTTAT 1781
Db 17 GATTTTAAAAATATAT 1

RESULT 189
AR057784/c
LOCUS AR057784 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1988 from patent US 5837542.
ACCESSION AR057784

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VERSION AR057784.1 GI:5983361
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1988 17-NOV-1998;
FEATURES Location/Qualifiers
source
1..17
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTCAGAGGAA 1553
Db 17 GGGTAATAGAGAGGAA 1

RESULT 192
AR104585
LOCUS AR104585
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION AR104585
VERSION AR104585.1 GI:12817293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 132 25-JUL-2000;
FEATURES Location/Qualifiers
source
1..17
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTCAGAGGAA 1553
Db 17 GGGTAATAGAGAGGAA 1

RESULT 190
AR104585
LOCUS AR104585
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION AR104585
VERSION AR104585.1 GI:12817293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 132 25-JUL-2000;
FEATURES Location/Qualifiers
source
1..17
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881
Db 1 TTTTATTTTGTGTTT 17

RESULT 191
AR115542/c
LOCUS AR115542/c
DEFINITION Sequence 1988 from patent US 6132967.
ACCESSION AR115542
VERSION AR115542.1 GI:14095864
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1988 17-OCT-2000;
FEATURES Location/Qualifiers
source
1..17
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881
Db 1 TTTTATTTTGTGTTT 17

RESULT 193
AR175846
LOCUS AR175846
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION AR175846
VERSION AR175846.1 GI:17917145
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 132 30-OCT-2001;
FEATURES Location/Qualifiers
source
1..17
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881
Db 1 TTTTATTTTGTGTTT 17

RESULT 194
AR241082/c
LOCUS AR241082/c
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION AR241082
VERSION AR241082.1 GI:33050852
KEYWORDS JP 2002525127-A/29.
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTCAGAGGAA 1553
Db 17 GGGTAATAGAGAGGAA 1

RESULT 192
AR141074
LOCUS AR141074
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION AR141074
VERSION AR141074.1 GI:14483570
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 5 27-MAR-2001;
FEATURES Location/Qualifiers
source
1..17
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881
Db 1 TTTTATTTTGTGTTT 17

RESULT 193
AR175846
LOCUS AR175846
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION AR175846
VERSION AR175846.1 GI:17917145
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 132 30-OCT-2001;
FEATURES Location/Qualifiers
source
1..17
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1881
Db 1 TTTTATTTTGTGTTT 17

RESULT 194
BD241082/c
LOCUS BD241082/c
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241082
VERSION BD241082.1 GI:33050852
KEYWORDS JP 2002525127-A/29.
```


SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 Lander, J.E., Jordan, B., Housman, D.E. and Charest, A.
 Methods and products related to genotyping and DNA analysis
 Patent: JP 2002525127-A 29 13-AUG-2002;
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY
 OS Homo sapiens (human)
 PN JP 2002525127-A/29
 PD 13-AUG-2002
 PF 24-SEP-1999 JP 2000572407
 PR 25-SEP-1998 US 60/101757
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N37/00, PC
 G01N37/00,
 PC C12N15/00
 CC Methods and products related to genotyping and DNA analysis FH
 Key
 FT source 1.3%; Score 13.8; DB 1; Length 17;
 Location/Qualifiers
 FT 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
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 QY 1379 TGGCTTGAAGAATGTTA 1395
 DB 17 TGGCTTGAAGAATGTTA 1

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 Lander, J.E., Jordan, B., Housman, D.E. and Charest, A.
 Methods and products related to genotyping and DNA analysis
 Patent: JP 2002525127-A 29 13-AUG-2002;
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY
 OS Homo sapiens (human)
 PN JP 2002525127-A/29
 PD 13-AUG-2002
 PF 24-SEP-1999 JP 2000572407
 PR 25-SEP-1998 US 60/101757
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N37/00, PC
 G01N37/00,
 PC C12N15/00
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 QY 1379 TGGCTTGAAGAATGTTA 1395
 DB 17 TGGCTTGAAGAATGTTA 1

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 Lander, J.E., Jordan, B., Housman, D.E. and Charest, A.
 Methods and products related to genotyping and DNA analysis
 Patent: JP 2002525127-A 29 13-AUG-2002;
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY
 OS Homo sapiens (human)
 PN JP 2002525127-A/29
 PD 13-AUG-2002
 PF 24-SEP-1999 JP 2000572407
 PR 25-SEP-1998 US 60/101757
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N37/00, PC
 G01N37/00,
 PC C12N15/00
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 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1379 TGGCTTGAAGAATGTTA 1395
 DB 17 TGGCTTGAAGAATGTTA 1

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 Lander, J.E., Jordan, B., Housman, D.E. and Charest, A.
 Methods and products related to genotyping and DNA analysis
 Patent: JP 2002525127-A 29 13-AUG-2002;
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY
 OS Homo sapiens (human)
 PN JP 2002525127-A/29
 PD 13-AUG-2002
 PF 24-SEP-1999 JP 2000572407
 PR 25-SEP-1998 US 60/101757
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N37/00, PC
 G01N37/00,
 PC C12N15/00
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 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1379 TGGCTTGAAGAATGTTA 1395
 DB 17 TGGCTTGAAGAATGTTA 1

Best Local Similarity 88.2%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1379 TGGCTTGAAGAATGTTA 1395
 DB 17 TGGCTTGAAGAATGTTA 1

RESULT 196
 LOCUS BD241132/c
 DEFINITION Methods and products related to genotyping and DNA analysis.
 ACCESSION BD241132
 VERSION BD241132.1 GI:33050902
 KEYWORDS JP 2002525127-A/79.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 Lander, J.E., Jordan, B., Housman, D.E. and Charest, A.
 Methods and products related to genotyping and DNA analysis
 Patent: JP 2002525127-A 79 13-AUG-2002;
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY
 OS Homo sapiens (human)
 PN JP 2002525127-A/79
 PD 13-AUG-2002
 PF 24-SEP-1999 JP 2000572407
 PR 25-SEP-1998 US 60/101757
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N37/00, PC
 G01N37/00,
 PC C12N15/00
 CC Methods and products related to genotyping and DNA analysis FH
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 FT source 1.3%; Score 13.8; DB 1; Length 17;
 Location/Qualifiers
 FT 1..17
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 Best Local Similarity 88.2%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1379 TGGCTTGAAGAATGTTA 1395
 DB 17 TGGCTTGAAGAATGTTA 1

RESULT 197
 LOCUS BD241617
 DEFINITION Methods and products related to genotyping and DNA analysis.
 ACCESSION BD241617
 VERSION BD241617.1 GI:33051387
 KEYWORDS JP 2002525127-A/564.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 17)
 Lander, J.E., Jordan, B., Housman, D.E. and Charest, A.
 Methods and products related to genotyping and DNA analysis
 Patent: JP 2002525127-A 564 13-AUG-2002;
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY
 OS Homo sapiens (human)
 PN JP 2002525127-A/564
 PD 13-AUG-2002
 PF 24-SEP-1999 JP 2000572407
 PR 25-SEP-1998 US 60/101757

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PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
GOIN37/00,
PC C12N15/00
CC Methods and products related to genotyping and DNA analysis FH
Key source Location/Qualifiers
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FEATURES
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1..17
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809
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Db 1 TGTGTGTGTGTGTGTCT 17

RESULT 198
BD254547
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254547
VERSION BD254547.1 GI:33064317
KEYWORDS JP 2002541795-A/2340.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2340 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2340
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1760 AGCAGATTTTATAAA 1776
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Db 1 AGAGAGATTTTATAAA 17

RESULT 200
I53133
LOCUS 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 874 from patent US 5646042.
ACCESSION I53133
VERSION I53133.1 GI:2474336
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myc targeted ribozymes
JOURNAL Patent: US 5646042-A 874 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..17
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
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QY 1765 GATTTTAAATTTAT 1781
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Db 1 GATTTTAAATATATAT 1

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BD255193
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255193
VERSION BD255193.1 GI:33064963
KEYWORDS JP 2002541795-A/2986.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2986 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2986
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
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CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1760 AGCAGATTTTATAAA 1776
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Db 1 AGAGAGATTTTATAAA 17

RESULT 200
I53133
LOCUS 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 874 from patent US 5646042.
ACCESSION I53133
VERSION I53133.1 GI:2474336
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myc targeted ribozymes
JOURNAL Patent: US 5646042-A 874 08-JUL-1997;
FEATURES Location/Qualifiers
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1765 GATTTTAAATTTAT 1781
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Db 1 GATTTTAAATATATAT 1

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RESULT 201
LOCUS AR187062 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2550 from patent US 6346398.
ACCESSION AR187062
VERSION AR187062.1 GI:20233027
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1864 CTTTATTATTTGTTTT 1880
Db 1 CTTTTTTTTTTTTTTT 17
RESULT 202
LOCUS AR190559 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6047 from patent US 6346398.
ACCESSION AR190559
VERSION AR190559.1 GI:20236524
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6047 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1639 TGTTCCTTAAGTCAGAA 1655
Db 1 TGTGCCTTAATTCAGAA 17
RESULT 203
LOCUS AR190561 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6049 from patent US 6346398.
ACCESSION AR190561
VERSION AR190561.1 GI:20236526
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6346398-A 6049 12-FEB-2002;
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source 1..17
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1643 CCTTAAGTCAGAACGC 1659
Db 1 CCTTAATTCAGAACCC 17
RESULT 204
LOCUS AR222463 17 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 23 from patent US 6429300.
ACCESSION AR222463
VERSION AR222463.1 GI:23329994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 23 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..17
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
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QY 1865 TTTTATTATTTGTTTT 1881
Db 1 TTTTATTATTTTTTTT 17
RESULT 205
LOCUS AR236087 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6462184.
ACCESSION AR236087
VERSION AR236087.1 GI:27279786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6462184-A 5 08-OCT-2002;
FEATURES Location/Qualifiers
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
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QY 1865 TTTTATTATTTGTTTT 1881
Db 1 TTTTATTATTTTTTTT 17
RESULT 206

AR323672 LOCUS 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1074 from patent US 6566127.
ACCESSION AR323672
VERSION AR323672.1 GI:33709480
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1864 CTTTATTTTGTGTTT 1880
Db 1 CTTTATTTTGTGTTT 17

RESULT 207
AR325482 LOCUS 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2884 from patent US 6566127.
ACCESSION AR325482
VERSION AR325482.1 GI:33711290
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2884 20-MAY-2003;
FEATURES Location/Qualifiers
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1639 TGTTCCTTAAGTCAGAA 1655
Db 1 TGTGCCTTAATTCAGAA 17

RESULT 208
AR325484 LOCUS 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2886 from patent US 6566127.
ACCESSION AR325484
VERSION AR325484.1 GI:33711292
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2886 20-MAY-2003;
FEATURES Location/Qualifiers

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Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1643 CCTTAAGTCAGACACG 1659
Db 1 CCTTAATTCAGAACCC 17

RESULT 209
AR433961 LOCUS 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 384 from patent US 6656700.
ACCESSION AR433961
VERSION AR433961.1 GI:40196804
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 384 02-DEC-2003;
FEATURES Location/Qualifiers
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1810
Db 1 GTGTGTGTGTGTGTGTG 17

RESULT 210
AR433962 LOCUS 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 385 from patent US 6656700.
ACCESSION AR433962
VERSION AR433962.1 GI:40196805
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 385 02-DEC-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1809
Db 1 TGTGTGTGTGTGTGTGTG 17

RESULT 211
AR433963 LOCUS 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 386 from patent US 6656700.

ACCESSION AR433963
VERSION AR433963.1 GI:40196806
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6556700-A 388 02-DEC-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTG 1810
Db 1 GTGTGTGTGTGTGTGTG 17
RESULT 212
ACCESSION AR433964
LOCUS AR433964
DEFINITION Sequence 387 from patent US 6656700.
ACCESSION AR433964
VERSION AR433964.1 GI:40196807
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6556700-A 387 02-DEC-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.4e+02;
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Db 1 TGTGTGTGTGTGTGTGT 17
RESULT 213
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LOCUS AR433965
DEFINITION Sequence 388 from patent US 6656700.
ACCESSION AR433965
VERSION AR433965.1 GI:40196808
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6556700-A 388 02-DEC-2003;
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/mol_type="genomic DNA"
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGT 1809
Db 1 TGTGTGTGTGTGTGTGT 17

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1798 GTGTGTGTGTGTGTGT 1814
Db 1 GTGTGTGTGTGTGTGT 17
RESULT 214
ACCESSION AR433966
LOCUS AR433966
DEFINITION Sequence 389 from patent US 6656700.
ACCESSION AR433966
VERSION AR433966.1 GI:40196809
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6556700-A 389 02-DEC-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1799 TGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTAT 17
RESULT 215
ACCESSION AX502780
LOCUS AX502780
DEFINITION Sequence 4087 from Patent EP1229046.
ACCESSION AX502780
VERSION AX502780.1 GI:23385073
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 4087 07-AUG-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2160 AACGATTTGTTCTACT 2176
Db 1 ATGCATTTGTTTCTAGT 17
RESULT 216
ACCESSION AX578222/c
LOCUS AX578222
DEFINITION Sequence 60 from Patent WO2011674.
ACCESSION AX578222
VERSION AX578222.1 GI:27647424
KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.
 TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)
 JOURNAL Patent: WO 0211674-A 60 14-FEB-2002;
 RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US); Thompson, James (US)

FEATURES
 source
 1. .17
 /organism="Homo sapiens"
 /mol_type="unassigned RNA"
 /db_xref="taxon:9606"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1821 TATATATGACAGTAT 1837
 Db 17 TATATATACAGATAT 1

RESULT 217
 AX634823/c
 LOCUS AX634823 17 bp RNA linear PAT 21-FEB-2003
 DEFINITION Sequence 1962 from Patent EP1260586.
 ACCESSION AX634823
 VERSION AX634823.1 GI:28470437
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.

REFERENCE 1
 AUTHORS Stinchcomb D.T., Dudycz L.W., Chowrika, B., Grimm, S., Drenzo, A., Karpeisky, A., Draper, K.G., Kisich, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.
 TITLE Method and reagent for inhibiting the expression of disease related genes
 JOURNAL Patent: EP 1260586-A 1962 27-NOV-2002;
 RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
 source
 1. .17
 /organism="unidentified"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1537 GTGTAATTGAGAGGAA 1553
 Db 17 GCGTAATAGAGAGGAA 1

RESULT 218
 AX692525
 LOCUS AX692525 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 5257 from Patent EP1281758.
 ACCESSION AX692525
 VERSION AX692525.1 GI:29415483
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 5257 05-FEB-2003;
 Aeomica, Inc. (US)

FEATURES
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 1. .17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1864 CTTTATTATTTTGT 1880
 Db 1 CTTTATTTTATTTT 17

RESULT 219
 AX735506
 LOCUS AX735506 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 1096 from Patent WO03025177.
 ACCESSION AX735506
 VERSION AX735506.1 GI:30514783
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Teleman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 JOURNAL Patent: WO 03025177-A 1096 27-MAR-2003;
 Molecular Engines Laboratories (FR)

FEATURES
 source
 1. .17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1695 GTTCAGGAATCGGAATC 1711
 Db 1 GATCAGAAATCGGAATC 17

RESULT 220
 AR050983
 LOCUS AR050983 15 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 52 from patent US 5830644.
 ACCESSION AR050983
 VERSION AR050983.1 GI:5974347
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 unclassified.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS West, M.D., Shay, J. and Wright, W.E.
 TITLE Method for screening for agents which increase telomerase activity in a cell
 JOURNAL Patent: US 5830644-A 52 03-NOV-1998;
 FEATURES
 source
 1. .15
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTGTG 15

RESULT 221
I84393
LOCUS I84393 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 52 from patent US 5645986.
ACCESSION I51784
VERSION I51784.1 GI:2472985
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
Wright,W.E., Blackburn,E.H. and Vaziri,H.
TITLE Therapy and diagnosis of conditions related to telomere length
and/or telomerase activity
JOURNAL Patent: US 5645986-A 52 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTGTG 15

RESULT 222
I84393
LOCUS I84393 15 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 51 from patent US 5695932.
ACCESSION I84393
VERSION I84393.1 GI:3021913
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS West,M.D., Shay,J., Wright,W., Blackburn,E.H. and McEachern,M.J.
TITLE Telomerase activity assays for diagnosing pathogenic infections
JOURNAL Patent: US 5695932-A 51 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTGTG 15

RESULT 223
AR204601
LOCUS AR204601 15 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 51 from patent US 6368789.
ACCESSION AR204601

VERSION AR204601.1 GI:21501969
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS West,M.D., Shay,J., Wright,W. and Blackburn,E.H.
TITLE Screening methods to identify inhibitors of telomerase activity
JOURNAL Patent: US 6368789-A 51 09-APR-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTGTG 15

RESULT 224
AR241795/c
LOCUS AR241795 15 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 83 from patent US 6472154.
ACCESSION AR241795
VERSION AR241795.1 GI:27287607
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 83 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATAT 1825
Db 15 TTTATATATATATAT 1

RESULT 225
AR307316
LOCUS AR307316 15 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 79 from patent US 6551774.
ACCESSION AR307316
VERSION AR307316.1 GI:31697843
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS West,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
Shay,J., Wright,W.E., Blackburn,E.H., Kim,N.W. and Vaziri,H.
TITLE Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
JOURNAL Patent: US 6551774-A 79 22-APR-2003;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1792 TTGTGTGTGTGTGTG 1806
Db 1 TGTGTGTGTGTGTG 15

RESULT 226
AX663411
LOCUS AX663411 15 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 37 from Patent WO2097126.
ACCESSION AX663411
VERSION AX663411.1 GI:29163751
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Weizenegger, M.
TITLE Method for detecting gram-positive bacteria
JOURNAL Patent: WO 02097126-A 37 05-DEC-2002;
Hain Lifescience GmbH (DE)
FEATURES Location/Qualifiers
source
1..15

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGT 1807
Db 1 TGTGTGGGTGTGTGT 15

RESULT 227
AR328665
LOCUS AR328665 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6067 from patent US 6566127.
ACCESSION AR328665
VERSION AR328665.1 GI:33714473
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6067 20-MAY-2003;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1791 ATTGTGTGTGTGTGT 1805
Db 2 ACTGTGTGTGTGTGT 16

RESULT 228
AR435926/c
LOCUS AR435926 16 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 185 from patent US 6656731.
ACCESSION AR435926

VERSION AR435926.1 GI:40199010
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)
AUTHORS Eckstein, F., Ludwig, J. and Beigelman, L.
TITLE Nucleic acid catalysts with endonuclease activity
JOURNAL Patent: US 6656731-A 185 02-DEC-2003;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGT 1879
Db 15 TTTTATTTTATTT 1

RESULT 229
AR046267
LOCUS AR046267 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1060 from patent US 5817796.
ACCESSION AR046267
VERSION AR046267.1 GI:5967732
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL Patent: US 5817796-A 1060 06-OCT-1998;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1813 TATATATATATATAT 1827
Db 2 TATATATATATACAT 16

RESULT 230
I53319
LOCUS I53319 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1060 from patent US 5646042.
ACCESSION I53319
VERSION I53319.1 GI:2474522
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 1060 08-JUL-1997;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.3%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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QY 1813 TATATATATATAT 1827
Db 2 TATATATATACAT 16

RESULT 231
AR074716/c 13 bp DNA linear PAT 28-AUG-2000
LOCUS
DEFINITION Sequence 13 from patent US 5955276.
ACCESSION AR074716
VERSION AR074716.1 GI:10001469
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 13 21-SEP-1999;
FEATURES Location/Qualifiers
source
1..13
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1805
Db 13 TGTGTGTGTGTGT 1

RESULT 232
AR074718
LOCUS
DEFINITION Sequence 15 from patent US 5955276.
ACCESSION AR074718
VERSION AR074718.1 GI:10001471
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 15 21-SEP-1999;
FEATURES Location/Qualifiers
source
1..13
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1805
Db 1 TGTGTGTGTGTGT 13

RESULT 233
AR199332
LOCUS
DEFINITION Sequence 41 from patent US 6355428.
ACCESSION AR199332
VERSION AR199332.1 GI:20249406
KEYWORDS
SOURCE
ORGANISM Unknown.
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Unclassified.
1 (bases 1 to 13)
Schroth,G.P., Bruce,T.Wayne, and Suh,Y.J.
Nucleic acid ligand interaction assays
JOURNAL Patent: US 6355428-A 41 12-MAR-2002;
FEATURES Location/Qualifiers
source
1..13
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806
Db 1 GTGTGTGTGTGTG 13

RESULT 234
AR218382
LOCUS
DEFINITION Sequence 41 from patent US 6420109.
ACCESSION AR218382
VERSION AR218382.1 GI:23319079
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Schroth,G.P., Bruce,T.W. and Suh,Y.J.
TITLE Nucleic acid ligand interaction assays
JOURNAL Patent: US 6420109-A 41 16-JUL-2002;
FEATURES Location/Qualifiers
source
1..13
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806
Db 1 GTGTGTGTGTGTG 13

RESULT 235
AR241795
LOCUS
DEFINITION Sequence 83 from patent US 6472154.
ACCESSION AR241795
VERSION AR241795.1 GI:27287607
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 83 29-OCT-2002;
FEATURES Location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
Db 1 ATATATATATATA 13
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RESULT 236
ARL170919
LOCUS          ARL170919          15 bp      DNA          linear          PAT 17-DEC-2001
DEFINITION     Sequence 1 from patent US 6297006.
ACCESSION      ARL170919
VERSION        ARL170919.1  GI:17909869
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Drmanac,R.T., Drmanac,S., Hou,A. and Hauser,B.
TITLE         Methods for sequencing repetitive sequences and for determining the
              order of sequence subfragments
JOURNAL        Patent: US 6297006-A 1 02-OCT-2001;
FEATURES       Location/Qualifiers
                1..15
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match    1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 237
ARL170920/C
LOCUS          ARL170920          15 bp      DNA          linear          PAT 17-DEC-2001
DEFINITION     Sequence 2 from patent US 6297006.
ACCESSION      ARL170920
VERSION        ARL170920.1  GI:17909870
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Drmanac,R.T., Drmanac,S., Hou,A. and Hauser,B.
TITLE         Methods for sequencing repetitive sequences and for determining the
              order of sequence subfragments
JOURNAL        Patent: US 6297006-A 2 02-OCT-2001;
FEATURES       Location/Qualifiers
                1..15
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match    1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 238
ARL175435
LOCUS          ARL175435          15 bp      DNA          linear          PAT 17-DEC-2001
DEFINITION     Sequence 2 from patent US 6309824.
ACCESSION      ARL175435
VERSION        ARL175435.1  GI:17916734
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Drmanac,R.T.
TITLE         Methods for analyzing a target nucleic acid using immobilized
              heterogeneous mixtures of oligonucleotide probes
JOURNAL        Patent: US 6309824-A 2 30-OCT-2001;
FEATURES       Location/Qualifiers
                1..15
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match    1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 239
ARL175436/C
LOCUS          ARL175436          15 bp      DNA          linear          PAT 17-DEC-2001
DEFINITION     Sequence 3 from patent US 6309824.
ACCESSION      ARL175436
VERSION        ARL175436.1  GI:17916735
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Drmanac,R.T.
TITLE         Methods for analyzing a target nucleic acid using immobilized
              heterogeneous mixtures of oligonucleotide probes
JOURNAL        Patent: US 6309824-A 3 30-OCT-2001;
FEATURES       Location/Qualifiers
                1..15
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match    1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 240
ARL1567/C
LOCUS          I61567            15 bp      DNA          linear          PAT 07-OCT-1997
DEFINITION     Sequence 121 from patent US 5658780.
ACCESSION      I61567
VERSION        I61567.1  GI:2479515
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE         Rel a targeted ribozymes
JOURNAL        Patent: US 5658780-A 121 19-AUG-1997;
FEATURES       Location/Qualifiers
                1..15
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match    1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2152 TCACCTGGAGCA 2164
Db 15 TCACCTGGAGCA 3
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/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1863  CCTTTTATTTTGTG 1876
          |||||
Db       1  CCTTTTNTTTTGTG 14

RESULT 244
AP242247/c
LOCUS      AR242247      15 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 10 from patent US 6472173.
ACCESSION  AR242247
VERSION     AR242247.1  GI:27288070
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS:   Ford, J. and Yeung, G.
TITLE      Chemokine receptor obtained from a cDNA library of fetal
           liver-spleen
JOURNALS   Patent: US 6472173-A 10 29-OCT-2002;
FEATURES   Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1863  CCTTTTATTTTGTG 1876
          |||||
Db       15  CCTTTTNTTTTGTG 2

RESULT 245
AX635886/c
LOCUS      AX635886      15 bp      RNA      linear      PAT 21-FEB-2000
DEFINITION Sequence 3025 from Patent EP1260586.
ACCESSION  AX635886
VERSION     AX635886.1  GI:28471500
KEYWORDS
SOURCE      unidentified
ORGANISM    unidentified
            unclassified.

REFERENCE   1
AUTHORS     Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Drenzo, A.,
           Karpeisky, A., Draper, K.G., Kisch, K., Matulic-Adamic, J.,
           McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M.,
           Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and
           Woolf, T.
TITLE      Method and reagent for inhibiting the expression of disease related
           genes
JOURNAL     Patent: EP 1260586-A 3025 27-NOV-2002;
FEATURES   RIBOZYME PHARMACEUTICALS, INC. (US)
            : Location/Qualifiers
            1..15
            /organism="unidentified"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32644"

source

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2152  TCACCTTGAAGCA 2164
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Db      15 TCACCTGGAAGCA 3

RESULT 246
LOCUS   AX636032/c
DEFINITION Sequence 3171 from Patent EP1260586.
ACCESSION AX636032
VERSION   AX636032.1 GI:28471646
KEYWORDS
SOURCE   unidentified
ORGANISM unidentified
REFERENCE
AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
          Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
          McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
          Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
          Woolf,T.
TITLE    Method and reagent for inhibiting the expression of disease related
          genes
JOURNAL  Patent: EP 1260586-A 3171 27-NOV-2002;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)
          source
          1. .15
          /organism="unidentified"
          /mol_type="unassigned RNA"
          /db_xref="taxon:32644"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2152 TCACCTGGAAGCA 2164
Db      15 TCACCTGGAAGCA 3

RESULT 247
LOCUS   AX636075/c
DEFINITION Sequence 3214 from Patent EPI260586.
ACCESSION AX636075
VERSION   AX636075.1 GI:28471689
KEYWORDS
SOURCE   unidentified
ORGANISM unidentified
REFERENCE
AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
          Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
          McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
          Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
          Woolf,T.
TITLE    Method and reagent for inhibiting the expression of disease related
          genes
JOURNAL  Patent: EP 1260586-A 3214 27-NOV-2002;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)
          source
          1. .15
          /organism="unidentified"
          /mol_type="unassigned RNA"
          /db_xref="taxon:32644"

Query Match      1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2152 TCACCTGGAAGCA 2164
Db      15 TCACCTGGAAGCA 3

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RESULT 248
LOCUS   AR435858
DEFINITION Sequence 117 from patent US 6856731.
ACCESSION AR435858
VERSION   AR435858.1 GI:40198942
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS   Eckstein,F., Ludwig,J. and Beigelman,L.
TITLE    Nucleic acid catalysts with endonuclease activity
JOURNAL  Patent: US 6856731-A 117 02-DEC-2003;
FEATURES Location/Qualifiers
          source
          1. .16
          /organism="unknown"
          /mol_type="unassigned RNA"

Query Match      1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. NO. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2268 TTTTTCCTATAAA 2280
Db      1 TTTTTCCTATAAA 13

RESULT 249
LOCUS   AR027678
DEFINITION Sequence 15 from patent US 5856435.
ACCESSION AR027678
VERSION   AR027678.1 GI:5938498
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS   Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
TITLE    Nucleic acid-containing composition, its preparation and use
JOURNAL  Patent: US 5856435-A 15 05-JAN-1999;
FEATURES Location/Qualifiers
          source
          1. .16
          /organism="unknown"
          /mol_type="unassigned DNA"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. NO. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1865 TTTTTCCTATAAA 1880
Db      1 TTTTTCCTATAAA 16

RESULT 250
LOCUS   AR037355
DEFINITION Sequence 2 from patent US 5801155.
ACCESSION AR037355
VERSION   AR037355.1 GI:5955211
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS   Kutayavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE    Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL  Patent: US 5801155-A 2 01-SEP-1998;
FEATURES Location/Qualifiers
          source
          1. .16
          /organism="unknown"

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KEYWORDS JP 2000060559-A/28.
SOURCE Haliotis discus discus
ORGANISM Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
          Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE Hideaki, T. and Masashi, S.
AUTHORS Method for isolating satellite sequence
TITLE Patent: JP 2000060559-A 28 29-FEB-2000;
JOURNAL NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT OS Haliotis discus discus
          PN JP 2000060559-A/28
          PD 29-FEB-2000
          PF 18-AUG-1998 JP 1998232153
          PR HIDEAKI TAKAHASHI, MASASHI SEKINO
          PC C12N15/09, C12Q1/68, C12N15/00
          CC CC
          FH key Location/Qualifiers
          FT source 1..16
          FT Location/Qualifiers
          FT 1..16
          FT /organism='Haliotis discus discus'
          FT /mol_type='genomic DNA'
          FT /sub_species='discus'
          FT /db_xref='taxon:91233'

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 16 TCTCTGTGTGTGTGTG 1

RESULT 254
I38676 138676 16 bp DNA linear PAT 13-MAY-1997
LOCUS
DEFINITION Sequence 36 from patent US 5614617.
ACCESSION 138676
VERSION 138676.1 GI:2084730
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook, P.D. and Sanghvi, V.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that
JOURNAL detect and modulate gene expression
PATENT Patent: US 5614617-A 36 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..16
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

RESULT 255
I38682 138682 16 bp DNA linear PAT 13-MAY-1997
LOCUS
DEFINITION Sequence 42 from patent US 5614617.
ACCESSION I38682
VERSION I38682.1 GI:2084736
KEYWORDS
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/mol_type='unassigned DNA'

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

RESULT 251
AR104584/c AR104584 16 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 131 from patent US 6093809.
ACCESSION AR104584
VERSION AR104584.1 GI:12817292
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech, T.R. and Lingner, J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 131 25-JUL-2000;
FEATURES Location/Qualifiers
source 1..16
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 252
AR175845/c AR175845 16 bp DNA linear PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 131 from patent US 6309867.
ACCESSION AR175845
VERSION AR175845.1 GI:17917144
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech, T.R. and Nakamura, T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 131 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..16
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 253
E32226/c E32226 16 bp DNA linear PAT 18-JUN-2001
LOCUS
DEFINITION Method for isolating satellite sequence.
ACCESSION E32226
VERSION E32226.1 GI:13021862
KEYWORDS
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 42 25-MAR-1997;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 256
LOCUS I38700 16 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 60 from patent US 5614617.
ACCESSION I38700
VERSION I38700.1 GI:2084754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 60 25-MAR-1997;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 257
LOCUS AR221692 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 2 from patent US 6426408.
ACCESSION AR221692
VERSION AR221692.1 GI:23328764
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 2 30-JUL-2002;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="genomic DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 258
LOCUS AR222462 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 22 from patent US 6429300.
ACCESSION AR222462
VERSION AR222462.1 GI:23329993
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 22 06-AUG-2002;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="genomic DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 259
LOCUS AR257437 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6486308.
ACCESSION AR257437
VERSION AR257437.1 GI:27307448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 2 26-NOV-2002;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="genomic DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 260
LOCUS AR328670 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6072 from patent US 6566127.
ACCESSION AR328670
VERSION AR328670.1 GI:33714478
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 42 25-MAR-1997;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 256
LOCUS I38700 16 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 60 from patent US 5614617.
ACCESSION I38700
VERSION I38700.1 GI:2084754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that detect and modulate gene expression
JOURNAL Patent: US 5614617-A 60 25-MAR-1997;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 257
LOCUS AR221692 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 2 from patent US 6426408.
ACCESSION AR221692
VERSION AR221692.1 GI:23328764
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 2 30-JUL-2002;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="genomic DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 258
LOCUS AR222462 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 22 from patent US 6429300.
ACCESSION AR222462
VERSION AR222462.1 GI:23329993
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 22 06-AUG-2002;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="genomic DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 259
LOCUS AR257437 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6486308.
ACCESSION AR257437
VERSION AR257437.1 GI:27307448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 2 26-NOV-2002;
FEATURES Location/Qualifiers
 1..16
 /organism="unknown"
 /mol_type="genomic DNA"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16
RESULT 260
LOCUS AR328670 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6072 from patent US 6566127.
ACCESSION AR328670
VERSION AR328670.1 GI:33714478
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)

AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 6072 20-MAY-2003;
 FEATURES Location/Qualifiers

source
 1..16
 /organism="unknown"
 /mol_type="unassigned RNA"

Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGT 1809
 Db 1 GTGTGTGTGTGTGT 16

RESULT 261
 AR328672 16 bp RNA linear PAT 17-AUG-2003
 LOCUS Sequence 6074 from patent US 6566127.
 DEFINITION AR328672
 ACCESSION AR328672
 VERSION AR328672.1 GI:33714480

KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)
 AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 6074 20-MAY-2003;
 FEATURES Location/Qualifiers

source
 1..16
 /organism="unknown"
 /mol_type="unassigned RNA"

Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGT 1809
 Db 1 GTGGGTGTGTGTGT 16

RESULT 262
 AR436263 16 bp RNA linear PAT 18-DEC-2003
 LOCUS Sequence 522 from patent US 6656731.
 DEFINITION AR436263
 ACCESSION AR436263
 VERSION AR436263.1 GI:40199347

KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)
 AUTHORS Eckstein,F., Ludwig,J. and Beigelman,L.
 TITLE Nucleic acid catalysts with endonuclease activity
 JOURNAL Patent: US 6656731-A 522 02-DEC-2003;
 FEATURES Location/Qualifiers

source
 1..16
 /organism="unknown"
 /mol_type="unassigned RNA"

Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1832 AGTTATCTAGTTAAT 1847
 Db 1 AGTTATGTATGTTAAT 16

RESULT 263
 AX039049/c 16 bp DNA linear PAT 16-NOV-2000
 LOCUS Sequence 2 from Patent WO0061594.
 DEFINITION AX039049
 ACCESSION AX039049
 VERSION AX039049.1 GI:11228345

KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Beier,M. and Hohenisel,J.
 TITLE Nucleoside derivatives with photo-unstable protective groups
 JOURNAL Patent: WO 0061594-A 2 19-OCT-2000;
 DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG (DE)

FEATURES Location/Qualifiers

source
 1..16
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Oligonucleotide"

Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
 Db 16 TTTTATTTTGTGTTT 1

RESULT 264
 AX135448/c 16 bp DNA linear PAT 29-MAY-2001
 LOCUS Sequence 5 from Patent EP1113080.
 DEFINITION AX135448
 ACCESSION AX135448
 VERSION AX135448.1 GI:14271796

KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Wang,X.B.
 TITLE Personal gene library
 JOURNAL Patent: EP 1113080-A 5 04-JUL-2001;
 Wang, Xiao Bing (US) ; Morisawa, Shinkatsu (JP)

FEATURES Location/Qualifiers
 source
 1..16
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Oligonucleotide primer"

Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2130 TCTATATAGCTGATCA 2145
 Db 16 TCTACAGAGCTGATCA 1

RESULT 265
 AX235176 16 bp DNA linear PAT 11-SEP-2001
 LOCUS Sequence 9 from Patent WO0163282.
 DEFINITION AX235176
 ACCESSION AX235176
 VERSION AX235176.1 GI:15593767

KEYWORDS synthetic construct
 SOURCE synthetic construct

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ORGANISM      synthetic construct
KEYWORDS      artificial sequences.
REFERENCE     1
AUTHORS       Cuzin,M., Pettie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
TITLE         Analysis of biological targets using a biochip comprising a
              fluorescent marker
JOURNAL       Patent: WO 0163282-A 9 30-AUG-2001;
              COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES      Location/Qualifiers
              1..16
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="sequence synthetique"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1865 TTTTATTGTTT 1880
Db      1 TTTTATTGTTT 16

RESULT 266
LOCUS      BD016420/c
DEFINITION Personal gene library.
ACCESSION  BD016420
VERSION     BD016420.1 GI:22557558
KEYWORDS    JP 2001186882-A/5.
SOURCE      unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Wang,X
TITLE        Personal gene library
JOURNAL      Patent: JP 2001186882-A 5 10-JUL-2001;
              XIAOBING WANG,SHINKATSU MORISAWA
COMMENT      OS Unidentified
              PN JP 2001186882-A/5
              PD 10-JUL-2001
              PP 17-NOV-2000 JP 2000350702
              PR 01-DEC-1999 US 60/168297,09-NOV-2000 US 09/708493 PI
              PC C12N15/09,C12N15/09,C12M1/00,C12M1/68,C12N15/00,C12N15/00 CC
              Strandedness: Single;
              CC Topology: Linear;
              CC Personal gene library
              FH Key Location/Qualifiers
              FT source 1..16
              /organism='Unidentified'.

FEATURES      source
              Location/Qualifiers
              1..16
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2130 TCTATATAGCTGATCA 2145
Db      16 TCTACAGAGCTGATCA 1

RESULT 267
LOCUS      BD167413/c
DEFINITION Surface-roughened slide glass and method of analyzing biological
              substance using the same.
ACCESSION  BD167413

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VERSION      BD167413.1 GI:27873225
KEYWORDS      JP 2002211954-A/1.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 16)
AUTHORS       Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE         Surface-roughened slide glass and method of analyzing biological
              substance using the same
JOURNAL       Patent: JP 2002211954-A 1 31-JUL-2002;
              TOYO KOHAN CO LTD
COMMENT       OS Artificial Sequence
              PN JP 2002211954-A/1
              PD 31-JUL-2002
              PP 30-OCT-2001 JP 2001332778
              PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
              KENICHI TAKAGI
              PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
              C12Q1/68,
              PC G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
              Surface-roughened slide glass and method of analyzing CC
              biological substance
              CC using the same
              FH Key Location/Qualifiers
              FT source 1..16
              /organism='Artificial Sequence'.

FEATURES      source
              Location/Qualifiers
              1..16
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1865 TTTTATTGTTT 1880
Db      16 TTTTATTGTTT 1

RESULT 268
LOCUS      BD167414/c
DEFINITION Surface-roughened slide glass and method of analyzing biological
              substance using the same.
ACCESSION  BD167414
VERSION     BD167414.1 GI:27873226
KEYWORDS    JP 2002211954-A/2.
SOURCE      unidentified
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 16)
AUTHORS       Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE         Surface-roughened slide glass and method of analyzing biological
              substance using the same
JOURNAL       Patent: JP 2002211954-A 2 31-JUL-2002;
              TOYO KOHAN CO LTD
COMMENT       OS Artificial Sequence
              PN JP 2002211954-A/2
              PD 31-JUL-2002
              PP 30-OCT-2001 JP 2001332778
              PI HIROSHI OKAMURA,MICHIFUMI TANGA,MITSUYOSHI OBA,KAORU YAMAKAWA,
              KENICHI TAKAGI
              PC C03C15/00,C03C17/245,C12M1/00,C12N11/14,C12N15/09,C12N15/09,
              C12Q1/68,
              PC G01N33/53,G01N33/53,G01N37/00,C12N15/00,C12N15/00 CC
              Surface-roughened slide glass and method of analyzing CC
              biological substance
              CC using the same
              FH Key Location/Qualifiers
              FT source 1..16
              /organism='Artificial Sequence'.

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LOCUS	AX578222	Sequence 60 from Patent WO0211674,	17 bp	DNA	linear	PAT 10-JAN-2000
DEFINITION	AX578222					
ACCESSION	AX578222					
VERSION	AX578222.1	GI:27647424				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE						
AUTHORS	Thompson, J., McSwiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.					
TITLE	Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)					
JOURNAL	Patent: WO 0211674-A 60 14-FEB-2002;					
FEATURES	RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)					
source	1. .17					
	/organism="Homo sapiens"					
	/mol_type="unassigned RNA"					
	/db_xref="taxon:9606"					
Query Match	1.2%; Score 12.8; DB 1; Length 17;					
Best Local Similarity	87.5%; Pred. No. 1.8e+02;					
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	1807 TGTGTGTATATATA 1822					
Db	2 TATCTGTATATATA 17					
RESULT 272						
LOCUS	AR050988	Sequence 57 from patent US 5830644.	14 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	AR050988					
ACCESSION	AR050988					
VERSION	AR050988.1	GI:5974352				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 14)					
AUTHORS	West, M.D., Shay, J. and Wright, W.E.					
TITLE	Method for screening for agents which increase telomerase activity in a cell					
JOURNAL	Patent: US 5830644-A 57 03-NOV-1998;					
FEATURES	Location/Qualifiers					
source	1. .14					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	1.2%; Score 12.4; DB 1; Length 14;					
Best Local Similarity	92.9%; Pred. No. 1.6e+02;					
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	1793 TGTGTGTGTGTGTG 1806					
Db	1 TGGGTGTGTGTGTG 14					
RESULT 273						
LOCUS	IS1789	Sequence 57 from patent US 5645986.	14 bp	DNA	linear	PAT 07-OCT-1999
DEFINITION	IS1789					
ACCESSION	IS1789					
VERSION	IS1789.1	GI:2472990				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 14)					
AUTHORS	West, M.D., Harley, C.B., Strahl, C.M., McEachern, M.J., Shay, J.,					

LOCUS	AX578222	Sequence 60 from Patent WO0211674,	17 bp	DNA	linear	PAT 10-JAN-2000
DEFINITION	AX578222					
ACCESSION	AX578222					
VERSION	AX578222.1	GI:27647424				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE						
AUTHORS	Thompson, J., McSwiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.					
TITLE	Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)					
JOURNAL	Patent: WO 0211674-A 60 14-FEB-2002;					
FEATURES	RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)					
source	1. .17					
	/organism="Homo sapiens"					
	/mol_type="unassigned RNA"					
	/db_xref="taxon:9606"					
Query Match	1.2%; Score 12.8; DB 1; Length 17;					
Best Local Similarity	87.5%; Pred. No. 1.8e+02;					
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
QY	1807 TGTGTGTATATATA 1822					
Db	2 TATCTGTATATATA 17					
RESULT 272						
LOCUS	AR050988	Sequence 57 from patent US 5830644.	14 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	AR050988					
ACCESSION	AR050988					
VERSION	AR050988.1	GI:5974352				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 14)					
AUTHORS	West, M.D., Shay, J. and Wright, W.E.					
TITLE	Method for screening for agents which increase telomerase activity in a cell					
JOURNAL	Patent: US 5830644-A 57 03-NOV-1998;					
FEATURES	Location/Qualifiers					
source	1. .14					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	1.2%; Score 12.4; DB 1; Length 14;					
Best Local Similarity	92.9%; Pred. No. 1.6e+02;					
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	1793 TGTGTGTGTGTGTG 1806					
Db	1 TGGGTGTGTGTGTG 14					
RESULT 273						
LOCUS	IS1789	Sequence 57 from patent US 5645986.	14 bp	DNA	linear	PAT 07-OCT-1999
DEFINITION	IS1789					
ACCESSION	IS1789					
VERSION	IS1789.1	GI:2472990				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 14)					
AUTHORS	West, M.D., Harley, C.B., Strahl, C.M., McEachern, M.J., Shay, J.,					

Wright, W.E., Blackburn, E.H. and Vaziri, H.
Therapy and diagnosis of conditions related to telomere length
and/or telomerase activity
Patent: US 5645986-A 57 08-JUL-1997;
JOURNAL Location/Qualifiers
FEATURES
source
1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTG 14

RESULT 274
184398 I84398 14 bp DNA linear PAT 04-APR-1998
LOCUS
DEFINITION Sequence 56 from patent US 5695932.
ACCESSION I84398
VERSION I84398.1 GI:3021918
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 14)
AUTHORS West, M.D., Shay, J., Wright, W., Blackburn, E.H. and McEachern, M.J.
TITLE Telomerase activity assays for diagnosing pathogenic infections
JOURNAL Patent: US 5695932-A 56 09-DEC-1997;
FEATURES Location/Qualifiers
source
1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTG 14

RESULT 275
AR204606 AR204606 14 bp DNA linear PAT 20-JUN-2002
LOCUS
DEFINITION Sequence 56 from patent US 6368789.
ACCESSION AR204606
VERSION AR204606.1 GI:21501975
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 14)
AUTHORS West, M.D., Shay, J., Wright, W. and Blackburn, E.H.
TITLE Screening methods to identify inhibitors of telomerase activity
JOURNAL Patent: US 6368789-A 56 09-APR-2002;
FEATURES Location/Qualifiers
source
1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTG 14

RESULT 276
AR307315 AR307315 14 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 78 from patent US 6551774.
ACCESSION AR307315
VERSION AR307315.1 GI:31697842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 14)
AUTHORS West, M.D., Harley, C.B., Weinrich, S.L., Strahl, C.M., McEachern, M.J.,
Shay, J., Wright, W.E., Blackburn, E.H., Kim, N.W. and Vaziri, H.
TITLE Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
JOURNAL Patent: US 6551774-A 78 22-APR-2003;
FEATURES Location/Qualifiers
source
1. .14
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTG 14

RESULT 277
BD185612 BD185612 14 bp DNA linear PAT 17-JUN-2003
LOCUS
DEFINITION Analysis of double stranded nucleic acid using scanning probe
microscope.
ACCESSION BD185612
VERSION BD185612.1 GI:31877812
KEYWORDS JP 2002360300-A/1
SOURCE Synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 14)
AUTHORS Takeuchi, M.
TITLE Analysis of double stranded nucleic acid using scanning probe
PATENT: JP 2002360300-A 1 17-DEC-2002;
JOURNAL OLYMPUS OPTICAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002360300-A/1
PD 17-DEC-2002
PF 06-JUN-2001 JP 2001171590
PI MINORU TAKEUCHI
PC C13Q1/68, C12N15/09, G01N33/483, G01N33/50, C12N15/00 CC
Analysis of double stranded nucleic acid using scanning probe CC
microscope
FH Key Location/Qualifiers
FT source 1. .14
/organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1. .14
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTG 1806
Db 1 TGTGTGTGTGTG 14

RESULT 278
 BD185613/c
 LOCUS
 DEFINITION
 ANALYSEs of double stranded nucleic acid using scanning probe
 microscope.
 ACCESSION
 BD185613
 VERSION
 BD185613.1 GI:31877813
 KEYWORDS
 JP 2002360300-A/2.
 SOURCE
 ORGANISM
 synthetic construct
 artificial sequences.
 REFERENCE
 1 (bases 1 to 14)
 AUTHORS
 Takeuchi, M.
 TITLE
 ANALYSEs of double stranded nucleic acid using scanning probe
 JOURNAL
 COMMENT
 OS Artificial Sequence
 PN JP 2002360300-A/2
 PD 17-DEC-2002
 PF 06-JUN-2001 JP 2001171590
 PI MINORU TAKEUCHI
 PC C1201/68, C12N15/09, G01N33/483, G01N33/50, C12N15/00 CC
 ANALYSEs of double stranded nucleic acid using scanning probe CC
 FH Key microscope Location/Qualifiers
 FT source. 1. .14
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 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 1.2%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 1.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTG 1806
 DB 14 TGTGTGTGTGTGTG 1
 RESULT 279
 AR056127
 LOCUS
 DEFINITION
 Sequence 331 from patent US 5837542.
 ACCESSION
 AR056127
 VERSION
 AR056127.1 GI:5981704
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 15)
 AUTHORS
 Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
 Draper, K.G.
 TITLE
 Intercellular adhesion molecule-1 (ICAM-1) ribozymes
 JOURNAL
 Patent: US 5837542-A 331 17-NOV-1998;
 FEATURES
 source
 1. .15
 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1801 TGTGTGTGTGTGTA 1814
 DB 1 TGTGTGTGTGTGTA 14
 RESULT 280
 AR113885
 LOCUS
 DEFINITION
 Sequence 331 from patent US 6132967.
 ACCESSION
 AR113885
 VERSION
 AR113885.1 GI:14094207
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 15)
 AUTHORS
 Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
 Draper, K.G.
 TITLE
 Ribozyme treatment of diseases or conditions related to levels of
 intercellular adhesion molecule-1 (ICAM-1)
 JOURNAL
 Patent: US 6132967-A 331 17-OCT-2000;
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 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1801 TGTGTGTGTGTGTA 1814
 DB 1 TGTGTGTGTGTGTA 14
 RESULT 281
 AR118773
 LOCUS
 DEFINITION
 Sequence 203 from patent US 6150087.
 ACCESSION
 AR118773
 VERSION
 AR118773.1 GI:14100683
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 15)
 AUTHORS
 Chien, D.Y.
 TITLE
 NANBV diagnostics and vaccines
 JOURNAL
 Patent: US 6150087-A 203 21-NOV-2000;
 FEATURES
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 1. .15
 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1378 CTGGCTTGAAGAAT 1391
 DB 1 CTGGCTTGAAGAAT 14
 RESULT 282
 AR179058
 LOCUS
 DEFINITION
 Sequence 1 from patent US 6326139.
 ACCESSION
 AR179058
 VERSION
 AR179058.1 GI:20220613
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 15)
 AUTHORS
 Soreq, H. and Zakut, H.
 TITLE
 Method of screening for genetic predisposition to
 anticholinesterase therapy
 JOURNAL
 Patent: US 6326139-A 1 04-DEC-2001;
 FEATURES
 source
 1. .15
 Location/Qualifiers

LOCUS
 DEFINITION
 Sequence 331 from patent US 6132967.
 ACCESSION
 AR113885
 VERSION
 AR113885.1 GI:14094207
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 15)
 AUTHORS
 Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
 Draper, K.G.
 TITLE
 Ribozyme treatment of diseases or conditions related to levels of
 intercellular adhesion molecule-1 (ICAM-1)
 JOURNAL
 Patent: US 6132967-A 331 17-OCT-2000;
 FEATURES
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 1. .15
 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1801 TGTGTGTGTGTGTA 1814
 DB 1 TGTGTGTGTGTGTA 14
 RESULT 281
 AR118773
 LOCUS
 DEFINITION
 Sequence 203 from patent US 6150087.
 ACCESSION
 AR118773
 VERSION
 AR118773.1 GI:14100683
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 15)
 AUTHORS
 Chien, D.Y.
 TITLE
 NANBV diagnostics and vaccines
 JOURNAL
 Patent: US 6150087-A 203 21-NOV-2000;
 FEATURES
 source
 1. .15
 Location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1378 CTGGCTTGAAGAAT 1391
 DB 1 CTGGCTTGAAGAAT 14
 RESULT 282
 AR179058
 LOCUS
 DEFINITION
 Sequence 1 from patent US 6326139.
 ACCESSION
 AR179058
 VERSION
 AR179058.1 GI:20220613
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 15)
 AUTHORS
 Soreq, H. and Zakut, H.
 TITLE
 Method of screening for genetic predisposition to
 anticholinesterase therapy
 JOURNAL
 Patent: US 6326139-A 1 04-DEC-2001;
 FEATURES
 source
 1. .15
 Location/Qualifiers

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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2174 ACTTGATATGACT 2187
Db 2 ACTTGCTAAGACT 15

RESULT 283
LOCUS I06405
DEFINITION Sequence 25 from Patent EP 0318216.
ACCESSION I06405
VERSION I06405.1 GI:590295
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Nanbv diagnostics and vaccines
JOURNAL Patent: EP 0318216-A1 25 31-MAY-1989;
FEATURES
    Location/Qualifiers
        source
            1..15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1378 CTGGTTTGAAGAT 1391
Db 1 CTGGCTTGAAGAT 14

RESULT 284
LOCUS I06416
DEFINITION Sequence 36 from Patent EP 0318216.
ACCESSION I06416
VERSION I06416.1 GI:590306
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Nanbv diagnostics and vaccines
JOURNAL Patent: EP 0318216-A1 36 31-MAY-1989;
FEATURES
    Location/Qualifiers
        source
            1..15
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                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1378 CTGGTTTGAAGAT 1391
Db 1 CTGGCTTGAAGAT 14

RESULT 285
LOCUS I39436
DEFINITION Sequence 474 from patent US 5616488.
ACCESSION I39436
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2174 ACTTGATATGACT 2187
Db 2 ACTTGCTAAGACT 15

RESULT 283
LOCUS I06405
DEFINITION Sequence 25 from Patent EP 0318216.
ACCESSION I06405
VERSION I06405.1 GI:590295
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Nanbv diagnostics and vaccines
JOURNAL Patent: EP 0318216-A1 25 31-MAY-1989;
FEATURES
    Location/Qualifiers
        source
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                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1378 CTGGTTTGAAGAT 1391
Db 1 CTGGCTTGAAGAT 14

RESULT 284
LOCUS I06416
DEFINITION Sequence 36 from Patent EP 0318216.
ACCESSION I06416
VERSION I06416.1 GI:590306
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Nanbv diagnostics and vaccines
JOURNAL Patent: EP 0318216-A1 36 31-MAY-1989;
FEATURES
    Location/Qualifiers
        source
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                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1378 CTGGTTTGAAGAT 1391
Db 1 CTGGCTTGAAGAT 14

RESULT 285
LOCUS I39436
DEFINITION Sequence 474 from patent US 5616488.
ACCESSION I39436
```

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VERSION I39436.1 GI:2083916
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 474 01-APR-1997;
FEATURES
    Location/Qualifiers
        source
            1..15
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1956 AAAGCATGAATGG 1969
Db 1 AAAGCATAAATGG 14

RESULT 286
LOCUS I39453
DEFINITION Sequence 491 from patent US 5616488.
ACCESSION I39453
VERSION I39453.1 GI:2083933
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 491 01-APR-1997;
FEATURES
    Location/Qualifiers
        source
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                /organism="unknown"
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Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1284 TTATTTAATCTGT 1297
Db 2 TTATTTAATCTGT 15

RESULT 287
LOCUS I77628/c
DEFINITION Sequence 335 from patent US 5693532.
ACCESSION I77628
VERSION I77628.1 GI:3013782
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS McSwiggen,J., Draper,K., Pavco,P. and Woolf,T.
TITLE Respiratory syncytial virus ribozymes
JOURNAL Patent: US 5693532-A 335 02-DEC-1997;
FEATURES
    Location/Qualifiers
        source
            1..15
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                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 12.4; DB 1; Length 15;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1378 CTGGTTTGAAGAT 1391
Db 1 CTGGCTTGAAGAT 14

RESULT 285
LOCUS I39436
DEFINITION Sequence 474 from patent US 5616488.
ACCESSION I39436
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Qy 1784 TGTAAATATTGTGT 1797
Db 14 TGTGAATATTGTGT 1

RESULT 288
AR241870 15 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 158 from patent US 6472154.
DEFINITION AR241870
ACCESSION AR241870
VERSION AR241870.1 GI:27287682
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 158 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGT 1879
Db 1 TTTTATTTTGTGT 15

RESULT 289
AX587098/c 15 bp DNA linear PAT 10-JAN-2003
LOCUS Sequence 120 from Patent WO02072883.
DEFINITION AX587098
ACCESSION AX587098
VERSION AX587098.1 GI:27655973
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Roetger,A.
TITLE Nucleotide carrier for diagnosing and treating oral diseases
JOURNAL Patent: WO 02072883-A 120 19-SEP-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Bacteria"

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1275 TAGCACAGTATT 1288
Db 15 TAGCACAGTATT 2

RESULT 290
AX633234 15 bp RNA linear PAT 21-FEB-2003
LOCUS Sequence 373 from Patent EP1260586.
DEFINITION AX633234
ACCESSION AX633234
VERSION AX633234.1 GI:28468848
KEYWORDS
SOURCE unidentified

ORGANISM unidentified
REFERENCE 1

Qy 1284 TTATTTAAATCTGT 1297
Db 2 TTATTTAAATCTGT 15

RESULT 292
AX635755 15 bp RNA linear PAT 21-FEB-2003
LOCUS Sequence 2894 from Patent EP1260586.
DEFINITION AX635755
ACCESSION AX635755
VERSION AX635755.1 GI:28471369
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1

Qy 1801 TGTGTGTGTGTGA 1814
Db 1 TGTGTGTGTGTGA 14

RESULT 291
AX635692 15 bp RNA linear PAT 21-FEB-2003
LOCUS Sequence 2831 from Patent EP1260586.
DEFINITION AX635692
ACCESSION AX635692.1 GI:28471306
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,X.G., Kisich,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,P.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 2831 27-NOV-2002;
FEATURES Location/Qualifiers
source 1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1284 TTATTTAAATCTGT 1297
Db 2 TTATTTAAATCTGT 15

RESULT 292
AX635755 15 bp RNA linear PAT 21-FEB-2003
LOCUS Sequence 2894 from Patent EP1260586.
DEFINITION AX635755
ACCESSION AX635755
VERSION AX635755.1 GI:28471369
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1

Qy 1284 TTATTTAAATCTGT 1297
Db 2 TTATTTAAATCTGT 15

RESULT 292
AX635755 15 bp RNA linear PAT 21-FEB-2003
LOCUS Sequence 2894 from Patent EP1260586.
DEFINITION AX635755
ACCESSION AX635755
VERSION AX635755.1 GI:28471369
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1

AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related genes

JOURNAL Patent: EP 1260586-A 2894 27-NOV-2002; RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES source
 Location/Qualifiers
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 /db_xref="taxon:32644"

Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1956 AAAGCATGAATGG 1969
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 1 AAAGCATGAATGG 14

Db

RESULT 293
 AX637904/c
 LOCUS AX637904 15 bp RNA linear PAT 21-FEB-2003
 DEFINITION Sequence 5043 from Patent EP1260586.
 ACCESSION AX637904
 VERSION AX637904.1 GI:28473518
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 UNCLASSIFIED.

REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related genes

JOURNAL Patent: EP 1260586-A 5043 27-NOV-2002; RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES source
 Location/Qualifiers
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 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 1.7e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1784 TGTAATATTGCT 1797
 |||||
 14 TGTAATATTGCT 1

Db

RESULT 294
 I31521/c
 LOCUS I31521 12 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 433 from patent US 5582979.
 ACCESSION I31521
 VERSION I31521.1 GI:1822312
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 12)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same

JOURNAL Patent: US 5582979-A 433 10-DEC-1996;
FEATURES source
 Location/Qualifiers
 1..12
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.1%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1805
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 12 GTGTGTGTGTGT 1

Db

RESULT 295
 AR208365
 LOCUS AR208365 12 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 21 from patent US 6383747.
 ACCESSION AR208365
 VERSION AR208365.1 GI:21509500
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 12)
AUTHORS Dawkins,R.Letts. and Abraham,L.Joseph.
TITLE Method for determining ancestral haplotypes using haplo-specific geometric elements within the major histocompatibility complex multigene cluster

JOURNAL Patent: US 6383747-A 21 07-MAY-2002;
FEATURES source
 Location/Qualifiers
 1..12
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.1%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTG 1804
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 1 TGTGTGTGTGTG 12

Db

RESULT 296
 AR261535/c
 LOCUS AR261535 12 bp DNA linear PAT 29-JAN-2003
 DEFINITION Sequence 2 from patent US 6322971.
 ACCESSION AR261535
 VERSION AR261535.1 GI:28072603
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 12)
AUTHORS Chetverin,A.B. and Kramer,F.R.
TITLE Oligonucleotide arrays and their use for sorting, isolating, sequencing, and manipulating nucleic acids

JOURNAL Patent: US 6322971-A 2 27-NOV-2001;
FEATURES source
 Location/Qualifiers
 1..12
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 1.1%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
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QY 1794 GTGTGTGTGTGT 1805
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 12 GTGTGTGTGTGT 1

Db

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RESULT 297
AX175249
LOCUS AX175249 12 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 13 from Patent WO0144465.
ACCESSION AX175249
VERSION AX175249.1 GI:14598617
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 13 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
1..12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTG 1804
| | | | |
Db 1 TGTGTGTGTGTG 12

RESULT 298
AX175250
LOCUS AX175250 12 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 14 from Patent WO0144465.
ACCESSION AX175250
VERSION AX175250.1 GI:14598618
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 14 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTG 1804
| | | | |
Db 1 TGTGTGTGTGTG 12

RESULT 299
AX239661/c
LOCUS AX239661 12 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 1 from Patent WO0164948.
ACCESSION AX239661
VERSION AX239661.1 GI:15797326
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van Haeringen,W.A. and van Haeringen,H.

TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 1 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1..12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="primer"
Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTG 1804
| | | | |
Db 12 TGTGTGTGTGTG 1

RESULT 300
AX644020/c
LOCUS AX644020 12 bp DNA linear PAT 27-FEB-2003
DEFINITION Sequence 1 from Patent WO02101088.
ACCESSION AX644020
VERSION AX644020.1 GI:28610172
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Dace,G.T., Kmerly,W.J., Goff,S.A. and Oeller,P.
TITLE In vitro capture of nucleic acids via modified oligonucleotides and
magnetic beads
JOURNAL Patent: WO 02101088-A 1 19-DEC-2002;
Syngenta Participations AG (CH)
FEATURES
source
1..12
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Hypothetical SSR"
Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTG 1804
| | | | |
Db 12 TGTGTGTGTGTG 1

RESULT 301
AX644021
LOCUS AX644021 12 bp DNA linear PAT 27-FEB-2003
DEFINITION Sequence 2 from Patent WO02101088.
ACCESSION AX644021
VERSION AX644021.1 GI:28610173
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Dace,G.T., Kmerly,W.J., Goff,S.A. and Oeller,P.
TITLE In vitro capture of nucleic acids via modified oligonucleotides and
magnetic beads
JOURNAL Patent: WO 02101088-A 2 19-DEC-2002;
Syngenta Participations AG (CH)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Hypothetical probe"
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Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGT 1805
|||||
Db 1 GTGTGTGTGT 12

RESULT 302

BD062286 12 bp DNA linear PAT 27-AUG-2002
LOCUS Method for identifying organism by genotype.

DEFINITION
ACCESSION BD062286
VERSION BD062286.1 GI:22607891
KEYWORDS JP 2001299398-A/11.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 12)
AUTHORS Nishigaki, K., Takasawa, T. and Hamano, K.
TITLE Method for identifying organism by genotype
JOURNAL Patent: JP 2001299398-A 11 30-OCT-2001;
TIE TECH KK

COMMENT OS Unknown
PN JP 2001299398-A/11
PD 30-OCT-2001
PF 23-APR-2000 JP 2000123755

PI KOICHI NISHIGAKI, TSUTOMU TAKASAWA, KEIICHI HAMANO PC
C1201/68, C12N15/09, G01N27/447, G01N27/447, G01N33/50 CC
FH Key Location/Qualifiers.

FEATURES

source

1. .12
/organism="unidentified"
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/db_xref="taxon:32644"

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATAT 1825
|||||
Db 1 ATATATATAT 12

RESULT 303

BD062286/c 12 bp DNA linear PAT 27-AUG-2002
LOCUS Method for identifying organism by genotype.

DEFINITION
ACCESSION BD062286
VERSION BD062286.1 GI:22607891
KEYWORDS JP 2001299398-A/11.
SOURCE unidentified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 12)
AUTHORS Nishigaki, K., Takasawa, T. and Hamano, K.
TITLE Method for identifying organism by genotype
JOURNAL Patent: JP 2001299398-A 11 30-OCT-2001;
TIE TECH KK

COMMENT OS Unknown
PN JP 2001299398-A/11
PD 30-OCT-2001
PF 25-APR-2000 JP 2000123755

PI KOICHI NISHIGAKI, TSUTOMU TAKASAWA, KEIICHI HAMANO PC
C1201/68, C12N15/09, G01N27/447, G01N27/447, G01N33/50 CC
FH Key Location/Qualifiers.

FEATURES

source

1. .12
/organism="unidentified"
/mol_type="genomic DNA"

/db_xref="taxon:32644"

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATAT 1825
|||||
Db 12 ATATATATAT 1

RESULT 304

BD106556/c 12 bp DNA linear PAT 18-SEP-2002
LOCUS Production of attenuated parainfluenza virus vaccines from cloned
DEFINITION nucleotide sequence.

ACCESSION BD106556
VERSION BD106556.1 GI:23201374
KEYWORDS JP 2002502241-A/50.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 12)
AUTHORS Murphy, B.R., Collins, P.L., Durbin, A.P., Skiadopoulos, M.H. and Ta, T.
TITLE Production of attenuated parainfluenza virus vaccines from cloned
JOURNAL nucleotide sequence
Patent: JP 2002502241-A 50 22-JAN-2002;

COMMENT THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
THE MERCK & CO INC DEPARTMENT OF HEALTH AND HUMANSERVICES
PN JP 2002502241-A/50
PD 22-JAN-2002
PF 22-MAY-1998 JP 1998550704

PR 23-MAY-1997 US 60/047575, 19-SEP-1997 US 60/059385 PI
BRIAN R MURPHY, PETER L COLLINS, ANNA P DURBIN, MARIO H PI
SKIADOPOULOS, TAO TAO
PC C12N15/45, C07K14/115, C12N5/10, C12N7/01, A61K39/155 CC
Strandedness: Single;
CC Topology: Linear;

FH Key Location/Qualifiers.

FEATURES

source

1. .12
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1844 TAATTAAAGTT 1855
|||||
Db 12 TAATTAAAGTT 1

RESULT 305

A09237/c 15 bp RNA linear PAT 14-OCT-1993
LOCUS Sabin:codon 286-290 mRNA.

DEFINITION
ACCESSION A09237
VERSION A09237.1 GI:492887
KEYWORDS Human poliovirus 3
SOURCE Human poliovirus 3

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 15)
AUTHORS Minor, P.D., Evans, D.M.A., Schild, G.C., Almond, J.W. and Ferguson, M.
TITLE Peptides useful in vaccination against enteroviruses
JOURNAL Patent: EP 0197772-A 1 15-OCT-1986;
NATIONAL RESEARCH DEVELOPMENT CORPORATION

FEATURES

source

1. .15
/organism="Human poliovirus 3"


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/mol_type="unassigned RNA"
/db_xref="taxon:12086"

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1634 CAAGTTGTTCT 1645
Db 12 CAAGTTGTTCT 1

RESULT 306
161566/c
LOCUS 161566 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 120 from patent US 5658780.
ACCESSION I61566
VERSION I61566.1 GI:2479514
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 120 19-AUG-1997;
FEATURES
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 307
161639/c
LOCUS 161639 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 193 from patent US 5658780.
ACCESSION I61639
VERSION I61639.1 GI:2479587
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 193 19-AUG-1997;
FEATURES
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 308
161755/c
LOCUS 161755 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 309 from patent US 5658780.
ACCESSION I61755
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161755.1 GI:2479703
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 309 19-AUG-1997;
FEATURES
source
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 309
166357
LOCUS 166357 15 bp DNA linear PAT 28-DEC-1997
DEFINITION Sequence 16 from patent US 5670330.
ACCESSION I66357
VERSION I66357.1 GI:2724334
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Sonenberg,N., Katze,M.G., Roy,S., Koromilas,A.E. and Barber,G.H.
TITLE Anti-tumor agent assay using PKR
JOURNAL Patent: US 5670330-A 16 23-SEP-1997;
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/mol_type="unassigned DNA"

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1784 TGTAATATTGT 1795
Db 3 TGTAATATTGT 14

RESULT 310
177325/c
LOCUS 177325 15 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 32 from patent US 5693532.
ACCESSION I77325
VERSION I77325.1 GI:3013479
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS McSwiggen,J., Draper,K., Pavco,P. and Woolf,T.
TITLE Respiratory syncytial virus ribozymes
JOURNAL Patent: US 5693532-A 32 02-DEC-1997;
FEATURES
source
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ACCESSION	AX636030				
VERSION	AX636030.1	GI:28471644			
KEYWORDS					
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1				
AUTHORS	Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpelsky,A., Draper,K.G., Kisich,K., Matulich-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.				
TITLE	Method and reagent for inhibiting the expression of disease related genes				
JOURNAL	PATENT: EP 1260586-A 3169 27-NOV-2002;				
FEATURES	RIBOZYME PHARMACEUTICALS, INC. (US)				
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Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	2153 CACCTGGAGCA 2164				
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RESULT 314					
AX636073/c					
LOCUS	AX636073	15 bp	RNA	linear	PAT 21-FEB-2003
DEFINITION	Sequence 3212 from Patent EPI260586.				
ACCESSION	AX636073				
VERSION	AX636073.1	GI:28471687			
KEYWORDS	unidentified				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1				
AUTHORS	Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpelsky,A., Draper,K.G., Kisich,K., Matulich-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.				
TITLE	Method and reagent for inhibiting the expression of disease related genes				
JOURNAL	PATENT: EP 1260586-A 3212 27-NOV-2002;				
FEATURES	RIBOZYME PHARMACEUTICALS, INC. (US)				
source	Location/Qualifiers				
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Query Match	1.1%; Score 12; DB 1; Length 15;				
Best Local Similarity	100.0%; Pred. No. 1.9e+02;				
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	2153 CACCTGGAGCA 2164				
Db	15 CACCTGGAGCA 4				
RESULT 315					
AX638069/c					
LOCUS	AX638069	15 bp	RNA	linear	PAT 21-FEB-2003
DEFINITION	Sequence 5208 from Patent EPI260586.				
ACCESSION	AX638069				
VERSION	AX638069.1	GI:28473683			
KEYWORDS					

SOURCE unidentified
 ORGANISM unidentified
 REFERENCE unclassified.
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 AUTHORS
 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
 Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
 Meswigen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
 Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
 Woolf,T.
 TITLE
 Method and reagent for inhibiting the expression of disease related
 genes
 JOURNAL
 Patent: EP 1260586-A 5208 27-NOV-2002;
 RIBOZYME PHARMACEUTICALS, INC. (US)
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 /mol_type="unassigned RNA"
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Query Match 1.1%; Score 12; DB 1; Length 15;
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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1347 TGTCAAAACAAAT 1358
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 Db 13 TGTCAAAACAAAT 2

RESULT 316
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 LOCUS AX638071 15 bp RNA linear PAT 21-FEB-2003
 DEFINITION Sequence 5210 from Patent EP1260586.
 ACCESSION AX638071
 VERSION AX638071.1 GI:28473685
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 1 unclassified.
 REFERENCE
 AUTHORS
 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
 Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
 Meswigen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
 Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
 Woolf,T.
 TITLE
 Method and reagent for inhibiting the expression of disease related
 genes
 JOURNAL
 Patent: EP 1260586-A 5210 27-NOV-2002;
 RIBOZYME PHARMACEUTICALS, INC. (US)
 FEATURES
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Query Match 1.1%; Score 12; DB 1; Length 15;
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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1347 TGTCAAAACAAAT 1358
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 Db 12 TGTCAAAACAAAT 1

Search completed: April 2, 2004, 14:35:26
 Job time : 6 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: April 2, 2004, 14:41:23 ; Search time 3 Seconds
(without alignment)
2.494 Million cell updates/sec

Title: us-10-006-191-19
Perfect score: 1049
Sequence: 1 ttgaactgattcacatctca.....gtgtatattttttctataaa 1049

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 169 seqs, 3566 residues

Total number of hits satisfying chosen parameters: 338

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 178 summaries

Database : rst.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	37	3.5	37	1	R06912
C 2	31	3.0	35	1	ACCSSION:R06912
C 3	23.4	2.2	26	1	ACCSSION:N41929
C 4	23.2	2.2	28	1	ACCSSION:AZ781130
C 5	23.2	2.2	28	1	ACCSSION:AZ405219
C 6	23.2	2.2	28	1	ACCSSION:AZ443611
C 7	22.8	2.2	28	1	ACCSSION:AZ648796
C 8	22.4	2.1	24	1	ACCSSION:AZ646963
C 9	22.4	2.1	25	1	ACCSSION:AZ446429
C 10	22.4	2.1	25	1	ACCSSION:AZ762101
C 11	22.4	2.1	28	1	ACCSSION:AZ780500
C 12	22.2	2.1	27	1	ACCSSION:AZ345426
C 13	22.2	2.1	27	1	ACCSSION:AZ638238
C 14	22.2	2.1	27	1	ACCSSION:AZ981811
C 15	22.2	2.1	26	1	ACCSSION:AZ774981
C 16	21.8	2.1	25	1	ACCSSION:BX563211
C 17	21.8	2.1	25	1	ACCSSION:BX39866
C 18	21.8	2.1	26	1	ACCSSION:BX569116
C 19	21.8	2.1	26	1	ACCSSION:AZ307889
C 20	21.8	2.1	26	1	ACCSSION:AZ345505
C 21	21.8	2.1	26	1	ACCSSION:AZ494537
C 22	21.8	2.1	26	1	ACCSSION:AZ503652
C 23	21.8	2.1	26	1	ACCSSION:AZ795803
C 24	21.8	2.1	26	1	ACCSSION:AZ806004
C 25	21.8	2.1	26	1	ACCSSION:AZ297558
C 26	21.8	2.1	27	1	ACCSSION:AZ329433
C 27	21.8	2.1	27	1	ACCSSION:AZ342492
C 28	21.8	2.1	27	1	ACCSSION:AZ404479
C 29	21.8	2.1	27	1	ACCSSION:AZ583081
C 30	21.8	2.1	27	1	ACCSSION:AZ758321
C 31	21.8	2.1	27	1	ACCSSION:AZ788874
C 32	21.8	2.1	27	1	ACCSSION:AZ801217
C 33	21.4	2.0	23	1	ACCSSION:BX557786

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C 37	21.4	2.0	23	1	ACCSSION:AZ829195
C 38	21.4	2.0	24	1	ACCSSION:BX559963
C 39	21.4	2.0	24	1	ACCSSION:AZ419602
C 40	21.4	2.0	24	1	ACCSSION:AZ621455
C 41	21.4	2.0	24	1	ACCSSION:AZ807762
C 42	21.4	2.0	24	1	ACCSSION:AZ813106
C 43	21.4	2.0	24	1	ACCSSION:AZ846178
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132 14.4 1.4 17 1 AM247165
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167 11.4 1.1 13 1 CF280421
168 11.4 1.1 13 1 CF299609
169 11.4 1.1 14 1 CF300543
170 11.4 1.1 14 1 CF328966
171 11 1.0 11 1 CF299360
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ALIGNMENTS

RESULT 1
R05912/c
LOCUS

DEFINITION
Yf12g05.s1 Soares fetal liver spleen INFILs Homo sapiens cDNA clone
IMAGE:126680 3', similar to gb:M92934 CONNECTIVE TISSUE GROWTH
FACTOR PRECURSOR (HUMAN) ; mRNA sequence.

37 bp mRNA linear EST 05-APR-1995
R06912
R05912.1 GI:758835
EST.
Homo sapiens (human)

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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COMMENT

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QY 2008 CCGTCAAAACAGATTGTTTGCAGAGGGAGGAGGCATCAG 2044

DB 37 CCGTCAAAACAGATTGTTTGCAGAGGGAGGAGGCATCAG 1

RESULT 2

LOCUS

DEFINITION

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

N41929
YY07502.r1 Soares melanocyte 2N5HM Homo sapiens cDNA clone

35 bp mRNA linear EST 24-JAN-1996

IMAGE:270507 5' similar to gb:M92934 CONNECTIVE TISSUE GROWTH
FACTOR PRECURSOR (HUMAN) ; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

N41929 1 GI:1165960
EST.
Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 35)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Travaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

The WashU-Merck EST Project

JOURNAL
COMMENT

Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: 17

High quality sequence stop: 1.

FEATURES
source

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/db_xref="GDB:3880149"
/db_xref="taxon:9606"
/clone="IMAGE:270507"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2N5HM"
/note="Vector: p773D (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTCACCACTGAGTGGAGCGCGCGAGTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

Query Match 3.0%; Score 31; DB 1; Length 35;
Best Local Similarity 91.2%; Pred. No. 5.6;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGTGTGTATATATATAT 1827
DB 1 GNGTGTGTGTGTGTGTGTGTGTATATATATATAT 34

RESULT 3

AZ781130

LOCUS

DEFINITION 2M0019A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0019A07 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

TITLE

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0019 row: A column: 07

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

FEATURES
source

1. .26
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0019A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pW42 (GI:4732114[gb]/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.2%; Score 23.4; DB 1; Length 26;

Best Local Similarity 96.0%; Pred. No. 22;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTATAT 1817
DB 1 TGTGTGTGTGTGTGTGTGTGTGTAT 25

RESULT 4

AZ405219

LOCUS

DEFINITION

IM0173N21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0173N21 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE
Niederhausern,A. and Wright,D.,Weiss,R.
JOURNAL
Mouse whole genome scaffolding with paired end reads from 10kb
COMMENT
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0242 row: A column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0242A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTGTGTGTGTAT 1815
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DB 1 TTGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 9
AZ762101
LOCUS
DEFINITION 1M0556K17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0556K17 R, genomic survey sequence.
ACCESSION AZ762101
VERSION AZ762101.1 GI:12871750
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0556 row: K column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.

FEATURES

source
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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0556K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 26;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTATA 1816
|||||
DB 2 TGTGTGTGTGTGTGTGTGTGTGTGA 25

RESULT 10
AZ780500/c
LOCUS
DEFINITION 2M0017J19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0017J19 R, genomic survey sequence.
ACCESSION AZ780500
VERSION AZ780500.1 GI:12912224
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 Row: K Column: 17
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0222K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 29;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATATAT 1819
|||||
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 13

AZ638238 27 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
IMC498H05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0498H05 F, genomic survey sequence.

ACCESSION

AZ638238
VERSION
KEYWORDS
SOURCE

GSS.
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 Row: H Column: 05
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source

1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0498H05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 29;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATATAT 1819
|||||
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 14

AZ981811/c 27 bp DNA linear GSS 27-APR-2001
LOCUS
DEFINITION
2M0262D23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0262D23 F, genomic survey sequence.

ACCESSION

AZ981811
VERSION
KEYWORDS
SOURCE

GSS.
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0262 row: D column: 23
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1. .27

FEATURES

source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0262D23"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22.2; DB 1; Length 27;
 Best Local Similarity 88.9%; Pred. No. 29;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
 |||||
 Db 27 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 15
 AZ774981/c
 LOCUS 26 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0004D22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004D22 R, genomic survey sequence.

ACCESSION AZ774981
 VERSION AZ774981.1
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)

REFERENCE
 DUNN, D., AYOAGI, A., BARBER, M., BEACORN, T., DUVAL, B., HAMIL, C., ISLAM, H., LONGACRE, S., MAHMOUD, M., MEENEN, E., PEDERSEN, T., REILLY, M., ROSE, M., ROSE, R., STOKES, R., TINGEY, A., VON NIEDERHAUSEN, A. and WRIGHT, D., WEISS, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0004 row: D column: 22
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
 1. .26

FEATURES

source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0004D22"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.1%; Score 22; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTA 1814
 |||||
 Db 25 TGTGTGTGTGTGTGTGTGTGTA 4

RESULT 16
 BX563211
 LOCUS 25 bp mRNA linear EST 10-OCT-2003
 DEFINITION BX563211 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse65b06_plc, mRNA sequence.

ACCESSION BX563211
 VERSION BX563211.1
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 25)

REFERENCE
 LAHANE, M.J., AKSOY, S., GIBSON, W., KERHORNOU, A., BERRIMAN, M., HAMILTON, J., SOARES, M.B., BONALDO, M.F., LEHANE, S. and HALL, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL
 Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. W.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
Location/Qualifiers
1. .25
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse65b06 plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 2.1%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 29;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817
|||||
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 17

AZ339866 25 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
1M0071H01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0071H01 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rally,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: H column: 01
Seq primer: CACACGAGAACCTATGACC
Class: plasmid ends
High quality sequence stop: 25.

FEATURES

source
Location/Qualifiers
1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0071H01"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrolytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI4732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 29;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817
|||||
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 18

LOCUS
DEFINITION
BX569116 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse97f02_plc, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BX569116 26 bp mRNA linear EST 14-OCT-2003
BX569116.1 GI:33437055
EST.
Glossina morsitans morsitans
Glossina morsitans morsitans

REFERENCE
AUTHORS
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes

JOURNAL
MEDLINE
PUBMED
COMMENT

Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
Location/Qualifiers
1. .26
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse97f02 plc"
/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 2.1%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 92.0%; Pred. No. 30;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGTATAT 1817
 |||||
 Db 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 19
 AZ307889
 LOCUS
 DEFINITION
 1M0010118F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0010118 F, genomic survey sequence.

ACCESSION
 AZ307889
 VERSION
 AZ307889.1 GI:10347331
 KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 UNPUBLISHED (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0010 row: 1 column: 18
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
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 Location/Qualifiers

/organism="Mus musculus"
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0010118"
 /sex="Male"
 /lab_host="F. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
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 of pWD42 (G[14732114]gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 92.0%; Pred. No. 30;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTGTATAT 1817
 |||||
 Db 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 20
 AZ345505/c
 LOCUS
 DEFINITION
 1M0080H01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0080H01 F, genomic survey sequence.

ACCESSION
 AZ345505
 VERSION
 AZ345505.1 GI:10424742
 KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
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 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: H column: 01
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
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/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080H01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
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 (http://www.jax.org/resources/documents/dnares/). The DNA
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Query Match 2.1%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 30;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTATAT 1817
|||||
Db 26 TGTGTGTGTGTGTGTGTGTGTGTGT 2

RESULT 21
AZ494537
LOCUS 26 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0329D24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0329D24 R, genomic survey sequence.

ACCESSION AZ494537

VERSION AZ494537.1 GI:10669212

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0329 row: D column: 24

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 26.

FEATURES Location/Qualifiers

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0329D24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 30;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTATAT 1817
|||||
Db 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 22

AZ503652

LOCUS 26 bp DNA linear GSS 05-OCT-2000

DEFINITION IM0343FOIR Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0343FOI R, genomic survey sequence.

ACCESSION AZ503652

VERSION AZ503652.1 GI:10684968

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0343 row: F column: 01

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 26.

FEATURES Location/Qualifiers

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0343FOI"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

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(http://www.jax.org/resources/documents/dnares/). The DNA

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Query Match 2.1%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 92.0%; Pred. No. 30;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
 |||||
 DB 2 TGTGTGTGTGTGTGTGTGTGT 26

RESULT 23
 AZ795803 26 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0051P11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0051P11 F, genomic survey sequence.
 ACCESSION AZ795803
 VERSION AZ795803.1 GI:12943205
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 26)
 Durr,D., Aoyagi,A., Barber,M., Mahmoud,M., Meenen,E., Pedersen,T.,
 Islam,H., Longacre,S., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0051 row: P column: 11
 Seq primer: CGTGTGAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0051P11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
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 10.5 kb range using preparative agarose gel
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 inducible derivative of plasmid R1. The vector was ligated
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 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source
 1..26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0051P11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
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Query Match 2.1%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 92.0%; Pred. No. 30;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
 |||||
 DB 1 TGTGTGTGTGTGTGTGTGTGT 25

RESULT 24
 AZ806004 26 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0067H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0067H16 R, genomic survey sequence.
 ACCESSION AZ806004
 VERSION AZ806004.1 GI:12966815
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 26)
 Durr,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0067 row: H column: 16
 Seq primer: CACACAGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0067H16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
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 1..26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0067H16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
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 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 26;

Matches

Matches	25; conservative	27; mismatches	27; errors
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8	8	8	8
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94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817
 Db 3 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 27
 AZ342492 27 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0075004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0075004 R, genomic survey sequence.
 ACCESSION AZ342492
 VERSION A2342492.1 GI:10419783
 KEYWORDS Mus musculus (house mouse)
 SOURCE GSS.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0075 row: 0 column: 04
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.

FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0075004"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 27;
 Best Local Similarity 92.0%; Pred. No. 31;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817
 Db 2 TGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 28
 AZ404479 27 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M017218R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M017218 R, genomic survey sequence.
 ACCESSION AZ404479
 VERSION AZ404479.1 GI:10528408
 KEYWORDS Mus musculus (house mouse)
 SOURCE GSS.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0172 row: F column: 18
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.

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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 27;
 Best Local Similarity 92.0%; Pred. No. 31;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817

Db 3 TGTGTGAGTGTGTGTGTGTGTAT 27

RESULT 29
AZ583081
LOCUS
DEFINITION
AZ583081 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0376L16 R, genomic survey sequence.

ACCESSION
AZ583081
VERSION
AZ583081.1 GI:11702607
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0376 row: L column: 16
Seq primer: CACACAGGAAACGATGACG
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
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/clone="UUGC1M0376L16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1793 TGTGTGTGTGTGTGTGTGTAT 1817

Db 3 TGTGTGAGTGTGTGTGTGTGTAT 27

RESULT 30
AZ758321
LOCUS
DEFINITION
AZ758321 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0550G18 F, genomic survey sequence.

ACCESSION
AZ758321
VERSION
AZ758321.1 GI:12863998
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0550 row: G column: 18
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0550G18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1793 TGTGTGTGTGTGTGTGTGTAT 1817

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RESULT 31
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LOCUS
DEFINITION
  2M0036H16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0036H16 F, genomic survey sequence.
ACCESSION
  AZ788874
VERSION
  AZ788874.1 GI:12929113
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 27)
REFERENCE
  Authors
    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
    Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
    Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
    Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel.: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0036 row: H column: 16
  Seq primer: CGTTGTAACACGCGCCAGT
  Class: plasmid ends
  High quality sequence stop: 27.
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    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0036H16"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
  
```

FEATURES

source

```

RESULT 32
AZ801217
LOCUS
DEFINITION
  2M0059P03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0059P03 R, genomic survey sequence.
ACCESSION
  AZ801217
VERSION
  AZ801217.1 GI:12953540
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 27)
REFERENCE
  Authors
    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
    Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
    Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
    Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel.: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0059 row: F column: 03
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  Class: plasmid ends
  High quality sequence stop: 27.
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    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
  
```

FEATURES

source

```

Query Match      2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 31;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1817
      |||||
DB 3 TGTGTGTGTGTGTGTGTGTGTGTGT 27

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RESULT 33
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LOCUS
DEFINITION  BX557786 Glossina morsitans morsitans adult infected gut Glossina
              morsitans morsitans cDNA clone Tse34f11_p1c, mRNA sequence.
ACCESSION  BX557786
VERSION    BX557786.1 GI:33428961
KEYWORDS
SOURCE     EST.
ORGANISM   Glossina morsitans morsitans
            Glossina morsitans morsitans
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            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
REFERENCE  1 (bases 1 to 23)
AUTHORS   Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
            Hamilton, J., Soares, M.B., Donald, M.F., Lehane, S. and Hall, N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PUBMED   14519136
COMMENT   Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J. Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all p1c reads are from
            the 3' end.
FEATURES
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            /clone_lib="Glossina morsitans morsitans adult infected
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            /notes="country: Zimbabwe; EST from adult gut infected with
            T.brucei"
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            Best Local Similarity 95.7%; Pred. No. 30;
            Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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            Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 23
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            ACCESSION  A2483624
            VERSION    A2483624.1 GI:10647786
            KEYWORDS
            SOURCE     GSS.
            ORGANISM   Mus musculus (house mouse)
            Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 23)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb

```

```

TITLE
JOURNAL
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduenne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0309 row: C column: 01
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
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            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /notes="Vector: pMD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD42 (GI4732114|GB|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
            Query Match 2.0%; Score 21.4; DB 1; Length 23;
            Best Local Similarity 95.7%; Pred. No. 30;
            Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
            QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
            Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 23
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            clone UUGC1M0496005 R, genomic survey sequence.
            ACCESSION  A2637290
            VERSION    A2637290.1 GI:11759480
            KEYWORDS
            SOURCE     GSS.
            ORGANISM   Mus musculus (house mouse)
            Mus musculus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 23)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb

```

plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0496 row: 0 column: 05
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.

FEATURES
 source

1. .23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0496C05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 30;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
 |||||
 DB 23 TGTGTGTGTGTGTGTGTAT 1

RESULT 36
 AZ789907/c
 LOCUS
 DEFINITION
 2M0038G13F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC2M0038G13 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

Unpublished (2000)

JOURNAL
 COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0038 row: G column: 13
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.

FEATURES
 source

1. .23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC2M0038G13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 30;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTAT 1815
 |||||
 DB 23 TGTGTGTGTGTGTGTAT 1

RESULT 37
 AZ829195/c

LOCUS
 DEFINITION
 2M0106M12R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC2M0106M12 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0106 row: M column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES

source

FEATURES

source

1. .23
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0106M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42hv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 30;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815

Db 23 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 38

BX559963

LOCUS

DEFINITION BX559963 Glossina morsitans morsitans adult infected gut Glossina

morsitans morsitans cDNA clone Tse47a03_plc, mRNA sequence.

ACCESSION

BX559963

VERSION

BX559963.1

KEYWORDS

EST.

SOURCE

Glossina morsitans morsitans

ORGANISM

Glossina morsitans morsitans

REFERENCE

1 (bases 1 to 24)

AUTHORS

Lehane, M.J., Soares, S., Gibson, W., Kerhornou, A., Berriman, M.,

Hamilton, J., Soares, S., Bonaldo, M.F., Lehane, S. and Hall, N.

TITLE

Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune

response genes

JOURNAL

Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED

COMMENT

14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

Location/Qualifiers

1. .24
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse47a03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 2.0%; Score 21.4; DB 1; Length 24;

Best Local Similarity 95.7%; Pred. No. 31;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815

Db 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 39

AZ419602

LOCUS

DEFINITION AZ419602 Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0196L12 F, genomic survey sequence.

ACCESSION

AZ419602

VERSION

AZ419602.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 24)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0196 row: L column: 12

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1. .24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"


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/db_xref="taxon:10090"
/clone="UUGC1M0196L12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
      |||||
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 40
AZ621455
LOCUS
DEFINITION
  IM0454K11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0454K11 R, genomic survey sequence.
ACCESSION
  AZ621455
VERSION
  AZ621455.1 GI:11743645
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 24)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0454 row: K column: 11
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 24.
  Location/Qualifiers
    1..24
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"

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/clone="UUGC1M0454K11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
      |||||
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 41
AZ807762
LOCUS
DEFINITION
  AZ807762 24 bp DNA linear GSS 20-FEB-2001
  2M0070014R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0070014 R, genomic survey sequence.
ACCESSION
  AZ807762
VERSION
  AZ807762.1 GI:12972432
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 24)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0070 row: O column: 14
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 24.
  Location/Qualifiers
    1..24
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0070014"

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
|||||
Db 1 TGTGTGTGTGTGTGTGTGT 23
|||||

RESULT 42
AZ813106/c
LOCUS
DEFINITION
2M0080A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0080A16 F, genomic survey sequence.

ACCESSION
AZ813106
VERSION
AZ813106.1 GI:12983014
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: A column: 16
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0080A16"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
|||||
Db 24 TGTGTGTGTGTGTGTGTGT 2
|||||

RESULT 43
AZ846178
LOCUS
DEFINITION
2M0146F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0146F14 F, genomic survey sequence.

ACCESSION
AZ846178
VERSION
AZ846178.1 GI:13016086
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0146 row: F column: 14
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0146F14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

```

/clone.lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match          2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
      |||||||
Db 2 TGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 44
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LOCUS                T. brucei sheared genomic DNA clone 163h11, forward sequence,
DEFINITION           genomic survey sequence.
ACCESSION            AL472248
VERSION              AL472248.1 GI:11837597
KEYWORDS
SOURCE               Trypanosoma brucei
ORGANISM              Trypanosoma brucei
REFERENCE             1 (bases 1 to 24)
AUTHORS              Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
                     Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
                     Meiville, S.B., Rajandream, M.A. and Barrell, B.G.
TITLE                Direct Submission
JOURNAL              Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                     project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                     Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                     nh@sanger.ac.uk
COMMENT              Constructed at the Institute for Genomic Research (TIGR),
                     Rockville, MD. Genomic DNA isolated from a cloned population of
                     Trypanosoma brucei (TREU927/4 Gnat 10.1) was mechanically sheared
                     to give a tight size distribution (
                     4 kb). The v + i method used for the library construction is
                     described in detail in Smith, H. and Venter, J.C. (Making small
                     insert libraries for whole genome shotgun sequencing projects. In
                     Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                     Barrell, Oxford University Press, 1999).
                     Email: nh@sanger.ac.uk
                     Details of T. brucei sequencing at the Sanger Centre are available
                     at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             1..24
                     source
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="163h11"

Query Match          2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
      |||||||
Db 2 TGTGTGTGTGTGTGTGTGTGTGT 24

/clone.lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match          2.0%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
      |||||||
Db 2 TGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 45
AZ345553             25 bp DNA linear GSS 29-SEP-2000
LOCUS                1M0080E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION           clone UUGC1M0080E16 F, genomic survey sequence.
ACCESSION            AZ345553
VERSION              AZ345553.1 GI:10424790
KEYWORDS              GSS.
SOURCE               Mus musculus (house mouse)
ORGANISM              Mus musculus
REFERENCE             1 (bases 1 to 25)
AUTHORS              Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                     Irlam, H., Jongacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                     Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
                     Niederhausern, A. and Wright, D., Weiss, R.
                     Mouse whole genome scaffolding with paired end reads from 10kb
                     plasmid inserts
                     Unpublished (2000)
                     Contact: Robert B. Weiss
                     University of Utah Genome Center
                     University of Utah
                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                     84112, USA
                     Tel: 801 585 5606
                     Fax: 801 585 7177
                     Email: dunn@genetics.utah.edu
                     Insert Length: 10000 Std Error: 0.00
                     Plate: 0080 row: E column: 16
                     Seq primer: CGTGTAAACGACGGCCAGT
                     Class: plasmid ends
                     High quality sequence stop: 25.
FEATURES             1..25
                     source
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080E16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptor DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptor mouse DNA was annealed to
                     adaptor vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

```

QY	1793	TGTGCTGTGTGTGTGTGTAT	1815
Db	24	TGTGTGTGTGTGTGTGTGTGT	2
RESULT 47			
AZ467470			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
1..25			
/organism="Mus musculus"			
/mol_type="genomic DNA"			
/strain="C57BL/6J"			
/db_xref="taxon:10090"			
/clone="UGGC1M027BE21"			
/sex="Male"			
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"			
/clone_lib="Mouse 10kb plasmid UUGC1M library"			
/note="Vector: PWD42nv; Purified genomic DNA from M.			
musculus C57BL/6J (male) was obtained from the Jackson			
Laboratory Mouse DNA Resource			
(http://www.jax.org/resources/documents/dnares/). The DNA			
was hydrodynamically sheared by repeated passage through a			
0.005 inch orifice at constant velocity. The sheared DNA			
was blunt end-repaired with T4 DNA polymerase and T4			
polynucleotide kinase. Adaptor oligonucleotides were			
ligated to the blunt ends in high molar excess. The			
adaptors were purified and size-selected for a 9.5 to			
10.5 kb range using preparative agarose gel			
electrophoresis. Vector DNA was prepared from a derivative			
of pMD42 (GI 4732114 gb AF129072.1), a copy-number			
inducible derivative of plasmid R1. The vector was ligated			
with adaptors complementary to the insert adaptors and			
purified. The sheared, adaptor mouse DNA was annealed to			
adaptor vector DNA, and transformed into			
chemically-competent E. coli XL10-Gold (Stratagene) cells			
and selected for ampicillin resistance."			
Query Match 2.0%; Score 21.4; DB 1; Length 25;			
Best Local Similarity 95.7%; Pred. No. 32;			
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1793	TGTGCTGTGTGTGTGTGTAT	1815

Db 3 TGTGTGTGTGTGTGTGTGT 25
|||||

RESULT 48
AZ769673
LOCUS
DEFINITION
1M0570D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0570D12 R, genomic survey sequence.
ACCESSION
AZ769673
VERSION
AZ769673.1 GI:12890050
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0570 row: D column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0570D12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. NO. 32;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
|||||

Db 2 TGTGTGTGTGTGTGTGTGT 24

RESULT 49
AZ771881
LOCUS
DEFINITION
1M0574P23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0574P23 F, genomic survey sequence.
ACCESSION
AZ771881
VERSION
AZ771881.1 GI:12894610
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0574 row: F column: 23
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.

FEATURES
source
1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0574P23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. NO. 32;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
|||||

Db 2 TGTGTGTGTGTGTGTGTGT 24

RESULT 50
 AZ419877/c
 LOCUS
 DEFINITION
 1M019N03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M019N03 R, genomic survey sequence.
 ACCESSION
 AZ419877
 VERSION
 AZ419877.1 GI:10543890
 KEYWORDS
 GSS
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0196 row: N column: 03
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES

source
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 /organism="Mus musculus"
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M019N03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 26;
 Best Local Similarity 95.7%; Pred. No. 33;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
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 DB 26 TGTGTGTGTGTGTGTGTGTAT 4

RESULT 51
 AZ467063
 LOCUS
 DEFINITION
 1M0278O07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0278O07 F, genomic survey sequence.
 ACCESSION
 AZ467063
 VERSION
 AZ467063.1 GI:10625188
 KEYWORDS
 GSS
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0278 row: O column: 07
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES

source
 1..26
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /clone="UUGC1M0278O07"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 26;
 Best Local Similarity 95.7%; Pred. No. 33;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
 |||||
 DB 4 TGTGTGTGTGTGTGTGTGT 26

RESULT 52
 AZ646850
 LOCUS
 DEFINITION
 1M0513106F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0513106 F, genomic survey sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 GSS.
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0513 row: L column: 06
 Seq primer: CGTTGTAAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
 source
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 /mol_type="genomic DNA"
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 /clone="UUGC1M0513106"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 26;
 Best Local Similarity 95.7%; Pred. No. 33;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
 |||||
 DB 3 TGTGTGTGTGTGTGTGTGTGT 25

RESULT 53

AZ830551
 LOCUS
 DEFINITION
 2M0109C19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0109C19 R, genomic survey sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 GSS.
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0109 row: C column: 19
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
 source
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0109C19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 2.0%; Score 21.4; DB 1; Length 26;
 Best Local Similarity 95.7%; Pred. No. 33;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
 |||||
 DB 3 TGTGTGTGTGTGTGTGTGTGT 25

RESULT 54
 AZ310642

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LOCUS      AZ310642                      21 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION clone UUGC1M0025N09 R, genomic survey sequence.
ACCESSION  AZ310642
VERSION    AZ310642
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 21)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D. Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
COMMENT    University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0025 row: N column: 09
            Seq primer: CACACAGGAACACGATGACG
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES   Location/Qualifiers
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0025N09"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 [G14732114|gb|AF129072.1], a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
            Query Match      2.0%; Score 21; DB 1; Length 21;
            Best Local Similarity 100.0%; Pred. No. 30;
            Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

            QY 1793 TGTGTGTGTGTGTGTGTGT 1813
                |||||
            Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 55
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LOCUS      AZ333309                      21 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION clone UUGC1M0062P13 F, genomic survey sequence.
ACCESSION  AZ333309
VERSION    AZ333309
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 21)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D. Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
COMMENT    University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0062 row: P column: 13
            Seq primer: CGTGTAAACGACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES   Location/Qualifiers
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                /strain="C57BL/6J"
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                /clone="UUGC1M0062P13"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 [G14732114|gb|AF129072.1], a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
            Query Match      2.0%; Score 21; DB 1; Length 21;
            Best Local Similarity 100.0%; Pred. No. 30;
            Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

            QY 1793 TGTGTGTGTGTGTGTGTGT 1813
                |||||
            Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 56
AZ762904
LOCUS      AZ762904                      21 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION 1M0558G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

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```

VERSION      AZ484090.1  GI:10648679
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0310 row: 1 column: 15
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0267D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
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Db 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 59
AZ985497
LOCUS      22 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0267D23F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0267D23 F, genomic survey sequence.
ACCESSION  AZ985497
VERSION     AZ985497.1 GI:13856724
KEYWORDS

```

```

GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: 2 column: 23
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0267D23"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
      ||||||||||||||||||
Db 2 TGTGTGTGTGTGTGTGTGTGT 22

RESULT 60
AZ328763
LOCUS      23 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0521L12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0521L12 R, genomic survey sequence.
ACCESSION  AZ328763
VERSION     AZ328763.1 GI:10388815
KEYWORDS

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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0052 row: L column: 12
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
FEATURES Location/Qualifiers
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 /clone="UUGC1M0052L12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
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DB 2 TGTGTGTGTGTGTGTGTGTGTGTGTGT 22

RESULT 61
AZ371475
LOCUS AZ371475
DEFINITION IM0122K19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0122K19 R, genomic survey sequence.
ACCESSION AZ371475
VERSION AZ371475.1 GI:10485175
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0122 row: K column: 19
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
FEATURES Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0122K19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
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DB 3 TGTGTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 62
AZ824638
LOCUS AZ824638
DEFINITION 2M0099A22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0099A22 F, genomic survey sequence.
ACCESSION AZ824638
VERSION AZ824638.1 GI:12994546
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
1 (bases 1 to 23)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: A column: 22
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0099A22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1913
DB 2 TGTGTGTGTGTGTGTGTGTGT 22

RESULT 63
AZ828969/c
LOCUS
DEFINITION
2M0106013F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0106013 F, genomic survey sequence.
ACCESSION
AZ828969
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
1 (bases 1 to 23)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0106 row: O column: 13
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
source

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0106013"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 2.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 22 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 64
AZ647335
LOCUS
DEFINITION
1M0513J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0513J15 R, genomic survey sequence.
ACCESSION
AZ647335
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0513 row: J column: 15
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24

FEATURES

source
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0513J15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

Best Local Similarity 2.0%; Score 21; DB 1; Length 24;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813

DB 3 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 65

AZ459694
 LOCUS
 DEFINITION 25 bp DNA linear GSS 04-OCT-2000
 clone UUGC1M0264P10 R, genomic survey sequence.
 ACCESSION AZ459694
 VERSION AZ459694.1 GI:10617819
 KEYWORDS GSS.
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 25)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0264 row: P column: 10
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1..25

FEATURES

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0264P10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

Best Local Similarity 2.0%; Score 21; DB 1; Length 25;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1814

DB 1 GTGTGTGTGTGTGTGTGTGT 21

RESULT 66

AZ506209
 LOCUS
 DEFINITION 25 bp DNA linear GSS 05-OCT-2000
 clone UUGC1M0347F10 F, genomic survey sequence.
 ACCESSION AZ506209
 VERSION AZ506209.1 GI:10687525
 KEYWORDS GSS.
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Ross, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0347 row: F column: 10
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Insert/Qualifiers

FEATURES

1. 25

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/mol_type="Genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0347F10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrolytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of FWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match          2.0%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1793 TGTGTGTGTGTGTGTGTGT 1813
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 pb 4 TGTGTGTGTGTGTGTGTGT 24

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RESULT 67
A2494629
LOCUS       26 bp DNA linear GSS 05-OCT-2000
DEFINITION  IM0330F01F Mouse 10kb plasmid UMGCM library Mus musculus genomic
              clone UMGCM0330F01 F, genomic survey sequence.
ACCESSION   A2494629
VERSION     A2494629.1 GI:10669392
KEYWORDS    GSS,

```

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 26) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0330 row: F column: 01
Seq primer: CCGTGAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. .26

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCIM0330F01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PMW42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMW42 [G14732114]p[AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match 2.0%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTTGTGTGTGTGTGTGTGTGT 1813
| | | | | | | | | |
pb 5 TGTGTGTGTGTGTGTGTGTGTGT 25

RESULT	68
AZ602037	
LOCUS	23 bp DNA linear GSS 13-DEC-2000
DEFINITION	1M042A10R Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGC1M042A10 R, genomic survey sequence.
ACCESSION	AZ602037
VERSION	AZ602037.1 GI:11724227
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Stokes, P., W. Pace, B. Mingev, A. von


```

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0119 row: 1 column: 12
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/mol_type="genomic DNA"
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/clone="UUGC1M0119112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 71
AZ465453 20 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION
IM0275F24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0275F24 F, genomic survey sequence.
ACCESSION
AZ465453
VERSION
AZ465453.1 GI:10623578
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

```

```

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: F column: 24
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0275F24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 72
AZ470768 20 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION
IM0285H09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0285H09 F, genomic survey sequence.
ACCESSION
AZ470768
VERSION
AZ470768.1 GI:10628893
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

```


COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: H column: 09
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1[4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTG 1812

Db 1 TGTGTGTGTGTGTGTGTGTG 20

RESULT 73

AZ580200

LOCUS

DEFINITION 1M0368A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0368A20 F, genomic survey sequence.

ACCESSION

AZ580200

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0368 row: A column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1[4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTG 1812

Db 1 TGTGTGTGTGTGTGTGTGTG 20

RESULT 74

AZ634201

LOCUS

DEFINITION

1M0489C19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0489C19 R, genomic survey sequence.

ACCESSION

AZ634201

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

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Rm. 368, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0489 row: C column: 19
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0489C19"
/sex="Male"
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/sex="male">E. Coli strain XL10-Gold, T1-resistant, F⁻ /clone.lib="Mouse 10kb Plasmid UUCGM1 library" /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels

1794	GTGTGTGTGTGTGTGTGT	1813
Qy		
1	GTGTGTGTGTGTGTGTGT	20
Dp		

RESULT 75
AZ946508/c

LOCUS	AZ946508	20 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	2M0208P13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0208P13 F, genomic survey sequence.				

ACCESSION AZ946508
VERSION AZ946508.1 GI:13815584
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM	Mus musculus
REFERENCE	1 (bases 1 to 20)
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS	TITLE
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
Unpublished (2000)
plasmid inserts
Mouse whole genome
111111

CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: gdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0208 row: P column: 13
Seq primer: GTTCTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

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/organism="Mus musculus"  
/mol_type="genomic DNA"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="UUGC2M0208P13"  
/sex="Female"  
lab host="E. coli strain"
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`/clone_lib=mouse 10kb plasmid JUGC2M library"`
`/notes=vector: PW4242nv; Purified genomic DNA from M.`
`musculus C57BL/6J (female); was obtained from the Jackson`
`Laboratory Mouse DNA Resource`
[\(http://www.jax.org/resources/documents/dnares/\)](http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PW424 [G14732119b/AP129072.1], a copy-number ligated
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

```
Query Match      1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 20; Conservative 0; Mismatches 0; Indels
```

QY 1793 TGTGTTGTGTGTGTG 1812
|||
db 20 TGTGTTGTGTGTGTGTG 1

RESULT 76
AZ959039/c

Accession	LOCUS	DEFINITION	Accession	LOCUS	DEFINITION
AF295903.1	LOCUS	20 bp DNA linear	AF295903.1	LOCUS	20 bp DNA linear
2M022610.5R	Mouse	10 kb plasmid UUCG2M library	2M022610.5R	Mouse	10 kb plasmid UUCG2M library
clone UUCG2M022610.5	R. genomic survey sequence.		clone UUCG2M022610.5	R. genomic survey sequence.	

ACCESSION AZ959039
VERSION AZ959039.1 GI:13830266
KEYWORDS GSS

NETWORKS
GSS:
Mus musculus (house mouse)
SOURCE

SOURCE ORGANISM

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ismail, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
Unpublished (2000)

**JOURNAL
COMMENT**

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0504 row: J column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

```

1. .21
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC1M0504J04"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 1.9%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1794 GTGTGTGTGTGTGTGTGTGT 1813
      |||
Db 1 GTGTGTGTGTGTGTGTGTGT 20

```

```

RESULT 79
AZ991225/c
LOCUS
DEFINITION
  AZ991225 2M0275K17F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
  clone UUGC2M0275K17 F, genomic survey sequence.
ACCESSION
  AZ991225
VERSION
  AZ991225.1 GI:13862452
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 21)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177

```

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0275 row: K column: 17
 Seq primer: CGTGTAAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

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1. .21
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC2M0275K17"
  /sex="Female"
  /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC2M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 1.9%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1794 GTGTGTGTGTGTGTGTGTGT 1813
      |||
Db 21 GTGTGTGTGTGTGTGTGTGT 2

```

```

RESULT 80
AZ514387/c
LOCUS
DEFINITION
  AZ514387 1M0361H03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0361H03 F, genomic survey sequence.
ACCESSION
  AZ514387
VERSION
  AZ514387.1 GI:10695703
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 22)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu

```

Insert Length: 10000 Std Error: 0.00

Plate: 0361 row: H column: 03

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0016J20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1795 TGTGTGTGTGTGTGTGTGT 1814

Db 22 TGTGTGTGTGTGTGTGTGT 3

RESULT 81

AZ780002/c

LOCUS

DEFINITION AZ780002 22 bp DNA linear GSS 16-FEB-2001
clone UUC2M0016J20 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0016 row: J column: 20

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0016J20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813

Db 22 GTGTGTGTGTGTGTGTGT 3

RESULT 82

AZ780118

LOCUS

DEFINITION AZ780118 22 bp DNA linear GSS 16-FEB-2001
clone UUC2M0017G07 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1. 22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0017G07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGGTGTGTGTGTGTGTGTG 1812
|||||
Db 3 TGTGTGTGTGTGTGTGTG 22

RESULT 83

AZ309945/c

LOCUS

DEFINITION

clone UUGC1M0017K22 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss

University of Utah Genome Center

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Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0017 row: K column: 22

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

FEATURES

source

1. 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0017K22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTG 1813
|||||
Db 21 GTGTGTGTGTGTGTGTGTG 2

RESULT 84

AZ452951

LOCUS

DEFINITION

clone UUGC1M0254M05 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0254 row: M column: 05

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

FEATURES
sourceLocation/Qualifiers
1. .23

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0254M05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 40;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGTGTGTGTGT 1813

Db 4 GTGTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 85

AZ645446

LOCUS

DEFINITION 24 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0510H22 R, genomic survey sequence.

ACCESSION AZ645446

VERSION A2645446.1 GI:11774942

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: H column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source

Location/Qualifiers

1. .24

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0510H22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGTGTGTG 1812

Db 1 TGTGTGTGTGTGTGTGTGTGTGTG 20

RESULT 86

AZ451588/c

LOCUS

DEFINITION

25 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0251I05 F, genomic survey sequence.

ACCESSION AZ451588

VERSION AZ451588.1 GI:10607541

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: I column: 05
Seq primer: CGTGTAAACACGCCGACGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

source

1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0251105"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1913
 |||||

Db 25 GTGTGTGTGTGTGTGTGT 6
 |||||

RESULT 87

A2513902/c

LOCUS

DEFINITION

A2513902

A2513902

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

21 bp DNA linear GSS 05-OCT-2000
 1M0360A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0360A13 F, genomic survey sequence.

A2513902.1 GI:10695218
 GSS.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: A column: 13
 Seq primer: GTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1. .25

FEATURES
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1. .25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0251105"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1913
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Db 25 GTGTGTGTGTGTGTGTGT 6
 |||||

RESULT 87

A2513902/c

LOCUS

DEFINITION

A2513902

A2513902

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

21 bp DNA linear GSS 05-OCT-2000
 1M0360A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0360A13 F, genomic survey sequence.

A2513902.1 GI:10695218
 GSS.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: A column: 13
 Seq primer: GTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1. .25

FEATURES
 source

1. .25

/organism="Mus musculus"

/mol_type="genomic DNA"

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/sex="Male"

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/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1913
 |||||

Db 25 GTGTGTGTGTGTGTGTGT 6
 |||||

RESULT 87

A2513902/c

LOCUS

DEFINITION

A2513902

A2513902

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

21 bp DNA linear GSS 05-OCT-2000
 1M0360A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0360A13 F, genomic survey sequence.

A2513902.1 GI:10695218
 GSS.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
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 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

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 plasmid inserts
 Unpublished (2000)
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 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: A column: 13
 Seq primer: GTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1. .25

FEATURES
 source

1. .25

/organism="Mus musculus"

/mol_type="genomic DNA"

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/db_xref="taxon:10090"

/clone="UUGC1M0251105"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Query Match 1.9%; Score 20; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1913
 |||||

Db 25 GTGTGTGTGTGTGTGTGT 6
 |||||

RESULT 87

A2513902/c

LOCUS

DEFINITION

A2513902

A2513902

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

21 bp DNA linear GSS 05-OCT-2000
 1M0360A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0360A13 F, genomic survey sequence.

A2513902.1 GI:10695218
 GSS.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

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 Unpublished (2000)
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 84112, USA
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 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: A column: 13
 Seq primer: GTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1. .25

FEATURES
 source

1. .25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0251105"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Query Match 1.9%; Score 20; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1913
 |||||

Db 25 GTGTGTGTGTGTGTGTGT 6
 |||||

RESULT 87

A2513902/c

LOCUS

DEFINITION

A2513902

A2513902

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

21 bp DNA linear GSS 05-OCT-2000
 1M0360A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0360A13 F, genomic survey sequence.

A2513902.1 GI:10695218
 GSS.
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)
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 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: A column: 13
 Seq primer: GTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1. .25

FEATURES
 source

1. .25

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0251105"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.9%; Score 20; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1913
 |||||

Db 25 GTGTGTGTGTGTGTGTGT 6
 |||||

RESULT 87

A2513902/c

LOCUS

DEFINITION

A2513902

A2513902

VERSION

KEYWORDS

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/sex="Male"
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/lab_lib="Mouse 10kb plasmid UUC1M library"
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Query Match 1.8%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
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DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 89
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LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0045H20R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0045H20 R, genomic survey sequence.
ACCESSION AZ793094
VERSION AZ793094.1 GI:12937525
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: H column: 20
Seq primer: CACACAGGAACAGC*ATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers 1. .22
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/mol_type="genomic DNA"

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0045H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/lab_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
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DB 2 TGTGTGTGTGTGTGTGTGTGT 22

RESULT 90
AZ801266
LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0059107R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0059107 R, genomic survey sequence.
ACCESSION AZ801266
VERSION AZ801266.1 GI:12953589
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: I column: 07
Seq primer: CACACAGGAACAGC*ATGACC
Class: plasmid ends
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Location/Qualifiers 1. .22
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/mol_type="genomic DNA"
/strain="C57BL/6J"


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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      1.8%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGT 1813
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Db 2 TGTGTGTGTGTGTGTGTGTGT 22

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DEFINITION
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  clone UUGC1M0097L07 F, genomic survey sequence.
ACCESSION
  AZ356191
VERSION
  AZ356191.1 GI:10469235
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 23)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Langacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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TITLE
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  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
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  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
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/clone="UUGC2M0059107"
/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      1.8%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 43;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGT 1813
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Db 2 TGTGTGTGTGTGTGTGTGTGT 22

RESULT 92
AZ822069
LOCUS
DEFINITION
  2M0095D03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0095D03 F, genomic survey sequence.
ACCESSION
  AZ822069
VERSION
  AZ822069.1 GI:12991977
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 24)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Langacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
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  84112, USA
  Tel: 801 585 5606
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  Email: ddunn@genetics.utah.edu
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  Plate: 0095 row: D column: 03
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    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0095D03"

```

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19.4; DB 1; Length 24;
 Best Local Similarity 95.2%; Pred. No. 46;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1813
 ||||| ||||| ||||| |||||
 DB 4 TGTGTGTGTGTGTGTGTGT 24

RESULT 93
 AZ648796 28 bp DNA linear GSS 14-DEC-2000
 LOCUS
 DEFINITION JM0518A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0518A05 F, genomic survey sequence.

ACCESSION
 AZ648796
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0518 row: A column: 05
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES
 Location/Qualifiers
 1..28
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0518A05"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19.2; DB 1; Length 28;
 Best Local Similarity 87.5%; Pred. No. 54;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1809 TGTGTATATATATATATATGTCAC 1832
 ||||| ||||| ||||| |||||
 DB 1 TATATATATATATATATATATCA 24

RESULT 94
 AZ431700 19 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION JM0216G318R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0216G318 R, genomic survey sequence.

ACCESSION
 AZ431700
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0216 row: G column: 18
 Seq primer: CACACAGGAACAGCATACAC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0216G18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (GI4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812
 |||||
 Db 1 GTGTGTGTGTGTGTGTG 19

RESULT 95
 AZ461642/c 19 bp DNA linear GSS 04-OCT-2000
 LOCUS
 DEFINITION 1M0267P06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0267P06 R, genomic survey sequence.

ACCESSION
 VERSION AZ461642.1 GI:10619767
 KEYWORDS
 SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0267 row: P column: 06
 Seq primer: CACACGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 1. .19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0267P06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (GI4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812
 |||||
 Db 19 GTGTGTGTGTGTGTGTG 1

RESULT 96
 AZ649147

LOCUS 19 bp DNA linear GSS 14-DEC-2000
 DEFINITION 1M0518B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0518B17 R, genomic survey sequence.

ACCESSION
 VERSION AZ649147.1 GI:11782334
 KEYWORDS
 SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0518 row: B column: 17
 Seq primer: CACACGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 1. .19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0518B17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811
|||||
DB 1 TGTGTGTGTGTGTGTGT 19

RESULT 97
LOCUS AZ774954/c
DEFINITION 2M0004N15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004N15 R, genomic survey sequence.

ACCESSION AZ774954
VERSION AZ774954.1 GI:12900943

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE 1 (bases 1 to 19)
AUTHORS Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0004 row: N column: 15
Seq primer: CACACGAAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source Location/Qualifiers

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004N15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812
|||||
DB 19 GTGTGTGTGTGTGTGTG 1

RESULT 98
LOCUS AZ795767

DEFINITION 2M0051112F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0051112 F, genomic survey sequence.

ACCESSION AZ795767
VERSION AZ795767.1 GI:12943132

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0051 row: I column: 12
Seq primer: CGTGTAAACACGCGCAGT

Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source Location/Qualifiers

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0051112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1794 GTGTGTGTGTGTGTGTGTG 1812
|||||
Db 1 GTGTGTGTGTGTGTGTGTG 19

RESULT 99
AZ822936
LOCUS
DEFINITION
2M0096E08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0096E08 R, genomic survey sequence.

ACCESSION
AZ822936
VERSION
AZ822936.1 GI:12992844

KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 19)
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: E column: 08
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0096E08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1794 GTGTGTGTGTGTGTGTGTG 1812
|||||
Db 1 GTGTGTGTGTGTGTGTGTG 19

RESULT 100
AZ827177
LOCUS
DEFINITION
2M0103A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0103A05 R, genomic survey sequence.

ACCESSION
AZ827177
VERSION
AZ827177.1 GI:12997085

KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 19)
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: A column: 05
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0103A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTGTGT 1811
 |||||
 Db 1 TGTGTGTGTGTGTGTGT 19

RESULT 101
 AZ785549 20 bp DNA linear GSS 16-FEB-2001
 LOCUS
 DEFINITION 2M0029F01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0029F01 R, Genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0029 row: F column: 01
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends

High quality sequence stop: 20.
 Location/Qualifiers

1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0029F01"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 44; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1792 TTGTGTGTGTGTGTGTGTG 1810
 |||||
 Db 2 TTGTGTGTGTGTGTGTGTG 20

RESULT 102
 AZ818214 21 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0088B08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0088B08 F, Genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

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 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0088 row: B column: 08
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends

High quality sequence stop: 21.
 Location/Qualifiers

1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0088B08"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811
|||||
Db 3 TGTGTGTGTGTGTGTGTGT 21

RESULT 103
AZ482421
LOCUS 20 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0307P01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0307P01 R, genomic survey sequence.

ACCESSION AZ482421
VERSION 1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0307 row: P column: 01
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source 1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0307P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

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Query Match 1.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1812
|||||
Db 1 TGTGTGTGTGTGTGTGTGT 20

RESULT 104

AZ632650

LOCUS 20 bp DNA linear GSS 13-DEC-2000

DEFINITION 1M0487H23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0487H23 F, genomic survey sequence.

ACCESSION AZ632650

VERSION 1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0487 row: H column: 23

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0487H23"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 49;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTGT 1811

Db 1 TTGTGTGTGTGTGTGTGT 20

RESULT 105

AZ654458

LOCUS

DEFINITION 20 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0528G10 R, genomic survey sequence.

ACCESSION

AZ654458

VERSION

AZ654458.1 GI:11791604

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 20)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A., and Wright, D., Weiss, R.

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Unpublished (2000)

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84112, USA

Tel.: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0528 row: G column: 10

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0528G10"

/sex="Male"

/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

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ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

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Query Match 1.8%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 49;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1812

Db 1 TGTGTGTGTGTGTGTGTGT 20

RESULT 106

AZ793887/c

LOCUS

DEFINITION 20 bp DNA linear GSS 16-FEB-2001

clone UUGC2M0047G21 F, genomic survey sequence.

ACCESSION

AZ793887

VERSION

AZ793887.1 GI:12939296

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 20)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A., and Wright, D., Weiss, R.

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plasmid inserts

Unpublished (2000)

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84112, USA

Tel.: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0047 row: G column: 21

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0047G21"

/sex="Male"

/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTGTGTGTGTGTGT 1811
|||||
Db 20 TTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 107
AZ415089
LOCUS 21 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0189G1R7R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0189G17 R, genomic survey sequence.

ACCESSION AZ415089
VERSION AZ415089.1 GI:10539102
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0189 row: G column: 17
Seq primer: CACACGGAACACTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
1. .21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0189G17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
|||||
Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGT 20

RESULT 108
AZ579599
LOCUS 21 bp DNA linear GSS 13-DEC-2000

DEFINITION 1M0367P06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0367P06 F, genomic survey sequence.

ACCESSION AZ579599
VERSION AZ579599.1 GI:11694028
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: P column: 06
Seq primer: GTTGTAAACGACGCCAGC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
1. .21
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0367P06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

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Query Match 1.8%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1808 GTGTGTATATATATATAT 1827
|||||
Db 1 GTGTATATATATATATCT 20

RESULT 109
AZ621072/c 21 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
1M0454M05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0454M05 F, genomic survey sequence.

ACCESSION
AZ621072
VERSION
AZ621072.1 GI:11743262
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

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84112 USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: M column: 05
Seq primer: CGTGTAAACGACGCGCAGT
Class: Plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0454M05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.8%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1796 GTGTGTGTGTGTGTGTAT 1815
|||||
Db 21 GTGTGTGTGTGTGTGTAT 2

RESULT 110
AZ665302/c 21 bp DNA linear GSS 14-DEC-2000
LOCUS
DEFINITION
1M0546J09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0546J09 R, genomic survey sequence.

ACCESSION
AZ665302
VERSION
AZ665302.1 GI:11802448
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

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Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0546 row: J column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
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1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0546J09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.7%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1790 TATTGTGTGTGTGTGTGTG 1810
| | | | | | | | | | | | | | | | | | | | |
Db 21 TTTTGTGTGTGTGTGTGTG 1

RESULT 111
PCH303878/c
LOCUS 21 bp DNA linear GSS 03-APR-2001
DEFINITION Plasmodium chabaudi genome survey sequence, clone PC4c11.plt,
genomic survey sequence.
ACCESSION AJ303878
VERSION AJ303878.1 GI:11140385
KEYWORDS GSS; genome survey sequence.
SOURCE Plasmodium chabaudi
ORGANISM Plasmodium chabaudi
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 21)
Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harris,D.,
Bowman,S., Phillips,R.S. and Turner,C.M.
TITLE Gene discovery in Plasmodium chabaudi by genome survey sequencing
JOURNAL Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
MEDLINE 21192558
PUBMED 11295179
REFERENCE 2 (bases 1 to 21)
Janssen,C.S.
AUTHORS Direct Submission
TITLE Submitted (06-NOV-2000) Division of Infection & Immunity,
University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
COMMENT bases 40 to 60 (SL to QR).
FEATURES
source
1..21
/organism="Plasmodium chabaudi"
/mol_type="genomic DNA"
/db_xref="taxon:5825"
/clone="PC4c11.plt"

Query Match 1.7%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1767 TTTTAAAAATTTATATGTA 1787
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Db 21 TTTTAAAAATTTATATTTTA 1

RESULT 112
AZ464442
LOCUS 22 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0273N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0273N14 R, genomic survey sequence.
ACCESSION AZ464442
VERSION AZ464442.1 GI:10622567
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weises,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0273 row: N column: 14
Seq primer: CACACAGGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0273N14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/duares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114[gb]/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0273N14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/duares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114[gb]/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.7%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1813
| | | | | | | | | | | | | | | | | | | | |
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 21

RESULT 113
AA995094/c
LOCUS 19 bp mRNA linear EST 27-AUG-1998
DEFINITION ou99909.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1635040 3',
similar to TR:Q69566 Q69566 ; contains TARI.t2 MER35 repetitive
element ; mRNA sequence.
ACCESSION AA995094
VERSION AA995094.1 GI:3181583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 CDNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1087 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1635040"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Kid3"
 /note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 1.7%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 58;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812
 Db 19 GGTGTGTGTGTGTGTG 1

RESULT 114
 AZ786779
 LOCUS
 DEFINITION 19 bp DNA linear GSS 16-FEB-2001
 2M0032C01R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGC2M0032C01 R, genomic survey sequence.

ACCESSION AZ786779
 VERSION AZ786779
 KEYWORDS GSS.
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0032 row: C column: 01
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0032C01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTGTA 1814
 Db 3 GTGTGTGTGTGTGTGTA 19

RESULT 115

AZ597939
 LOCUS
 DEFINITION 21 bp DNA linear GSS 13-DEC-2000
 1M0412F22F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGC1M0412F22 F, genomic survey sequence.
 ACCESSION AZ597939
 VERSION AZ597939
 KEYWORDS GSS.
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0412 row: F column: 22
 Seq primer: CGTTGTAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

```

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1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cloned="UUCG1M0412F22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATATGTA 1830
DB 1 TATATATATATATATATA 20

RESULT 116
AZ597939/c
LOCUS
DEFINITION
1M0412F22F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0412F22 F, genomic survey sequence.
ACCESSION
AZ597939
VERSION
AZ597939.1 GI:11720129
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0412 row: F column: 22
Seq primer: CGTTGTAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
Location/Qualifiers
1. .21
/organism="Mus musculus"

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cloned="UUCG1M0412F22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATATGTA 1830
DB 1 TATATATATATATATATA 20

RESULT 117
AZ401252
LOCUS
DEFINITION
1M0167E20R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0167E20 R, genomic survey sequence.
ACCESSION
AZ401252
VERSION
AZ401252.1 GI:10516326
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: E column: 20
Seq primer: CACACAGGAACACGATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES
Location/Qualifiers
1. .19
/organism="Mus musculus"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0167E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      1.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 2 TATATATATATATATATA 19

RESULT 118
AZ401252/c
LOCUS          19 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION    IM0167E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0167E20 R, genomic survey sequence.
ACCESSION     AZ401252
VERSION       AZ401252.1  GI:10516326
KEYWORDS      .GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: E column: 20
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0167E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      1.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
DB 19 TATATATATATATATATA 2

RESULT 119
AZ630416
LOCUS          19 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION    IM0484B03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0484B03 F, genomic survey sequence.
ACCESSION     AZ630416
VERSION       AZ630416.1  GI:11752606
KEYWORDS      .GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0484 row: B column: 03
Seq primer: CGTTGTAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

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/db_xref="taxon:10090"
/clone="UUGC1M0484B03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
|||||
Db 2 TATATATATATATATA 19

RESULT 120
AZ630416/c
LOCUS
DEFINITION
A2630416 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0484B03 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

1.19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0484B03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATGTA 1830
|||||
Db 19 TATATATATATATATA 2

RESULT 121
AZ799396/c
LOCUS
DEFINITION
A2799396
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

1.19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0056N18"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGid library"
 /notes="Vector: pWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.5%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 79;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

b'p

5 GTGTGTGTGTGTCT 20

Accession	LOCUS	DEFINITION	Accession	LOCUS	DEFINITION
AZ3345795/C			AZ3345795	19 bp DNA linear	GSS 29-SEP-2000
			IMC080H09R	Mouse 10kb plasmid UUC1M library	Mus musculus genomic clone UUC1M080H09 R genomic survey sequence.

VERSION	AZ345795.1	GI:10425032
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: H column: 09
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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source
I. .13
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0080H09"
/sex="Male"
/lab_host="E. Coli strain"

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/clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.5%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 79;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTAA 1883
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 Db 19 TTTTATTTTGTGTTTAA 1

RESULT 124
 AZ491644 19 bp DNA linear GSS 05-OCT-2000
 LOCUS IM0325A20F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 DEFINITION clone UUGCLM0325A20 F, Genomic survey sequence.

ACCESSION AZ491644
 VERSION AZ491644.1 GI:10663543
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0325 row: A column: 20
 Seq primer: CGTTGTAACAGCGGCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

1. .19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0325A20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"

FEATURES

source

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.5%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 79;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTGTG 1810
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 Db 1 TCOCGTGTGTGTGTGTG 19

RESULT 125
 AZ650575/c

LOCUS IM0520P13R Mouse 10kb plasmid UUGCLM library Mus musculus genomic

DEFINITION clone UUGCLM0520P13 R, genomic survey sequence.

ACCESSION AZ650575

VERSION AZ650575.1 GI:11785200

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0520 row: P column: 13

Seq primer: CACACAGAAACACGATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM0520P13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.5%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 79;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTAA 1883

DB 19 TTTTATTTTGTGTTTAA 1

RESULT 126

CF276637/c

LOCUS

DEFINITION

14ETL--01-N18-g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION

CF276637

VERSION

CF276637.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 17)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..17

source

/organism="Oryza sativa"

/mol_type="cDNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ETL--01-N18"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity

94.1%; Pred. No. 79;

Matches 16; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

0;

0;

QY 1865 TTTTATTTTGTGTTT 1881

DB 17 TTTTATTTTGTGTTT 1

RESULT 127

AZ654747

LOCUS

DEFINITION

IM0525F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0525F08 F, genomic survey sequence.

ACCESSION

AZ654747

VERSION

AZ654747.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah

Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000

Std Error: 0.00

Plate: 0529

row: F

column: 08

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0525F08"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

Best Local Similarity

94.1%; Pred. No. 86;

Matches 16; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

0;

0;

QY 1865 TTTTATTTTGTGTTT 1881

Db 1 TTTTATTTTTTTTT 17

RESULT 128

CF301151

LOCUS 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--05-005, mRNA sequence.

CF301151

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nam B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1...18

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--05-005"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

RT-PCR."

Query Match

Best Local Similarity 1.4%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Ory

Db 1 TTTTATTTTTTTTT 18

1865 TTTTATTTTTTTTT 1882

1 TTTTATTTTTTTTT 18

1 TTTTATTTTTTTTT 18

1 TTTTATTTTTTTTT 18

1 TTTTATTTTTTTTT 18

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1 TTTTATTTTTTTTT 18

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1 TTTTATTTTTTTTT 18

1 TTTTATTTTTTTTT 18

1 TTTTATTTTTTTTT 18

1 TTTTATTTTTTTTT 18

1 TTTTATTTTTTTTT 18

of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1...18

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HD--11-E22"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
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 derived from rice Histone Deacetylase overexpression
 line."

line."

Query Match

Best Local Similarity 1.4%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Ory

Db 1 CTTTATTTTTTTTT 1881

1 CTTTATTTTTTTTT 18

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1 CTTTATTTTTTTTT 18

/sex="Male"
 /tissue_type="melanocyte"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares melanocyte 2NDM"
 /vector="p773D (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 CCGGACCTACCATCTGAAGTCGGCGCGCGAGTCTTTTCTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified p773 vector
 (Pharmacia). Library constructed by Bento Soares and
 Fatima Bonaldo. RNA from normal foreskin melanocytes
 (FS374) was kindly provided by Dr. Anthony P. Albino.

Query Match 1.48; Score 14.8; DB 1; Length 35;

LOCUS
DEFINITION
2819675.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819675 3',
mRNA sequence.
17 bp mRNA
linear EST 07-JAN-2000
AW247165

	EST.	Homo sapiens (human)
KEYWORDS		
SOURCE		Homo sapiens
ORGANISM		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Other ESTs: 2819675.5prime
 Contact: Robert Strausberg. ph.D.

Trimming: cross_match from University of Washington Genome Center.
 PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu> Low Quality Sequence: 17
 contiguous PHRED high quality bases following vector sequence. Very
 Low Quality Sequence: Trace file contained 17 contiguous distinct
 peaks following vector sequence.
 Plate: LiCM2 row: D column: 12
 High quality sequence stop: 17.

```

/tissue_type="small cell carcinoma"
/lac_host="DH10B (phage-resistant)"
/clone_lib="NH_MGC_7"
/notes="Organ: lung; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average

```

```

Query Match
Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTTT 1881
      |||||
      1 TTTTATTTTGTGTTTT 16

Db

RESULT 134
AW248574 17 bp mRNA linear EST 07-JAN-2000
LOCUS 2821096.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821096 3',
DEFINITION mRNA sequence.
ACCESSION AW248574.1 GI:6591567
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Other ESTs: 2821096.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin laboratory cDNA library Arrayed by: The I.M.A.G.E.
Consortium (ILMI). DNA sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/ILMI at:
www-bio.llnl.gov/bbr/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center. Vector
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 8 contiguous
PHRED high quality bases following vector sequence. Very low
Quality Sequence: Trace file contained 17 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: L10M5 row: 0 column: 17
High quality sequence stop: 8.
Location/Qualifiers
1. 17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821096"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match
Best Local Similarity 1.4%; Score 14.4; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1866 TTTTATTTTGTGTTTT 1881
      |||||
      1 TTTTATTTTGTGTTTT 16

Db

RESULT 134
AZ579599/c 21 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0367P06f Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION Clone UUGC1M0367P06 F, genomic survey sequence.
ACCESSION AZ579599
VERSION 1 GI:11694028
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
TITLE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Iellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: 0 column: 06
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0367P06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```

Query Match
Best Local Similarity 1.4%; Score 14.2; DB 1; Length 21;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

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QY 1814 ATATATATATATATGAC 1832
DB 20 AGATATATATATATAC 2

RESULT 135
BQ590128 17 bp mRNA linear EST 06-DEC-2002
LOCUS E012843-024-019-E19-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-019-E19 3-PRIME, mRNA sequence.
ACCESSION BQ590128
VERSION BQ590128
KEYWORDS EST.
SOURCE BQ590128.1 GI:26119711
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weissehaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissehaar@piz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 19 row: E column: 19
Seq primer: T7; GTAATACGACTCATATAGGCG.
Location/Qualifiers
1. .17
/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db xref="GABI:189986"
/db xref="taxon:161934"
/clone="024-019-E19"
/tissue_type="storage root"
/lab host="EMDH10B"
/clone lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTTTTA 1882
DB 1 TTTTATTTTGTTTTA 17

RESULT 136
BQ590687/c 17 bp mRNA linear EST 06-DEC-2002
LOCUS S013717-024-018-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-018-B24 3-PRIME, mRNA sequence.
ACCESSION BQ590687
VERSION BQ590687
KEYWORDS EST.
SOURCE BQ590687.1 GI:26120760
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weissehaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissehaar@piz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 19 row: E column: 19
Seq primer: T7; GTAATACGACTCATATAGGCG.
Location/Qualifiers
1. .17
/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db xref="GABI:189986"
/db xref="taxon:161934"
/clone="024-019-E19"
/tissue_type="storage root"
/lab host="EMDH10B"
/clone lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

ACCESSION BQ590687
VERSION BQ590687.1 GI:26120760
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weissehaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissehaar@piz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 18 row: B column: 24
Seq primer: T7; GTAATACGACTCATATAGGCG.
Location/Qualifiers
1. .17
/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db xref="GABI:189986"
/db xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage root"
/lab host="EMDH10B"
/clone lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTTTT 1881
DB 17 TTTTATTTTGTTTT 1

RESULT 137
BQ591177
LOCUS E012715-024-017-B22-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-017-B22 3-PRIME, mRNA sequence.
ACCESSION BQ591177
VERSION BQ591177
KEYWORDS EST.
SOURCE BQ591177.1 GI:26120760
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weissehaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissehaar@piz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 18 row: B column: 24
Seq primer: T7; GTAATACGACTCATATAGGCG.
Location/Qualifiers
1. .17
/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db xref="GABI:189986"
/db xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage root"
/lab host="EMDH10B"
/clone lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Leirach, H. and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J 32 (5), 845-857 (2002)
 MEDLINE 22342189
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@piz-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 17 row: B column: 22
 Seq primer: T7; GAAATACGACTCACTATAGGGC.
 Location/Qualifiers
 1. .17

FEATURES
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 1. .17
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:188948"
 /db_xref="taxon:161934"
 /clone="024-017-B22"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MPIZ-ADIS-024-storage root"
 /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-SalI-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1865 TTTTATTTTGTGTTT 1881
 1 TTTTATTTTGTGTTT 17
 Db 1 TTTTATTTTGTGTTT 17

RESULT 138
 LOCUS CF290854 17 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-A21, mRNA sequence.
 ACCESSION CF290854
 VERSION CF290854.1 GI:33659887
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 source
 1. .17
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ROOT--01-A21"
 /tissue_type="root"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1865 TTTTATTTTGTGTTT 1881
 1 TTTTATTTTGTGTTT 17
 Db 1 TTTTATTTTGTGTTT 17

RESULT 139
 LOCUS CF294668 17 bp mRNA linear EST 14-AUG-2003
 DEFINITION 30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--04-E17, mRNA sequence.
 ACCESSION CF294668
 VERSION CF294668.1 GI:33663701
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 source
 1. .17
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--04-E17"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
 Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1866 TTTTATTTTGTGTTT 1882
 1 TTTTATTTTGTGTTT 17
 Db 1 TTTTATTTTGTGTTT 17


```

RESULT 140
CF295988      17 bp mRNA linear EST 14-AUG-2003
LOCUS       30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION   sativa cDNA clone 30DGS--06-C17, mRNA sequence.
ACCESSION   CF295988
VERSION     CF295988.1 GI:33665021
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
             1..17
             /organism="Oryza sativa"
             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:4530"
             /clone="30DGS--06-C17"
             /tissue_type="leaf"
             /dev_stage="30 days after germination"
             /lab_host="E.coli DH10B"
             /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
             /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
             with oligoribonucleotides and then used as templates for
             RT-PCR."

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1866 TTTTATTTTGTGTTTTA 1882
Db      1 TTTTATTTTGTGTTTTA 17

RESULT 141
CF298589      17 bp mRNA linear EST 15-AUG-2003
LOCUS       7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION   sativa cDNA clone 7LEAF--02-A18, mRNA sequence.
ACCESSION   CF298589
VERSION     CF298589.1 GI:33670350
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
             1..17
             /organism="Oryza sativa"
             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:4530"
             /clone="30DGS--06-C17"
             /tissue_type="leaf"
             /dev_stage="30 days after germination"
             /lab_host="E.coli DH10B"
             /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
             /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
             with oligoribonucleotides and then used as templates for
             RT-PCR."

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1866 TTTTATTTTGTGTTTTA 1882
Db      1 TTTTATTTTGTGTTTTA 17

RESULT 142
CF310219      17 bp mRNA linear EST 15-AUG-2003
LOCUS       ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION   library (ABF) Oryza sativa cDNA clone ABF--04-M02, mRNA sequence.
ACCESSION   CF310219
VERSION     CF310219.1 GI:33681980
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
             1..17
             /organism="Oryza sativa"
             /mol_type="mRNA"
             /cultivar="Nackdong"
             /db_xref="taxon:4530"
             /clone="ABF--04-M02"
             /tissue_type="leaf"
             /dev_stage="14 days after germination"
             /lab_host="E.coli DH10B"
             /clone_lib="ABF3-overexpressing transgenic rice plasmid
             cDNA library (ABF)"
             /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
             for 2hrs. Oligo-capped mRNA was reverse transcribed and
             then used for PCR. mRNA was prepared from ABA-responsive
             element binding transcription factor 3 overexpression
             line."

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1865 TTTTATTTTGTGTTTTT 1881
Db      1 TTTTATTTTGTGTTTTT 17

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```

Db      1  TTTT TTTT TTTT TTTT 17

RESULT 143
CF334566      17 bp  mRNA  linear  EST 18-AUG-2003
LOCUS      JMT--03-013.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION      library (JMT) Oryza sativa cDNA clone JMT--03-013, mRNA sequence.
ACCESSION      CF334566.1 GI:33817460
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-013"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1865 TTTT TTTT TTTT TTTT 1881
Db      1  TTTT TTTT TTTT TTTT 17

RESULT 144
CF336950      17 bp  mRNA  linear  EST 18-AUG-2003
LOCUS      JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION      library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.
ACCESSION      CF336950.1 GI:33822280
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-013"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1865 TTTT TTTT TTTT TTTT 1881
Db      1  TTTT TTTT TTTT TTTT 17

RESULT 145
CF334566      16 bp  mRNA  linear  EST 09-MAR-1999
LOCUS      tf51h06.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2102843 3'
DEFINITION      similar to TR:Q69566 Q69566; mRNA sequence.
ACCESSION      AI424037
VERSION      AI424037.1 GI:4269968
KEYWORDS      EST.
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 16)
AUTHORS      NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL      Unpublished (1998)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2102843"
/tissue_type="glicblastoma (pooled)"

```

```

COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-D04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1866 TTTT TTTT TTTT TTTT 1882
Db      1  TTTT TTTT TTTT TTTT 17

RESULT 145
CF334566      16 bp  mRNA  linear  EST 09-MAR-1999
LOCUS      tf51h06.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2102843 3'
DEFINITION      similar to TR:Q69566 Q69566; mRNA sequence.
ACCESSION      AI424037
VERSION      AI424037.1 GI:4269968
KEYWORDS      EST.
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 16)
AUTHORS      NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL      Unpublished (1998)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2102843"
/tissue_type="glicblastoma (pooled)"

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/lab_host="DH108"
/clone_lib="NCI CGAP Brn23"
/note="Organ: Brain; Vector: pTT73D-Pac (Pharmacina) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - cligo(dn) primer [5'
TGTTCACATCTCAAGTGGAGCGCGGCATATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacina), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pTT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

```

Query Match 1.3%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 1.1e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGT 1807

DB 15 TGTGTGTGTGTGTGT 1

RESULT 146
 A1685758/c
 LOCUS
 DEFINITION
 tu37g09.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2253280 3'
 similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL
 SEQUENCE MOTIF PROTEIN 1 ;contains element LTR4 repetitive element
 ; mRNA sequence.

ACCESSION A1685758 16 bp mRNA linear EST 27-MAY-1999
 VERSION tu37g09.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2253280 3'
 KEYWORDS EST. similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 E5 CENTRAL
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 16)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -400P from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 source

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1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2253280"
/sex="male"
/dev stage="adult"
/lab_host="DH108"
/clone_lib="NCI CGAP Pr28"
/note="Organ: Prostate; Vector: pTT73D-Pac (Pharmacina)
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normalized library NCI-CGAP-Pr22 was prepared, and as
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonesIDs
985608-986759, 110192-110199, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

```

Query Match 1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGT 1808

DB 16 TGTGTGTGTGTGTGT 1

RESULT 147

B0590166

LOCUS
 DEFINITION
 E012844-024-019-K18-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-K18 3-PRIME, mRNA sequence.

ACCESSION B0590166 16 bp mRNA linear EST 06-DEC-2002

VERSION B0590166 16 bp mRNA linear EST 06-DEC-2002

KEYWORDS EST. GI:26119749

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE
 AUTHORS
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 16)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stabi,D., Wruck,W., Menzel,A., O'Brien,J., Lehrach,H.

and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 0492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 19 row: K column: 18

Seq primer: T7; GTAATACGACTCATATAGGCG.

Location/Qualifiers

1. .16

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:189955"

/db_xref="taxon:161934"

/clones="024-019-K18"

/tissue_type="storage root"

/lab_host="EMDH108"

/clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCNSPORT6; Site1: Sali; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

1.2%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGT 1880

DB 1 TTTTATTTTGTGT 16

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RESULT 148
BQ590507
LOCUS
DEFINITION
  E012844-024-019-M04-T7 MP12-ADIS-024-storage root Beta vulgaris
  cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION
  BQ590507
VERSION
  BQ590507.1 GI:26120090
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
ORGANISM
  Beta vulgaris
REFERENCE
  1 (bases 1 to 16)
AUTHORS
  Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
TITLE
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
  Plant J. 32 (5), 845-857 (2002)
MEDLINE
  22362189
PUBMED
  12472698
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
  Insert Length: 16 Std Error: 0.00
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  Seq primer: T7; GTAATACGCTCACTATAGGCG.
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    /mol_type="mRNA"
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    /db_xref="taxon:161934"
    /clone="024-019-M04"
    /tissue_type="storage root"
    /lab_host="EMDH10B"
    /clone_lib="MP12-ADIS-024-storage root"
    /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
    cDNA library from sugar beet. Library provided by KWS
    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.2%; Score 12.8; DB 1; Length 16;
  Best Local Similarity 87.5%; Pred. No. 1.2e+02;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1867 TTTATTGTTGTTT 1882
Db 1 TTTTATTTTATTTT 16

RESULT 149
BQ592600/c
LOCUS
DEFINITION
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  vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.
ACCESSION
  BQ592600
VERSION
  BQ592600.1 GI:26122183
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
ORGANISM
  Beta vulgaris
REFERENCE
  1 (bases 1 to 16)
AUTHORS
  Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
TITLE
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
  Plant J. 32 (5), 845-857 (2002)
MEDLINE
  22362189
PUBMED
  12472698
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
  Insert Length: 16 Std Error: 0.00
  Plate: 19 row: M column: 04
  Seq primer: T7; GTAATACGCTCACTATAGGCG.
FEATURES
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    /organism="Beta vulgaris"
    /mol_type="mRNA"
    /cultivar="KWS2320 (double haploid, monogerm breeding
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    cDNA library from sugar beet. Library provided by KWS
    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.2%; Score 12.8; DB 1; Length 16;
  Best Local Similarity 87.5%; Pred. No. 1.2e+02;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1867 TTTATTGTTGTTT 1882
Db 1 TTTTATTTTATTTT 16

RESULT 150
BQ592965
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ACCESSION
  BQ592965
VERSION
  BQ592965.1 GI:26122548
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
ORGANISM
  Beta vulgaris
REFERENCE
  1 (bases 1 to 16)
AUTHORS
  Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
TITLE
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
  Plant J. 32 (5), 845-857 (2002)
MEDLINE
  22362189
PUBMED
  12472698
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
  Insert Length: 16 Std Error: 0.00
  Plate: 28 row: F column: 08
  Seq primer: SP6R; ATTAGGTGACACTATAGAGA.
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    /db_xref="GABI:194262"
    /db_xref="taxon:161934"
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    /lab_host="EMDH10B"
    /clone_lib="MP12-ADIS-024-developing root"
    /notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
    cDNA library from sugar beet. Library provided by KWS
    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.2%; Score 12.8; DB 1; Length 16;
  Best Local Similarity 87.5%; Pred. No. 1.2e+02;
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QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
AUTHORS
  Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
  Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
  and Radelof, U.
TITLE
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
  Plant J. 32 (5), 845-857 (2002)
MEDLINE
  22362189
PUBMED
  12472698
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
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    /clone="024-028-F08"
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    /lab_host="EMDH10B"
    /clone_lib="MP12-ADIS-024-developing root"
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    cDNA library from sugar beet. Library provided by KWS
    Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
    orientation:
    SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet
    project, local PI: Dr. Katharina Schneider, coordinator:
    Prof. Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
  Query Match 1.2%; Score 12.8; DB 1; Length 16;
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  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

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22362189 MEDLINE
12472698 PUBMED
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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/db_xref="taxon:161934"
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/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-developing root"
/notes="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

RESULT 151
BO595369 16 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
cDNA clone 024-022-P02-T7 MPiZ-ADIS-024-developing root Beta vulgaris
ACCESSION
BO595369
VERSION
BO595369.1 GI:26124952
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

RESULT 151
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LOCUS
DEFINITION
cDNA clone 024-022-P02-T7 MPiZ-ADIS-024-developing root Beta vulgaris
ACCESSION
BO595369
VERSION
BO595369.1 GI:26124952
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
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fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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/clone_lib="MPiZ-ADIS-024-developing root"
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

RESULT 152
BO595717/c 16 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION
cDNA clone 024-022-H07-SP6 MPiZ-ADIS-024-developing root Beta vulgaris
ACCESSION
BO595717
VERSION
BO595717.1 GI:26125300
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Seq primer: SP6; CATACGATTAGGTCACACTAG.
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de, cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 153
CF279325
LOCUS
DEFINITION
14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION
CF279325
VERSION
CF279325.1 GI:33656711
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/lab_host="E.coli DH10B"
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/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 16

RESULT 155
CF311057
LOCUS
DEFINITION
ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.
ACCESSION
CF311057
VERSION
CF311057.1 GI:33682818
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/lab_host="E.coli DH10B"
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/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

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RESULT 154
CF296130
LOCUS
DEFINITION
30DGS--06-F22.b1 Rice leaf plasmid cDNA library 1 (30DGS) Oryza
sativa cDNA clone 30DGS--06-F22, mRNA sequence.
ACCESSION
CF296130
VERSION
CF296130.1 GI:33665163
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa"
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/lab_host="E.coli DH10B"
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/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1867 TTTTATTTTGTGTTT 1882
Db 1 TTTTATTTTGTGTTT 16

RESULT 155
CF311057
LOCUS
DEFINITION
ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.
ACCESSION
CF311057
VERSION
CF311057.1 GI:33682818
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

```

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
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Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880

Db 1 TTTTATTTTGTGTTT 16

RESULT 156

CF314013

LOCUS HD--02-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-G01, mRNA sequence.

ACCESSION CF314013

VERSION CF314013.1 GI:33685774

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-02-G01"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1867 TTTTATTTTGTGTTT 1882

Db 1 TTTTATTTTGTGTTT 16

RESULT 157

CF314377

LOCUS HD--02-G01.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-G01, mRNA sequence.

ACCESSION CF314377

VERSION CF314377.1 GI:33686138

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.2%; Score 12.8; DB 1; Length 16;

Best Local Similarity 87.5%; Pred. No. 1.2e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880

Db 1 TTTTATTTTGTGTTT 16

RESULT 158

CF315789

LOCUS HD--04-N10.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--04-N10, mRNA sequence.

ACCESSION CF315789

VERSION CF315789.1 GI:33687550

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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 line."

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
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Db 1 TTTTATTTTGTGTTT 16

RESULT 159
CF316056 16 bp mRNA linear EST 15-AUG-2003
LOCUS HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.
ACCESSION CF316056
VERSION EST.
KEYWORDS SOURCE
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
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/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
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 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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 line."

Query Match 1.2%; Score 12.8; DB 1; Length 16;
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 TTTTATTTTGTGTTT 16

RESULT 160
CF317718 16 bp mRNA linear EST 15-AUG-2003
LOCUS HD--07-I05.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--07-I05, mRNA sequence.

ACCESSION CF317718
VERSION EST.
KEYWORDS SOURCE
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
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 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
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 line."

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
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Db 1 TTTTATTTTGTGTTT 16

RESULT 161
CF320356 16 bp mRNA linear EST 15-AUG-2003
LOCUS HD--11-D14.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.

ACCESSION CF320356
VERSION EST.
KEYWORDS SOURCE
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
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 /lab_host="E.coli DH10B"

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
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Db 1 TTTTATTTTGTGTTT 16

RESULT 161
CF320356 16 bp mRNA linear EST 15-AUG-2003
LOCUS HD--11-D14.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.

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ACCESSION   CF320356
VERSION     CF320356.1  GI:33692117
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTATTGTTTT 1880
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      1 TTTTATTATTGTTTT 16

Db

RESULT 162
CF327722
LOCUS       NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION  sativa cDNA clone NACL--02-F06, mRNA sequence.
ACCESSION   CF327722
VERSION     CF327722.1  GI:33803695
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.

ACCESSION   CF320356
VERSION     CF320356.1  GI:33692117
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
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     line."
Query Match      1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTATTGTTTT 1880
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      1 TTTTATTATTGTTTT 16

Db

RESULT 162
CF327722
LOCUS       NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION  sativa cDNA clone NACL--02-F06, mRNA sequence.
ACCESSION   CF327722
VERSION     CF327722.1  GI:33803695
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db

RESULT 163
CF329320
LOCUS       NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION  sativa cDNA clone NACL--04-J17, mRNA sequence.
ACCESSION   CF329320
VERSION     CF329320.1  GI:33806877
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1867 TTTTATTATTGTTTT 1882
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Db

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University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK

bases 40 to 60 (SL to OR)

Location/Qualifiers

1. .21

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/clone="PC4c11.pit"

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Best Local Similarity 75.0%; Pred. No. 1.6e+02;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1772 TAAATTTTATTTGTAATA 1791

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Db 1 TAAATATAAAATTTTAAAA 20

RESULT 166

LOCUS R06912 37 bp mRNA linear EST 05-APR-1995

DEFINITION Yf12g05.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:126680 3' similar to GB:M92934 CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (HUMAN); mRNA sequence.

ACCESSION R06912

VERSION R06912.1 GI:758835

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 37)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasaki,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 1597

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality

Insert Length: 1597 Std Error: 0.00

Seq primer: -21mi3

High quality sequence stop: 1.

Location/Qualifiers

1. .37

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/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal liver spleen INFLS"

/note="Organ: Liver and spleen; Vector: p773D (Pharmacia) with a modified polylinker; Site: 1: Pac 1; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAATTAAGATCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

FEATURES

source

1. .37

/organism="Homo sapiens"

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/db_xref="GDB:478841"

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/sex="male"

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/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal liver spleen INFLS"

/note="Organ: Liver and spleen; Vector: p773D (Pharmacia) with a modified polylinker; Site: 1: Pac 1; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTAATTAAGATCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

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Query Match      1.1%; Score 11.8; DB 1; Length 37;
Best Local Similarity 61.3%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1320 TCCACCCATTCAACATGTGCCATGTC 1350
      ||||| ||||| ||||| ||||| |||||
Db 5 TGCCTCCCTTTCGAACAATCTGTTTGAC 35

RESULT 167
CF299609/c      13 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-L04.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION Oryza sativa cDNA clone 7LEAF--03-L04, mRNA sequence.
ACCESSION CF280421
VERSION 1
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-L04"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 TTTTAAAAATTT 1779
      ||||| ||||| ||||| ||||| |||||
Db 13 TTTTAAAAATTT 1

RESULT 169
CF300543      14 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--05-B01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION CF300543
VERSION 1
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-B01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 TTTTAAAAATTT 1779
      ||||| ||||| ||||| ||||| |||||
Db 13 TTTTAAAAATTT 1

RESULT 168
CF299609/c      13 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-L04.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-L04, mRNA sequence.
ACCESSION CF299609
VERSION 1
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

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with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1764 AGATTTTAAAAA 1776
|||||
Db 2 AGAATTTTAAAA 14

RESULT 170
CF328966/c
LOCUS
DEFINITION NACL--04-B19.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-B19, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--04-B19"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 1.1%; Score 11.4; DB 1; Length 14;

Best Local Similarity 92.3%; Pred. No. 1.5e+02;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 TTTTAAAAATTT 1779

|||||

Db 14 TTTTAAAAATTT 2

RESULT 171
CF299360/c
LOCUS
DEFINITION 7LEAF--03-F15.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-F15, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 11)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

1..11

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--03-F15"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 1.0%; Score 11; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1768 TTTTAAAAATTT 1778

|||||

Db 11 TTTTAAAAATTT 1

RESULT 172

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF291168 13 bp mRNA linear EST 14-AUG-2003
14ROOT--01-H20.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-H20, mRNA sequence.

CF291168
CF291168.1 GI:33660201

EST.

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers

1..13

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ROOT--01-H20"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

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/note="Vector: PCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1865 TTTTATATTTT 1875
DB 11 TTTTATATTTT 1

RESULT 173
CF320273/c      12 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--04-J19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--04-J19, mRNA sequence.
ACCESSION CF320273
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-K23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 TTTTATAAATT 1778
DB 12 TTTTATAAATT 1

RESULT 175
CF329947/c      12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--05-H12.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--05-H12, mRNA sequence.
ACCESSION CF329947
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-J19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2262 TGTATATTTT 2273
DB 12 TTTATATTTT 1

RESULT 174
CF328670/c      12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--03-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--03-K23, mRNA sequence.
ACCESSION CF328670
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-K23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 TTTTATAAATT 1778
DB 12 TTTTATAAATT 1

RESULT 175
CF329947/c      12 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--05-H12.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--05-H12, mRNA sequence.
ACCESSION CF329947
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..12
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-H12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"

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/clone lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 TTTTAAATTT 1778
DB 12 TTTTAAATTT 1

RESULT 176
AI744941/c
LOCUS      13 bp      mRNA      linear      EST 21-JUN-1999
DEFINITION      tr17603.x1 NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:2218588 3',
similar to TR:Q33563 Q33563 ENTP164 KINETOPLAST ;, mRNA sequence.
ACCESSION      AI744941
VERSION      AI744941.1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 13)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgapdb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
cDNA Library Arrayed by: Washington University Genome Sequencing Center
DNA distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40Up from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2218588"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Ov23"
/notes="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dm.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

Query Match      1.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1869 TATTTTGTGTTT 1880
DB 13 TATTTTGTGTTT 2

RESULT 177
CF299938/c
LOCUS      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--04-C12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-C12, mRNA sequence.
ACCESSION      CF299938
VERSION      CF299938.1
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-C12"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2262 TGTATATTTT 2273
DB 13 TTTATATTTT 2

RESULT 178
CF300659/c
LOCUS      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--05-D14.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-D14, mRNA sequence.
ACCESSION      CF300659
VERSION      CF300659.1
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
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Location/Qualifiers
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 232 seqs, 3894 residues
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Minimum DB seq length: 8
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Post-processing: Minimum Match 0%
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Listing first 254 summaries

Database : rni.seq:*

Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	25	2.4	25	1	US-09-292-036-9
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C 6	23	2.2	24	1	US-08-849-021-87
C 7	22.2	2.1	27	1	US-08-222-177A-143
C 8	22	2.1	22	1	US-08-849-021-88
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c 141	13.8	1.3	17	1	US-09-827-998-387	Sequence 387, App	c 215	12	1.1	15	1	US-08-334-847-33	Sequence 33, Appl
c 142	13.8	1.3	17	1	US-09-827-998-388	Sequence 388, App	c 216	12	1.1	15	1	US-08-334-847-33	Sequence 33, Appl
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c 171	12.8	1.2	16	1	US-07-971-978-42	Sequence 42, Appl	245	11.4	1.1	14	1	US-08-832-021-5	Sequence 5, Appl
c 172	12.8	1.2	16	1	US-07-971-978-60	Sequence 60, Appl	246	11.4	1.1	14	1	US-08-832-021-16	Sequence 16, Appl
c 173	12.8	1.2	16	1	US-08-415-370-2	Sequence 2, Appl	247	11.4	1.1	14	1	US-08-724-466B-14	Sequence 14, Appl
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c 179	12.8	1.2	16	1	US-09-430-323-131	Sequence 131, App	252	11.4	1.1	14	1	US-08-882-164D-17	Sequence 17, Appl


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; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 400:
US-09-225-201B-400

Query Match          3.1%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1732 CTTGTGGCAAGTGAATTCCTGTACAAAGCC 1763
Db 32 CTTGTGGCAAGTGAATTCCTGTACAAAGCC 1

RESULT 4
US-09-292-036-9/c
; Sequence 9, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIB01100-1
; CURRENT APPLICATION NUMBER: US/09/292,036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense CTGF oligonucleotide
US-09-292-036-9

Query Match          2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1718 ATTAGACTGGACAGCTTGCGCAAG 1742
Db 25 ATTAGACTGGACAGCTTGCGCAAG 1

RESULT 5
US-09-292-036-10/c
; Sequence 10, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIB01100-1
; CURRENT APPLICATION NUMBER: US/09/292,036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense CTGF oligonucleotide
US-09-292-036-10

Query Match          2.2%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 14;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1742 GTGAATTCCTGTACAAAGCCAGA 1766
Db 25 GTGAATTCCTGTACAAAGCCAGA 1

RESULT 6
US-08-849-021-87/c
; Sequence 87, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
```

```

; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-849-021-87

Query Match          2.2%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1805 TGTGTGTGTATATATATATAT 1827
DB 24 TGTGTGTGTATATATATATAT 2

RESULT 7
US-08-222-177A-143/c
; Sequence 143, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L. POLYMORPHISMS IN
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd311s
US-08-222-177A-143

Query Match          2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTATAT 1819
DB 27 TGTGTGTGTGTGTGTGTGTGTGTGT 1

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RESULT 8
US-08-849-021-88/c
; Sequence 88, Application US/08849021
; Patent No. 5953276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-849-021-88

Query Match          2.1%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1801 TGTGTGTGTGTATATATATAT 1822
DB 22 TGTGTGTGTGTATATATATAT 1

RESULT 9
US-08-222-177A-146/c
; Sequence 146, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin

```

```

; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mfd32rs
;
US-08-222-177A-146
Query Match 2.1%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 25 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 10
US-08-455-627-23/c
; Sequence 23, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-455-627-23
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 12
US-08-455-627-23/c
; Sequence 23, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-689-856-23/c
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 11
US-08-689-856-23/c
; Sequence 23, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-689-856-23
Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1817
Db 26 TGTGTGTGTGTGTGTGTGTGT 2
```

RESULT 12

```

US-08-787-321-23/c
; Sequence 23, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-787-321-23
Query Match          2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1817
      |||||
Db 26 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 13
US-08-222-177A-454/c
; Sequence 454, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 454:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-222-177A-445
Query Match          2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 23;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
      |||||
Db 24 TGTGTGTGTGTGTGTGTGT 2

RESULT 15
PCT-US92-10792-44
; Sequence 44, Application PC/TUS9210792
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Triple Helix Formation at

```



```

; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: m1251s
US-08-222-177A-125

Query Match 2.0%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGT 1813
Db 21 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 18
US-08-787-321-22/c
; Sequence 22, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-787-321-22

Query Match 2.0%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGT 1813
Db 22 TGTGTGTGTGTGTGTGTGTGT 2

RESULT 19
US-08-849-021-89/c
; Sequence 89, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-849-021-89

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1799 TGTGTGTGTGTGTGTATATA 1818
Db 20 TGTGTGTGTGTGTGTATATA 1

RESULT 20
US-08-863-639A-32/c
; Sequence 32, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel Wordperfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

TOPLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-32

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGT 1

RESULT 23
US-09-180-903-8
Sequence 8, Application US/09180903
Patent No. 6316190
GENERAL INFORMATION:
APPLICANT: Rein, Alan
Casas-Finet, Jose
Fisher, Robert
Fivash, Matthew
Henderson, Louis E.
TITLE OF INVENTION: Oligonucleotides Which Specifically Bind
Retroviral Nucleocapsid Proteins
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,903
FILING DATE: 12-Jul-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,128
FILING DATE: 20-MAY-1996
APPLICATION NUMBER: WO PCT/US97/08936
FILING DATE: 19-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Kathleen L.
REGISTRATION NUMBER: 43,433
REFERENCE/DOCKET NUMBER: 015280-279100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-180-903-8

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1812
DB 1 TGTGTGTGTGTGTGTGTGT 20

RESULT 24
US-08-529-878B-9
Sequence 9, Application US/08529878B
Patent No. 5932556
GENERAL INFORMATION:
APPLICANT: Tam, Robert C.

TOPLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-32

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGT 1

RESULT 21
US-09-407-675-5/c
Sequence 5, Application US/09407675
Patent No. 6169176
GENERAL INFORMATION:
APPLICANT: Bruice, Thomas C.
APPLICANT: Arya, Dev P.
TITLE OF INVENTION: DEOXYNUCLEIC ALKYL THIUREA COMPOUNDS AND USES THEREOF
FILE REFERENCE: 30448.65US02
CURRENT APPLICATION NUMBER: US/09/407,675
CURRENT FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 09/347,443
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091,481
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/111,800
PRIOR FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Oligo 5
US-09-407-675-5

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1812
DB 20 TGTGTGTGTGTGTGTGTGT 1

RESULT 22
US-09-488-671-88/c
Sequence 88, Application US/09488671A
Patent No. 6187545
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyatt
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
FILE REFERENCE: RTS-0123
CURRENT APPLICATION NUMBER: US/09/488,671A
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 177
SEQ ID NO 88
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-671-88

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
;; TITLE OF INVENTION: REGULATION OF CD28 EXPRESSION
;; NUMBER OF SEQUENCES: 48
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: Crockett & Fish
;; STREET: 3000 S. Augusta Court
;; CITY: La Habra
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 90631
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 6.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/529,878B
;; FILING DATE: 13-SEP-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fish, Robert D.
;; REGISTRATION NUMBER: 33,880
;; REFERENCE/DOCKET NUMBER: 213/003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 714-525-3433
;; TELEFAX: 714-525-3303
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
US-08-529-878B-9
Query Match 1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGT 20
RESULT 25
US-08-136-118-10/c
; Sequence 10, Application US/08136118
; Patent No. 5580969
; GENERAL INFORMATION:
; APPLICANT: HOKE, Glenn D
; APPLICANT: BRADLEY, Matthews O
; APPLICANT: WILLIAMS, Taify J
; APPLICANT: LEE, Che-Hung
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES DIRECTED
; TITLE OF INVENTION: AGAINST HUMAN ICAM-1
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.
; STREET: 8901 Wisconsin Ave.
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,118
; FILING DATE:
; CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/918,259
;; FILING DATE: 24-JUL-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Spavack, A. David
;; REGISTRATION NUMBER: 24,743
;; REFERENCE/DOCKET NUMBER: N.C. 75,776
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 295-6759
;; TELEFAX: (202) 295-1022
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; HYPOTHETICAL: NO
;; ANTI-SENSE: YES
US-08-136-118-10
Query Match 1.8%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTGTGT 1813
DB 21 TGTGTGTGTGTGTGTGTGT 1
RESULT 26
US-08-222-177A-442/c
; Sequence 442, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-ca)n.(ag-ct)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-222-177A-442

```
Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1811
    |||||
    19 TGTGTGTGTGTGTGTGT 1

Db

RESULT 27
US-08-849-021-74
; Sequence 74, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-849-021-74

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTATAT 1817
    |||||
    1 TGTGTGTGTGTGTATAT 19

Db

RESULT 28
US-08-915-609-3/c
; Sequence 3, Application US/08915609
; Patent No. 6054300
; GENERAL INFORMATION:
; APPLICANT: McKendree Jr., William L.

; TITLE OF INVENTION: Single-Site Amplification (SSA) Method for Accelerated
; FILE REFERENCE: 0115.97
; CURRENT APPLICATION NUMBER: US/08/915,609
; CURRENT FILING DATE: 1997-08-21
; EARLIER APPLICATION NUMBER: 60/028,775
; EARLIER FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0 - beta
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: primer_bind
; LOCATION: (1)..(19)
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)..(19)
; NAME/KEY: primer_bind
; LOCATION: (1)..(19)
US-08-915-609-3

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812
    |||||
    19 GTGTGTGTGTGTGTGTG 1

Db

RESULT 29
US-08-915-609-4
; Sequence 4, Application US/08915609
; Patent No. 6054300
; GENERAL INFORMATION:
; APPLICANT: McKendree Jr., William L.
; TITLE OF INVENTION: Single-Site Amplification (SSA) Method for Accelerated
; FILE REFERENCE: 0115.97
; CURRENT APPLICATION NUMBER: US/08/915,609
; CURRENT FILING DATE: 1997-08-21
; EARLIER APPLICATION NUMBER: 60/028,775
; EARLIER FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: primer_bind
; LOCATION: (1)..(19)
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)..(19)
US-08-915-609-4

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812
    |||||
    1 GTGTGTGTGTGTGTGTG 19

Db

RESULT 30
US-09-314-246-1
; Sequence 1, Application US/09314246
```

```
Patent No. 6180349
GENERAL INFORMATION:
APPLICANT: Ginzinger, David G.
APPLICANT: Godfrey, Tony E.
APPLICANT: Jensen, Ronald H.
APPLICANT: Gray, Joe W.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A Quantitative PCR Method to Enumerate DNA Copy Number
FILE REFERENCE: 2307AA-096200US
CURRENT APPLICATION NUMBER: US/09/314,246
CURRENT FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:TM-TaqMan
OTHER INFORMATION: dual-labeled fluorogenic oligonucleotide probe
OTHER INFORMATION: complementary to amplification products of
OTHER INFORMATION: CA-repeat
NAME/KEY: modified_base
LOCATION: (1)
OTHER INFORMATION: 5'-t attached to 6-carboxy fluorescein (FAM)
NAME/KEY: modified_base
LOCATION: (21)
OTHER INFORMATION: 3'-t attached to 6-carboxy tetramethyl rhodamine
(TAMRA)
US-09-314-246-1

Query Match 1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-314-246-2
QY 1794 GTGTGTGTGTGTGTGTG 1812
Db 2 GTGTGTGTGTGTGTGTG 20

RESULT 31
US-09-314-246-2
Sequence 2, Application US/09314246
Patent No. 6180349
GENERAL INFORMATION:
APPLICANT: Ginzinger, David G.
APPLICANT: Godfrey, Tony E.
APPLICANT: Jensen, Ronald H.
APPLICANT: Gray, Joe W.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A Quantitative PCR Method to Enumerate DNA Copy Number
FILE REFERENCE: 2307AA-096200US
CURRENT APPLICATION NUMBER: US/09/314,246
CURRENT FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:TM-TaqMan
OTHER INFORMATION: dual-labeled fluorogenic oligonucleotide probe
OTHER INFORMATION: complementary to amplification products of
OTHER INFORMATION: CA-repeat
NAME/KEY: modified_base
LOCATION: (1)
OTHER INFORMATION: 5'-t attached to reporter dye
NAME/KEY: modified_base
LOCATION: (21)
OTHER INFORMATION: 3'-t attached to quenching dye
US-09-314-246-2
```

```
Query Match 1.8%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1812
Db 2 GTGTGTGTGTGTGTGTG 20

RESULT 32
US-08-734-973-4/c
Sequence 4, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Mt Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No
US-08-734-973-4

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
Db 18 ATTGTGTGTGTGTGTG 1

RESULT 33
US-08-734-973-5/c
Sequence 5, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-5

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1791 ATTGTGTGTGTGTGTGTG 1808
Db 18 ATTGTGTGTGTGTGTGTG 1

RESULT 34
US-08-700-530-1/c
; Sequence 1, Application US/08700530
; Patent No. 6316186
; GENERAL INFORMATION:
; APPLICANT: EKINS, Roger P
; TITLE OF INVENTION: Binding assay using binding agents with tail groups
; FILE REFERENCE: 0380-P01180US0
; CURRENT APPLICATION NUMBER: US/08/700,530
; CURRENT FILING DATE: 1996-10-23
; PRIOR APPLICATION NUMBER: PCT/GB95/00521
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: GB 9404709.9
; PRIOR FILING DATE: 1994-03-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-08-700-530-1

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTG 1810
Db 18 TGTGTGTGTGTGTGTGTG 1

RESULT 35
US-08-700-530-2
; Sequence 2, Application US/08700530
; Patent No. 6316186
; GENERAL INFORMATION:
; APPLICANT: EKINS, Roger P
; TITLE OF INVENTION: Binding assay using binding agents with tail groups
; FILE REFERENCE: 0380-P01180US0
; CURRENT APPLICATION NUMBER: US/08/700,530
; CURRENT FILING DATE: 1996-10-23
; PRIOR APPLICATION NUMBER: PCT/GB95/00521
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: GB 9404709.9
; PRIOR FILING DATE: 1994-03-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-08-700-530-2

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGTGT 1811
Db 1 GTGTGTGTGTGTGTGTGT 18

RESULT 36
US-08-976-427-28
; Sequence 28, Application US/08976427A
; Patent No. 6322968
; GENERAL INFORMATION:
; APPLICANT: Head, Steven R.
; APPLICANT: Geolet, Philip
; APPLICANT: Karn, Jonathan
; APPLICANT: Boyce-Jacino, Michael
; TITLE OF INVENTION: De No. 6322968 or "Universal" Sequencing Array
; FILE REFERENCE: 04990.0049
; CURRENT APPLICATION NUMBER: US/08/976,427A
; CURRENT FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-976-427-28

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTG 1810
Db 1 TGTGTGTGTGTGTGTGTG 18

RESULT 37
US-09-648-312-28
; Sequence 28, Application US/09648312
; Patent No. 6337188
; GENERAL INFORMATION:
; APPLICANT: Head, Steven R.

APPLICANT: Goelet, Philip
APPLICANT: Karn, Jonathan
APPLICANT: Boyce-Jacino, Michael
TITLE OF INVENTION: De No. 63371880 or "Universal" Sequencing Array
FILE REFERENCE: 04990.0049
CURRENT APPLICATION NUMBER: US/09/648,312
CURRENT FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic primer
US-09-648-312-28

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
DB 1 TGTGTGTGTGTGTGTGTG 18

RESULT 38
US-09-488-671-120
Sequence 120, Application US/09488671A
Patent No. 6187545
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyatt
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPC-CYTOSOLIC EXPRESSION
FILE REFERENCE: RTS-0123
CURRENT APPLICATION NUMBER: US/09/488,671A
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 177
SEQ ID NO 120
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-671-120

Query Match 1.7%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTG 1812
DB 1 GTGTGTGTGTGTGTGTGTG 19

RESULT 39
US-09-496-694B-235/c
Sequence 235, Application US/09496694B
Patent No. 6335194
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Eric B. Swayze
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFERENCE: ISPH-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 09/163,162

PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 249
SEQ ID NO 235
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-496-694B-235

Query Match 1.7%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 53;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATGT 1829
DB 19 TGTATATATATATGT 1

RESULT 40
US-08-222-177A-448/c
Sequence 448, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n.(dg-gt)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 448:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-222-177A-448

Query Match 1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809
DB 17 TGTGTGTGTGTGTGTGT 1

RESULT 41
US-08-885-126-9
; Sequence 9, Application US/08885126A
; Patent No. 595597
; GENERAL INFORMATION:
; APPLICANT: Arnold, Lyle J.
; APPLICANT: Riley, Timothy A.
; APPLICANT: Reynolds, Mark A.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: CHIRALLY ENRICHED SYNTHETIC PHOSPHATE
; TITLE OF INVENTION: OLIGOMERS
; FILE REFERENCE: GENTA.020FW2
; CURRENT APPLICATION NUMBER: US/08/885,126A
; CURRENT FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/343,018
; EARLIER FILING DATE: 1994-11-21
; EARLIER APPLICATION NUMBER: 08/154,013
; EARLIER FILING DATE: 1993-11-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized oligomer
US-08-885-126-9

Query Match 1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTGA 1814
DB 1 GTGTGTGTGTGTGTGA 17

RESULT 42
US-08-960-111-11
; Sequence 11, Application US/08960111
; Patent No. 6060456
; GENERAL INFORMATION:
; APPLICANT: Arnold Jr., Lyle J.
; APPLICANT: Reynolds, Mark A.
; APPLICANT: Giachetti, Christina
; TITLE OF INVENTION: Chimeric Oligonucleoside Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth St.
; CITY: Los Angeles
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 90017
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,111
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,177
; FILING DATE: 04-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meier, Paul H.
; REGISTRATION NUMBER: 32,274
; REFERENCE/DOCKET NUMBER: 207/174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213/489-1600
; TELEFAX: 213/955-0440

TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FEATURE:
; NAME/KEY: GT oligomers 2517-1, 2516-1
; IDENTIFICATION METHOD: synthesis experiments
; OTHER INFORMATION: complementary to synthetic RNA
; OTHER INFORMATION: target
US-08-960-111-11

Query Match 1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTGA 1814
DB 1 GTGTGTGTGTGTGTGA 17

RESULT 43
US-09-490-774-11
; Sequence 11, Application US/09490774
; Patent No. 6262036
; GENERAL INFORMATION:
; APPLICANT: Arnold Jr., Lyle J.
; APPLICANT: Reynolds, Mark A.
; APPLICANT: Giachetti, Christina
; TITLE OF INVENTION: Chimeric Oligonucleoside Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth St.
; CITY: Los Angeles
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 90017
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/960,111
; FILING DATE:
; APPLICATION NUMBER: US/08/238,177
; FILING DATE: 04-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meier, Paul H.
; REGISTRATION NUMBER: 32,274
; REFERENCE/DOCKET NUMBER: 207/174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213/489-1600
; TELEFAX: 213/955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no

```
; ANTI-SENSE: yes
; FEATURE:
; NAME/KEY: CT oligomers 2517-1, 2516-1
; IDENTIFICATION METHOD: synthesis experiments
; OTHER INFORMATION: complementary to synthetic RNA
; OTHER INFORMATION: target
US-09-490-774-11

Query Match
Best Local Similarity 1.6%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1798 GTGTGTGTGTGTGTGA 1814
Db 1 GTGTGTGTGTGTGTGA 17

RESULT 44
US-09-958-221A-16
; Sequence 16, Application US/09958221A
; Patent No. 5686160
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; APPLICANT: Haeringen van, Hendrik
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/09/958,221A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 16
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-16

Query Match
Best Local Similarity 1.6%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1792 TTGTGTGTGTGTGTGTG 1808
Db 1 TTGTGTGTGTGTGTGTG 17

RESULT 45
US-08-734-973-1/c
; Sequence 1, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 3 :
; SEQUENCE CHARACTERISTICS :
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
; US-08-734-973-3
```

```
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 1 :
; SEQUENCE CHARACTERISTICS :
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
; US-08-734-973-1

Query Match
Best Local Similarity 1.6%; Score 17; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1792 TTGTGTGTGTGTGTGTG 1808
Db 17 TTGTGTGTGTGTGTGTG 1

RESULT 46
US-08-734-973-3/c
; Sequence 3, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 3 :
; SEQUENCE CHARACTERISTICS :
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
; US-08-734-973-3
```

Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1808
DB 17 TTGTGTGTGTGTGTG 1

RESULT 47
US-08-734-973-28/c
; Sequence 28, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 28 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
; US-08-734-973-28

Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1808
DB 17 TTGTGTGTGTGTGTG 1

RESULT 48
US-08-734-973-30/c
; Sequence 30, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 28 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
; US-08-734-973-28

ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 30 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No
US-08-734-973-30

Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1810
DB 17 GTGTGTGTGTGTGTG 1

RESULT 49
US-08-734-973-31/c
; Sequence 31, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; US-08-734-973-30

INFORMATION FOR SEQ ID NO: 31 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-31

Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1794 GTGTGTGTGTGTGTG 1810
Db 17 GTGTGTGTGTGTGTG 1

RESULT 50
US-08-734-973-32/c

Sequence 32, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021

TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 32 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-32

Query Match 1.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1794 GTGTGTGTGTGTGTG 1810
Db 17 GTGTGTGTGTGTGTG 1

RESULT 51
US-09-475-947A-337/c

Sequence 337, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 337
LENGTH: 20
TYPE: DNA
ORGANISM: human
US-09-475-947A-337

Query Match 1.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1792 TTGTGTGTGTGTGTGT 1811
Db 20 TGGGGTGTGTGTGTGTGT 1

RESULT 52

US-08-849-021-87
Sequence 87, Application US/08849021
Patent No. 5955276
GENERAL INFORMATION:
APPLICANT: MORGANTE, MICHELE
APPLICANT: VOGEL, JULIE M.
TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: DETECTION OF GENETIC
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND
ADDRESSEE: COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1064-A
TELEPHONE: 302-892-8112
TELEFAX: 302-992-7949
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

```

US-08-849-021-87
Query Match          1.6%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1813 TATATATATATATATAC 1832
DB 1 TATATATATATATATAC 20

RESULT 53
US-08-734-973-7/c
; Sequence 7, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; US-08-734-973-8

Query Match          1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 ACTGTGTGTGTGTGTG 1

RESULT 55
US-08-734-973-29/c
; Sequence 29, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; US-08-734-973-7

Query Match          1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 ACTGTGTGTGTGTGTG 1

RESULT 54
US-08-734-973-8/c
; Sequence 8, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability

```

TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 29 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-29

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1810
DB 18 TCTGTGTGTGTGTGTG 1

RESULT 56
US-08-734-973-33/c
Sequence 33, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 33 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-35

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 AATGTGTGTGTGTGTG 1

RESULT 58
US-08-734-973-37/c
Sequence 37, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 AATGTGTGTGTGTGTG 1

RESULT 57
US-08-734-973-35/c
Sequence 35, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 35 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-35

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 AATGTGTGTGTGTGTG 1

RESULT 58
US-08-734-973-37/c
Sequence 37, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 37 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-37

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 AATGTGTGTGTGTGTG 1

RESULT 59
US-08-734-973-38/c
Sequence 38, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoller, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 38 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-38

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1791 ATTGTGTGTGTGTGTG 1808
DB 18 AATGTGTGTGTGTGTG 1

RESULT 60
US-09-475-947A-104
Sequence 104, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 104
LENGTH: 18
TYPE: DNA
ORGANISM: human
US-09-475-947A-104

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1810 GTGTATATATATATATAT 1827
DB 1 GTATATATATATATATAT 18

RESULT 61
US-09-475-947A-104/c
Sequence 104, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 104
LENGTH: 18
TYPE: DNA
ORGANISM: human
US-09-475-947A-104

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTAC 1831
DB 18 ATATATATATATATATAC 1

RESULT 62
US-08-222-177A-439/c
Sequence 439, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:

RESULT 63
 US-09-371-772B-6069
 Sequence 6069, Application US/09371772B
 Patent No. 6566127
 GENERAL INFORMATION:
 APPLICANT: Ribozyme Pharmaceuticals, Inc.
 APPLICANT: Pavco, Pam
 APPLICANT: McSwiggen, Jim
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
 FILE REFERENCE: MEHB00,876-J (237/198)
 CURRENT APPLICATION NUMBER: US/09/371,772B
 CURRENT FILING DATE: 1999-08-10
 PRIOR APPLICATION NUMBER: US 60/005,974
 PRIOR FILING DATE: 1995-10-26
 PRIOR APPLICATION NUMBER: US 08/584,040
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 14225
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 6069
 LENGTH: 16
 TYPE: RNA

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 2 TGTGTGTGTGTGTGTG 17

RESULT 66
US-09-958-221A-19/c
; Sequence 19, Application US/09958221A
; Patent No. 6686160
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; APPLICANT: Haeringen van, Hendrik
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/09/958,221A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-19

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 67
US-09-958-221A-20/c
; Sequence 20, Application US/09958221A
; Patent No. 6686160
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; APPLICANT: Haeringen van, Hendrik
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/09/958,221A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-20

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 68
US-09-958-221A-21/c
; Sequence 21, Application US/09958221A
; Patent No. 6686160
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; APPLICANT: Haeringen van, Hendrik
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/09/958,221A
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-21

Query Match 1.5%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 69
US-08-734-973-2/c
; Sequence 2, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA: US/08/734,973
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 nucleotides
; TYPE: nucleic acid

STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No
US-08-734-973-2

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
|||||
DB 16 TGTGTGTGTGTGTG 1

RESULT 70

US-08-734-973-6/c
Sequence 6, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Mt Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734, 973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No

US-08-734-973-6/c
Sequence 6, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Mt Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734, 973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808
|||||
DB 16 TGTGTGTGTGTGTG 1

RESULT 71

US-08-734-973-34/c
Sequence 34, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.

APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Mt Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734, 973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No

US-08-734-973-34
Sequence 34, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Mt Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734, 973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808
|||||
DB 16 TGTGTGTGTGTGTG 1

RESULT 72

US-08-734-973-36/c
Sequence 36, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Mt Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734, 973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:

US-08-734-973-36/c
Sequence 36, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Mt Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734, 973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:

NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 36 :
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-36

Query Match 1.5%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
DB 16 TGTGTGTGTGTGTG 1

RESULT 73
US-08-849-021-7/c
; Sequence 7, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELEPHONE: 302-992-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-849-021-7

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1807
DB 15 TGTGTGTGTGTGTG 1

RESULT 74
US-08-849-021-8/c
; Sequence 8, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELEPHONE: 302-992-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-849-021-8

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1808
DB 15 GTGTGTGTGTGTG 1

RESULT 75
US-08-849-021-9
; Sequence 9, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.

;; TITLE OF INVENTION: COMPOUND MICROSATELLITE
;; TITLE OF INVENTION: PRIMERS FOR THE
;; TITLE OF INVENTION: DETECTION OF GENETIC
;; TITLE OF INVENTION: POLYMORPHISMS
;; NUMBER OF SEQUENCES: 89
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
;; ADDRESSEE: COMPANY
;; STREET: 1007 MARKET STREET
;; CITY: WILMINGTON
;; STATE: DELAWARE
;; COUNTRY: U.S.A.
;; ZIP: 19898
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; COMPUTER: IBM PC COMPATIBLE
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/849,021
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION FORM:
;; APPLICATION NUMBER: 08/346,456
;; FILING DATE: 28 NOVEMBER 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FLOYD, LINDA AXAMETHY
;; REGISTRATION NUMBER: 33,692
;; REFERENCE/DOCKET NUMBER: BB-1064-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 302-992-8112
;; TELEFAX: 302-992-7949
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-849-021-9
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGT 1807
Db 1 TGTGTGTGTGTGTGT 15
RESULT 76
US-08-849-021-10
; Sequence 10, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/849,021
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/346,456
;; FILING DATE: 28 NOVEMBER 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FLOYD, LINDA AXAMETHY
;; REGISTRATION NUMBER: 33,692
;; REFERENCE/DOCKET NUMBER: BB-1064-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 302-992-8112
;; TELEFAX: 302-992-7949
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-849-021-10
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTG 1808
Db 1 GTGTGTGTGTGTGTG 15
RESULT 77
US-08-787-321-24/c
; Sequence 24, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: HOIR, THOMAS
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 24
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-787-321-24
Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1794 GTGTGTGTGTGTGTG 1808
Db 15 GTGTGTGTGTGTGTG 1
RESULT 78
US-09-081-646-733
; Sequence 733, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert

APPLICANT: Zhang, Lin
APPLICANT: Zhou, Wei
TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
FILE REFERENCE: 01107.74664
CURRENT APPLICATION NUMBER: US/09/081,646
EARLIER FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: 60/047,352
EARLIER FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 871
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 733
LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
US-09-081-646-733

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2231 CATGTTTGACCTT 2245
Db 1 CATGTTTGACCTT 15

RESULT 79
US-07-971-978-2
Sequence 2, Application US/07971978
Patent No. 5614617
GENERAL INFORMATION:
APPLICANT: Cook and Sanghvi
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate
TITLE OF INVENTION: Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5614617ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: July 27, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-0333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2

OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: 6-aza-thymidine substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: 6-aza-thymidine substitution
US-07-971-978-2

Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1813 TATATATATATAT 1827
Db 2 TATATATATATAT 16

RESULT 80
US-07-971-978-2/c
Sequence 2, Application US/07971978
Patent No. 5614617
GENERAL INFORMATION:
APPLICANT: Cook and Sanghvi
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate
TITLE OF INVENTION: Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5614617ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: July 27, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-0333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 2
 OTHER INFORMATION: 6-aza-thymidine substitution
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 4
 OTHER INFORMATION: 6-aza-thymidine substitution
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: 6-aza-thymidine substitution
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 8
 OTHER INFORMATION: 6-aza-thymidine substitution
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 10
 OTHER INFORMATION: 6-aza-thymidine substitution
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 12
 OTHER INFORMATION: 6-aza-thymidine substitution
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 14
 OTHER INFORMATION: 6-aza-thymidine substitution
 US-07-971-978-2

Query Match 1.4%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
 |||||
 Db 15 TATATATATATAT 1

RESULT 81
 US-09-371-772B-6068
 ; Sequence 6068, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MEH00,876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; PRIOR FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 6068
 ; LENGTH: 16
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-371-772B-6068

Query Match 1.4%; Score 15; DB 1; Length 16;
 Best Local Similarity 46.7%; Pred. No. 74;
 Matches 7; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 QY 1793 TGCTGTGTGTGTGT 1807
 Db 2 UGUGUGUGUGUGUGU 16
 RESULT 82
 US-09-371-772B-6070
 ; Sequence 6070, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor
 ; FILE REFERENCE: MEH00,876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; PRIOR FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 6070
 ; LENGTH: 16
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-371-772B-6070

Query Match 1.4%; Score 15; DB 1; Length 16;
 Best Local Similarity 53.3%; Pred. No. 74;
 Matches 8; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGT 1808
 |||||
 Db 1 GUGUGUGUGUGUGUG 15

RESULT 83
 US-08-853-998-400
 ; Sequence 400, Application US/08859998
 ; Patent No. 5994076
 ; GENERAL INFORMATION:
 ; APPLICANT: Chenchik, Alex
 ; APPLICANT: Jekhadze, George
 ; APPLICANT: Bibilashvili, Robert
 ; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL EXPRESSION
 ; NUMBER OF SEQUENCES: 1375
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 2200 Sand Hill Road, Suite 100
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/859,998
 ; FILING DATE: 21-MAY-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

```
;
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-0875
; TELEFAX: 415-322-5070
; INFORMATION FOR SEQ ID NO: 400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
;
US-08-859-998-400

Query Match      1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1731 GCTTGTGCGCAAGTGAATTGCTGTAACAAG 1761
      |||||
Db 2 GCTTGTACAGGCAAAATTCATTGCCACAAG 32

RESULT 84
US-09-225-928-400
; Sequence 400, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
;      Jokhadze, George
;      Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;      EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-0875
; TELEFAX: 415-322-5070
; INFORMATION FOR SEQ ID NO: 400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
```

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;
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 400:
US-09-225-928-400

Query Match      1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1731 GCTTGTGCGCAAGTGAATTGCTGTAACAAG 1761
      |||||
Db 2 GCTTGTACAGGCAAAATTCATTGCCACAAG 32

RESULT 85
US-09-225-201B-400
; Sequence 400, Application US/09225201B
; Patent No. 8489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
;      Jokhadze, George
;      Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;      EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 400:
US-09-225-201B-400

Query Match      1.4%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1731 GCTTGTGCGCAAGTGAATTGCTGTAACAAG 1761
      |||||
Db 2 GCTTGTACAGGCAAAATTCATTGCCACAAG 32

RESULT 86
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US-09-344-520-40/c
 ; Sequence 40, Application US/09344520
 ; Patent No. 6037176
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank Bennett
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Lex M. Cowser
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF integrin beta 3 EXPRESSION
 ; FILE REFERENCE: RTS-0070
 ; CURRENT APPLICATION NUMBER: US/09/344,520
 ; CURRENT FILING DATE: 1999-06-25
 ; NUMBER OF SEQ ID NOS: 47
 ; SEQ ID NO 40
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-344-520-40

Query Match 1.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 91;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1794 GTGTGTGTGTGTGTGT 1811
 Db 18 GTGTGTGTGTGTGTGT 1

RESULT 87
 US-08-153-051B-58
 ; Sequence 58, Application US/08153051B
 ; Patent No. 5645986
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael D. West
 ; APPLICANT: Jerry W. Shay
 ; APPLICANT: Woodring E. Wright
 ; APPLICANT: Elizabeth Blackburn
 ; APPLICANT: Nam Woo Kim
 ; APPLICANT: Calvin B. Harley
 ; APPLICANT: Scott L. Weinrich
 ; APPLICANT: Catherine Strahl
 ; APPLICANT: Michael J. McEachern
 ; APPLICANT: Homayoun Vaziri
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
 ; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
 ; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/153,051B
 FILING DATE: No. 5645986ember 12, 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/038,766
 FILING DATE: March 24, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 204/195
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-153-051B-58
 Query Match 1.4%; Score 14.4; DB 1; Length 16;
 Best Local Similarity 93.8%; Pred. No. 87;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTG 1808
 Db 1 TGGGTGTGTGTGTGTG 16

RESULT 88
 US-08-060-952C-57
 ; Sequence 57, Application US/08060952C
 ; Patent No. 5695932
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael D. West
 ; APPLICANT: Jerry W. Shay
 ; APPLICANT: Woodring E. Wright
 ; APPLICANT: Elizabeth Blackburn
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
 ; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
 ; TITLE OF INVENTION: TELOMERASE ACTIVITY
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/060,952C
 FILING DATE: May 13, 1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/882,438
 FILING DATE: May 13, 1992
 APPLICATION NUMBER: 08/038,766
 FILING DATE: March 24, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 202/045
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-060-952C-57

Query Match 1.4%; Score 14.4; DB 1; Length 16;

Best Local Similarity 93.8%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808
Db 1 TGGGTGTGTGTGTG 16

RESULT 89
US-08-151-477A-58
; Sequence 58, Application US/08151477A
; Patent No. 5830644
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,477A
; FILING DATE: March 24, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/169
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808
Db 1 TGGGTGTGTGTGTG 16

RESULT 90

US-08-819-867-80
; Sequence 80, Application US/08819867
; Patent No. 6007989
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine M. Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Jerry Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth H. Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO
; TITLE OF INVENTION: TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,867
; FILING DATE: March 14, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/153,051
; FILING DATE: No. 6007989ember 12, 1993
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-819-867-80
Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1808
Db 1 TGGGTGTGTGTGTG 16

RESULT 91
US-08-464-011B-57
; Sequence 57, Application US/08464011B
; Patent No. 6368789
; GENERAL INFORMATION:
; APPLICANT: Michael D. West

Jerry W. Shay
Woodring E. Wright
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
RELATED TO TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,011B
FILING DATE: 05-Jun-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-08-464-011B-57

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
DB 1 TGGGTGTGTGTGTGTG 16

RESULT 92
US-09-378-535-80
Sequence 80, Application US/09378535
Patent No. 6551774
GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. McEachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF

CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-378-535-80

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
DB 1 TGGGTGTGTGTGTGTG 16

RESULT 93
US-09-371-772B-6071
Sequence 6071, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
ated to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MEH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 6071

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; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6071

Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GGTGTGTGTGTGTCT 1809
DB 1 GUGUGUGUGUGUGGU 16

RESULT 94
US-08-105-483-235
; Sequence 235, Application US/08105483
; Patent No. 5494807
; GENERAL INFORMATION:
; APPLICANT: Paolotti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; TITLE OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,483
; FILING DATE: 12-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 08-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 235:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-105-483-235

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792
DB 1 TTTATATTGTAATAT 16

RESULT 95
US-08-373-124A-1058/c
; Sequence 1058, Application US/08373124A
; Patent No. 5546042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.

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; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1058:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-1058

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826
Db 17 TGTATATATATATATA 2

RESULT 99
US-08-486-969-52
; Sequence 52, Application US/08486969
; Patent No. 5843456
; GENERAL INFORMATION:
; APPLICANT: Paolotti, Enzo
; APPLICANT: Maki, Joanne
; TITLE OF INVENTION: RECOMBINANT POXVIRUS - RABIES
; TITLE OF INVENTION: COMPOSITIONS AND COMBINATION COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,969
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-486-969-52

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1777 TTTATATTGTAATAT 1792
Db 1 TTTATATTGTAATAT 16
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```

RESULT 100
US-08-584-040-4159
; Sequence 4159, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-4159

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1749 TGCTGTAAACGA 1764
Db 2 UGCCUGUACCAAGCCA 17

RESULT 101
US-09-321-005A-13/c
; Sequence 13, Application US/09321005A
; Patent No. 6503710
; GENERAL INFORMATION:
; APPLICANT: Gut, Ivo
; TITLE OF INVENTION: Mutation Analysis Using Mass Spectrometry
; FILE REFERENCE: E0004/7065
; CURRENT APPLICATION NUMBER: US/09/321,005A
; CURRENT FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 17
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Hypothetical Sequence for Exemplary Purposes
; Patent No. 6503710
US-09-321-005A-13

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred.No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1891 ATATTTCATGTTAGC 1906
    |||:|||||
Db 16 ATATTTCATGTCAGC 1

RESULT 102
US-09-371-772B-1926
; Sequence 1926, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1926
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1926

Query Match 1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred.No. 94;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1749 TGCTGTATCAAGCCA 1764
    :|||:|||||
Db 2 UGCCUGUACCAAGCCA 17

RESULT 103
US-09-371-772B-6656
; Sequence 6656, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040

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; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6656
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6656

Query Match      1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred.No.94;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1750 GCCTGTAAACAGCCAG 1765
        |||..|||
Db       1 GCUGUACCAGCCAG 16

RESULT 104
US-09-496-694B-235
; Sequence 235, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swazyce
; APPLICANT: Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 235
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-496-694B-235

Query Match      1.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred.No.1.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1814 ATATATATATATGTCACA 1832
        |||||||
Db       1 ACATATATATATTAACA 19

RESULT 105
US-08-222-177A-436/c
; Sequence 436, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-da)n.(gg-ct)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/222,177A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/341,562
;; FILING DATE: 21-APR-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sara, Charles S.
;; REGISTRATION NUMBER: 30,492
;; REFERENCE/DOCKET NUMBER: 09865.601
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (608) 831-2100
;; TELEFAX: (608) 831-2106
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 436:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-222-177A-436

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1807
Db 14 GTGTGTGTGTGT 1

RESULT 106
US-09-913-514-27
; Sequence 27, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine
; FILE REFERENCE: 0216-0454P
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Varicella virus
US-09-913-514-27

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATA 1826
Db 1 TATATATATATA 14

RESULT 107
US-09-913-514-27/c
; Sequence 27, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:

;; APPLICANT: GOMI, Yasuyuki
;; APPLICANT: SUNAMACHI, Hiroki
;; APPLICANT: TAKAHASHI, Michiaki
;; APPLICANT: YAMANISHI, Koichi
;; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine
;; FILE REFERENCE: 0216-0454P
;; CURRENT APPLICATION NUMBER: US/09/913,514
;; CURRENT FILING DATE: 2001-12-07
;; PRIOR APPLICATION NUMBER: PCT/JP01/00678
;; PRIOR FILING DATE: 2001-01-31
;; PRIOR APPLICATION NUMBER: JP 2000-62734
;; PRIOR FILING DATE: 2000-01-31
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 27
;; LENGTH: 14
;; TYPE: DNA
;; ORGANISM: Varicella virus
US-09-913-514-27

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATA 1826
Db 14 TATATATATATA 1

RESULT 108
PCT-US92-00282-27
; Sequence 27, Application PC/TUS9200282
; GENERAL INFORMATION:
; APPLICANT: OWENS, IDA S.
; APPLICANT: RITTER, JOSEPH K.
; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION THEREIN.
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00282
; FILING DATE: 19920110
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US92-00282-27

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;

Matches	14;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy 1813 TATATATATATATA 1826
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Db 1 TATATATATATATA 14

RESULT 109

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PCT-US92-00282-27/c
; Sequence 27, Application PC/TUS9200282
;
; GENERAL INFORMATION:
;
; APPLICANT: OWENS, IDA S.
; APPLICANT: RITTER, JOSEPH K.
; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION
; TITLE OF INVENTION: THEREIN.
;

```

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBAY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
325 200326 5201

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; ZIP# 20036-5801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In License #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APLICATION NUMBER SCT#159/100392

```

REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 91532-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944
TELEX: 6714527 CUSH
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
DOC: US92-00382-37

Query Match 1.3%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No.89;
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 1813 TATATATATATA 1826
 |||||
 Db 14 TATATATATATA 1

RESULT 110

US-09-479-005A-336
Sequence 336, Application US/09479005A
Patent No. 6656731
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBH00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/444,209
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: US 09/159,274
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: US 60/059,473

```

; PRIOR FILING DATE: 1997-09-22
;
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: Patent version 3.0
; SEQ ID NO 336
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-479-005A-336

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Query Match 1.3%; Score 14; DB 1; Length 16;
Best Local Similarity 71.4%; Pred. No. 96;
Matches 10; Conservative 4; Mismatches 0; Indels

Qy 1392 GTTAAGACTTGACA 1405
| | | | | : : :
Db 1 GUUAAGACUUGACA 14

RESULT 111
US-08-373-124A-1060/c
; Sequence 1060, Application US/08373124A
; Patent No. 5646042

```

/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Draper, Kenneth
/ APPLICANT: McGwiggan, James
/ APPLICANT: Jarvis, Thale
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
/ TREATMENT OF RESTENOSIS AND
/ TITLE OF INVENTION: CANCER USING RIBOZYMES
/ NUMBER OF SEQUENCES: 2627.
/ CORRESPONDENCE ADDRESS:
/

```

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

```

1 ZIP: 90071
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
6
7 MEDIUM TYPE:
8
9 COMPUTER: IBM Compatible
10
11 OPERATING SYSTEM: IBM P.C. DOS 5.0
12
13 SOFTWARE: Word Perfect 5.1
14
15 CURRENT APPLICATION DATA:
16
17 APPLICATION NUMBER: US/08/373,124A
18
19 FILING DATE: January 13, 1995
20
21 PRIOR APPLICATION DATA:

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? ERROR REFLECTION DATA.
?
? APPLICATION NUMBER: 08/245,466
? FILING DATE: May 18, 1994
? APPLICATION NUMBER: 08/192,943
? FILING DATE: February 7, 1994
? APPLICATION NUMBER: 07/987,132
? FILING DATE: December 7, 1992
? APPLICATION NUMBER: 07/936,422
? FILING DATE: November 26, 1992
?

```

FILED DATE: AUGUST 07, 1954
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCES/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1060:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-1060

US-08-373-124A-1060

Query Match 1.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1811 TGTATATATATATA 1824
 DB 15 TGTATATATATATA 2

RESULT 112

US-08-373-124A-1855
 ; Sequence 1855, Application US/08373124A
 ; Patent No. 5646042

GENERAL INFORMATION:
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Jarvis, Thale
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
 ; TREATMENT OF RESTENOSIS AND
 ; TITLE OF INVENTION: CANCER USING RIBOZYMES
 ; NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage

COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/373,124A
 ; FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994
 ; APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994
 ; APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992
 ; APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992
 ; ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440

TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 1855:

SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs

TYPE: nucleic acid
 ; STRANDEDNESS: single

TOPOLOGY: linear
 ; US-08-373-124A-1855

Query Match 1.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 57.1%; Pred. No. 1e+02;
 Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAAA 1776
 DB 4 CAGAUUUUUAAAA 17

RESULT 113

US-08-373-124A-1857
 ; Sequence 1857, Application US/08373124A
 ; Patent No. 5646042

GENERAL INFORMATION:
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Jarvis, Thale
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
 ; TREATMENT OF RESTENOSIS AND
 ; TITLE OF INVENTION: CANCER USING RIBOZYMES
 ; NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage

COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/373,124A
 ; FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994
 ; APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994
 ; APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992
 ; APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992
 ; ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440

TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 1857:

SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs

TYPE: nucleic acid
 ; STRANDEDNESS: single

TOPOLOGY: linear
 ; US-08-373-124A-1857

Query Match 1.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 57.1%; Pred. No. 1e+02;
 Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAAA 1776
 DB 3 CAGAUUUUUAAAA 16

RESULT 114

US-08-373-124A-1859
 ; Sequence 1859, Application US/08373124A
 ; Patent No. 5646042

GENERAL INFORMATION:
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1859:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-373-124A-1859

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1e-02;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776

Db 2 CAGAUUUUUAAAA 15

RESULT 115

US-08-373-124A-1861
Sequence 1861, Application US/08373124A

Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwiggen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND

CANCER USING RIBOZYMES

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A

FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1861:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-373-124A-1861

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1e-02;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776

Db 1 CAGAUUUUUAAAA 14

RESULT 116

US-08-435-628-1060/c
Sequence 1060, Application US/08435628

Patent No. 5817796

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwiggen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND

CANCER USING RIBOZYMES

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/435,628
;; FILING DATE: 05-MAY-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/373,124
;; FILING DATE: January 13, 1995
;; APPLICATION NUMBER: 08/245,466
;; FILING DATE: May 18, 1994
;; APPLICATION NUMBER: 08/192,943
;; FILING DATE: February 7, 1994
;; APPLICATION NUMBER: 07/987,132
;; FILING DATE: December 7, 1992
;; APPLICATION NUMBER: 07/936,422
;; FILING DATE: August 26, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 209/035
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1060:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-435-628-1060

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1811 TGTATATATATATA 1824
DB 15 TGTATATATATATA 2

RESULT 117
US-08-435-628-1855
; Sequence 1855, Application US/08/435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124

;; FILING DATE: January 13, 1995
;; APPLICATION NUMBER: 08/245,466
;; FILING DATE: May 18, 1994
;; APPLICATION NUMBER: 08/192,943
;; FILING DATE: February 7, 1994
;; APPLICATION NUMBER: 07/987,132
;; FILING DATE: December 7, 1992
;; APPLICATION NUMBER: 07/936,422
;; FILING DATE: August 26, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 209/035
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 1855:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-435-628-1855

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAAA 1776
DB 4 CAGAUUUUUAAAA 17

RESULT 118
US-08-435-628-1857
; Sequence 1857, Application US/08/435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132

REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1859:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-1859

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1e-02;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776
Db 2 CAGAUUUUUAAAA 15

RESULT 120
US-08-435-628-1861
Sequence 1861, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: U.S.A.
90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1861:

FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1857:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-1857

Query Match 1.3%; Score 14; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 1e-02;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776
Db 3 CAGAUUUUUAAAA 16

RESULT 119
US-08-435-628-1859
Sequence 1859, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: U.S.A.
90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327

```
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 17 base pairs
/ ; TYPE: nucleic acid
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
US-08-435-628-1861

Query Match
Best Local Similarity 1.3%; Score 14; DB 1; Length 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1763 CAGATTTTAAAA 1776
|||||:|||||
Db 1 CAGAUUUUUAAAA 14

RESULT 121
US-08-849-021-16/c
; Sequence 16, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESS: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-849-021-16

Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
|||||:|||||
Db 17 TGTGTGTGTGTGTG 4

; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-874/c

Query Match
Best Local Similarity 1.3%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1765 GATTTTAAAAATTTAT 1781
|||||:|||||
Db 17 GATTTTAAAAATATAT 1

RESULT 123
US-08-435-628-874/c
; Sequence 874, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEEX: 67-3510
; INFORMATION FOR SEQ ID NO: 874:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-874
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628

FILING DATE: 05-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124

FILING DATE: January 13, 1995

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 874:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-435-628-874

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.le+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1765 GATTTTAAATTTAT 1781

Db 17 GATTTTAAATATAT 1

RESULT 124

US-08-292-620A-1988/c

Sequence 1988, Application US/08292620A

Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

APPLICANT: Sean Sullivan

APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF

DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: INTRACELLULAR ADHESION

TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1988:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1988

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.le+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTGAGAGGAA 1553

Db 17 GGTAAATAGAGAGGAA 1

RESULT 125

US-08-851-843A-132

Sequence 132, Application US/08851843A

Patent No. 6093809

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin

APPLICANT: Andrews, William H.

TITLE OF INVENTION: No. 6093809el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/846,017
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/844,419
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/724,643
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-851-843A-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
DB 1 TTTTATTTTGTGTTTT 17

RESULT 126
US-09-071-845-1988/c
; Sequence 1988, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US/08/292,620
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1988:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1988

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 GTGTAATTGAGAGGAA 1553
DB 17 GGGTAAATGAGAGGAA 1

RESULT 127
US-09-250-075-5
; Sequence 5, Application US/09250075
; Patent No. 6207819
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Mathiah
; APPLICANT: Maier, Martin A
; TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of
; TITLE OF INVENTION: Mixed Backbone Oligomeric Compounds
; FILE REFERENCE: ISIS3299
; CURRENT APPLICATION NUMBER: US/09/250,075
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(17)
; OTHER INFORMATION: 2'-methoxyethoxy (MOE); modified linkage
; OTHER INFORMATION: Description of Artificial Sequence: No. 6207819el
; OTHER INFORMATION: Sequence
US-09-250-075-5

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTTT 1881
DB 1 TTTTATTTTGTGTTTT 17

RESULT 128

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US-08-854-050-132
; Sequence 132, Application US/08894050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-430-323-132
; Query Match 1.3%; Score 13.8; DB 1; Length 17;
; Best Local Similarity 88.2%; Pred. No. 1.1e+02;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTATTTGTTTT 1881
DB 1 TTTTATTATTTT 17
RESULT 129
US-09-430-323-132
; Sequence 132, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-08-584-040-2550
; Sequence 2550, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES OR
```

;; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
;; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
;; TITLE OF INVENTION: GROWTH FACTOR
;; NUMBER OF SEQUENCES: 8502
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles
;; CITY: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 2550:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-584-040-2550
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 5.9%; Pred. No. 1.1e+02;
Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;
QY 1864 CTTTATTATTTGTTT 1880
Db 1 CUUUUUUUUUUUUUU 17
;;
;; RESULT 131
;; US-08-584-040-6047
;; Sequence 6047, Application US/08584040
;; Patent No. 6346398
;; GENERAL INFORMATION:
;; APPLICANT: Pavco, Pamela
;; APPLICANT: McSwiggen, James
;; APPLICANT: Stinchcomb, Dan T.
;; APPLICANT: Escobedo, Jaime
;; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
;; TITLE OF INVENTION: TREATMENT OF DISEASES OR
;; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
;; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
;; TITLE OF INVENTION: GROWTH FACTOR
;; NUMBER OF SEQUENCES: 8502
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles
;; CITY: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 6047:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-584-040-6047
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 5.9%; Pred. No. 1.1e+02;
Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 6047:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-584-040-6047
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1639 TGTTCCTTAAGTCAGAA 1655
Db 1 UGUCCCUAAUUCAGAA 17
;;
;; RESULT 132
;; US-08-584-040-6049
;; Sequence 6049, Application US/08584040
;; Patent No. 6346398
;; GENERAL INFORMATION:
;; APPLICANT: Pavco, Pamela
;; APPLICANT: McSwiggen, James
;; APPLICANT: Stinchcomb, Dan T.
;; APPLICANT: Escobedo, Jaime
;; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
;; TITLE OF INVENTION: TREATMENT OF DISEASES OR
;; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
;; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
;; TITLE OF INVENTION: GROWTH FACTOR
;; NUMBER OF SEQUENCES: 8502
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Suite 4700
;; STATE: Los Angeles
;; CITY: California
;; COUNTRY: U.S.A.
;; ZIP: 90071-2066
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/584,040
;; FILING DATE: January 11, 1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/005,974
;; FILING DATE: October 26, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 218/064
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 6047:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
US-08-584-040-6047
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6049:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-6049

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1643 CCTTAAGTCAGAACAGC 1659
Db 1 CCUUAUUCAGAACCC 17

RESULT 133
US-09-619-103-23/c
; Sequence 23, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-23

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1881
Db 17 TTTTATTTTGTGTTT 1

RESULT 134
US-09-726-096A-5
; Sequence 5, Application US/09726096A
; Patent No. 6462184
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Maier, Martin A.
; TITLE OF INVENTION: Compounds Processes And Intermediates For Synthesis Of Mixed Back
; FILE REFERENCE: IS154528
; CURRENT APPLICATION NUMBER: US/09/726,096A
; CURRENT FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate
; OTHER INFORMATION: internucleoside linkage
US-09-726-096A-5

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1881
Db 1 TTTTATTTTGTGTTT 17

RESULT 135
US-09-371-772B-1074
; Sequence 1074, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1074
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1074

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 5.9%; Pred. No. 1.1e+02;
Matches 1; Conservative 14; Mismatches 2; Indels 0; Gaps 0;

Qy 1864 CTTTATTTTGTGTTT 1880
Db 1 CUUUUUUUUUUUUUUUU 17

RESULT 136
US-09-371-772B-2884
; Sequence 2884, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10

```

, PRIOR APPLICATION NUMBER: US 60/005,974
, PRIOR FILING DATE: 1995-10-26
, PRIOR APPLICATION NUMBER: US 08/584,040
, PRIOR FILING DATE: 1996-01-08
, NUMBER OF SEQ ID NOS: 14225
, SOFTWARE: Patent in version 3.0
, SEQ ID NO 2884
, LENGTH: 17
, TYPE: RNA
, ORGANISM: Mus sp.
US-09-371-772B-2884

```

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 2; Indels

RESULT 137

```

RES01113,
US-09-371-772B-2886
; Sequence 2886, Application US/09371772B
; Patent No. 5566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for
; FILE REFERENCE: Levels of Vascular E
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2886
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2886

```

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.1e+02;
Matches 12; Conservative 3; Mismatches 2; Indels

RESULT 138

```

RESULI 138
US-09-827-998-384
; Sequence 384, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881

```

```

; SOFTWARE: Aemica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 384
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-827-998-384

```

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels

RESULT 139

```

RES001 139
US-09-827-998-385
; Sequence 385, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL
; FILE REFERENCE: MDAMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 385
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-385

```

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.e+02;
Matches 15; Conservative 0; Mismatches 2; Indels

RESULT 140

```

RESULI 140
US-09-827-998-386
; Sequence 386, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 386
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-386

```


Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTG 1810
 ||||| ||||| |||||
 DB 1 GTGTGTGTGTGTGTGTG 17

RESULT 141
 US-09-827-998-387
 ; Sequence 387, Application US/09827998
 ; Patent No. 6656700
 ; GENERAL INFORMATION:
 ; APPLICANT: Gu, Yizhong
 ; APPLICANT: Shannon, Mark
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: MDMORF-8
 ; CURRENT APPLICATION NUMBER: US/09/827,998
 ; CURRENT FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Aecomica Sequence Listing Engine
 ; Patent No. 6656700
 ; SEQ ID NO 387
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-827-998-387

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809
 ||||| ||||| |||||
 DB 1 TGTGTGTGTGTGTGTGT 17

RESULT 142
 US-09-827-998-388
 ; Sequence 388, Application US/09827998
 ; Patent No. 6656700
 ; GENERAL INFORMATION:
 ; APPLICANT: Gu, Yizhong
 ; APPLICANT: Shannon, Mark
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: MDMORF-8
 ; CURRENT APPLICATION NUMBER: US/09/827,998
 ; CURRENT FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Aecomica Sequence Listing Engine
 ; Patent No. 6656700
 ; SEQ ID NO 388
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-827-998-388

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTGTA 1814
 ||||| ||||| |||||

DB 1 GTGTGTGTGTGTGTGTA 17

RESULT 143
 US-09-827-998-389
 ; Sequence 389, Application US/09827998
 ; Patent No. 6656700
 ; GENERAL INFORMATION:
 ; APPLICANT: Gu, Yizhong
 ; APPLICANT: Shannon, Mark
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: MDMORF-8
 ; CURRENT APPLICATION NUMBER: US/09/827,998
 ; CURRENT FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Aecomica Sequence Listing Engine
 ; Patent No. 6656700
 ; SEQ ID NO 389
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-827-998-389

Query Match 1.3%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTGTAT 1815
 ||||| ||||| |||||
 DB 1 TGTGTGTGTGTGTGTAT 17

RESULT 144
 US-08-153-051B-52
 ; Sequence 52, Application US/08153051B
 ; Patent No. 5645986
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael D. West
 ; APPLICANT: Jerry M. Shay
 ; APPLICANT: Woodring E. Wright
 ; APPLICANT: Elizabeth Blackburn
 ; APPLICANT: Nam Woo Kim
 ; APPLICANT: Calvin B. Harley
 ; APPLICANT: Scott L. Weinrich
 ; APPLICANT: Catherine Strahl
 ; APPLICANT: Michael J. McEachern
 ; APPLICANT: Homayoun Vaziri
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
 ; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
 ; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/153,051B
 ; FILING DATE: No. 5645986ember 12, 1993
 ; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 204/195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-153-051B-52

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1792 TTGTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTGTG 15

RESULT 145
US-08-060-952C-51
; Sequence 51, Application US/08060952C
; Patent No. 5695932
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/060,952C
; FILING DATE: May 13, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-060-952C-51

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1792 TTGTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTGTG 15

RESULT 146
US-08-151-477A-52
; Sequence 52, Application US/08151477A
; Patent No. 5830644
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,477A
; FILING DATE: No. 5830644ember 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-151-477A-52

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

```

QY 1792 TTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTG 15

RESULT 147
US-08-819-867-79
Sequence 79, Application US/08819867
Patent No. 6007989
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine M. Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Jerry Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth H. Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO
TITLE OF INVENTION: TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 6007989ember 12, 1993
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-867-79

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTG 15

RESULT 148
US-08-464-011B-51
Sequence 51, Application US/08464011B
Patent No. 6369789
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
RELATED TO TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,011B
FILING DATE: 05-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-08-464-011B-51
Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1806
Db 1 TGGTGTGTGTGTG 15

RESULT 149
US-09-475-947A-83/c
Sequence 83, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes

FILE REFERENCE: UTS0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 83
LENGTH: 15
TYPE: DNA
ORGANISM: human
US-09-475-947A-83

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATAT 1825
DB 15 TTTATATATATAT 1

RESULT 150
US-09-378-535-79
Sequence 79, Application US/09378535
Patent No. 6551774
GENERAL INFORMATION:
APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-AUG-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/819,867
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-378-535-79

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1792 TTGTGTGTGTGTG 1806
DB 1 TGGTGTGTGTGTG 15

RESULT 151
US-09-371-772B-6067
Sequence 6067, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00.876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 6067.
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-6067

Query Match 1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
QY 1791 ATTGTGTGTGTGTG 1805
DB 2 ACUGUGUGUGUGUGU 16

RESULT 152
US-09-479-005A-185/c
Sequence 185, Application US/09479005A
Patent No. 6656731
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MBH00-984-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/444,209
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: US 09/159,274
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: US 60/059,473
PRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: Patentin version 3.0
SEQ ID NO 185
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens
US-09-479-005A-185

Query Match 1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGT 1879
DB 15 TTTTATTTTATTT 1

RESULT 153
US-08-373-124A-1060
; Sequence 1060, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1060:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-1060

Query Match 1.3%; Score 13.4; DB 1; Length 17;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
DB 2 UAUUAUUAUUAUACAU 16

RESULT 154
US-08-435-628-1060
; Sequence 1060, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1060:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1060

Query Match 1.3%; Score 13.4; DB 1; Length 17;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
DB 2 UAUUAUUAUUAUACAU 16

RESULT 155
US-08-849-021-13/c
; Sequence 13, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:

```

; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
;
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; US-08-849-021-13

```

```

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1793 TGTGTGTGTGTGT 1805
Db 13 TGTGTGTGTGTGT 1

```

```

RESULT 156
US-08-849-021-15
; Sequence 15, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
;
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; US-08-849-021-15

```

```

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1793 TGTGTGTGTGTGT 1805
Db 1 TGTGTGTGTGTGT 13

```

```

RESULT 157
US-09-393-783A-41
; Sequence 41, Application US/09393783A
; Patent No. 6355428
; GENERAL INFORMATION:
; APPLICANT: Schroth, Gary P.
; APPLICANT: Bruice, Thomas Wayne
; APPLICANT: Suh, Young J.
; TITLE OF INVENTION: Nucleic Acid Ligand Interaction Assays
; FILE REFERENCE: 4600-0128.30
; CURRENT APPLICATION NUMBER: US/09/393,783A
; CURRENT FILING DATE: 1999-10-09
; PRIOR APPLICATION NUMBER: US 09/151,890
; PRIOR FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)-(13)
; OTHER INFORMATION: synthesized test oligonucleotide for binding
; OTHER INFORMATION: studies
;
; US-09-393-783A-41

```

```

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1794 GTGTGTGTGTGTGT 1806
Db 1 GTGTGTGTGTGTGT 13

```

```

RESULT 158

```

```

US-09-151-890B-41
; Sequence 41, Application US/09151890B
; Patent No. 6420109
; GENERAL INFORMATION:
; APPLICANT: Gary P. Schroth
; APPLICANT: Thomas Wayne Bruice
; APPLICANT: Young J. Suh
; TITLE OF INVENTION: Nucleic Acid Ligand Interaction Assays
; FILE REFERENCE: 4600-0128
; CURRENT APPLICATION NUMBER: US/09/151,890B
; CURRENT FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)...(13)
; OTHER INFORMATION: synthesized test oligonucleotide for binding
; OTHER INFORMATION: studies
US-09-151-890B-41

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806
DB 1 GTGTGTGTGTGTG 13

RESULT 159
US-09-475-947A-83
; Sequence 83, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 15
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-83

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
DB 1 ATATATATATATA 13

RESULT 160
US-08-291-932A-121/c
; Sequence 121, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF

```

```

; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; PRIOR APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-291-932A-121

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2152 TCACCTGGAAGCA 2164
DB 15 TCACCTGGAAGCA 3

RESULT 161
US-08-291-932A-194/c
; Sequence 194, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-291-932A-194

Query Match 1.2% Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2152 TCACCTGGAAGCA 2164
Db 15 TCACCTGGAAGCA 3

RESULT 162
US-08-291-932A-310/c
; Sequence 310, Application US/08/291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514

```

Two

```

; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 310:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-291-932A-310

Query Match 1.2% Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2152 TCACCTGGAAGCA 2164
Db 15 TCACCTGGAAGCA 3

RESULT 163
US-08-812-951B-1
; Sequence 1, Application US/08812951B
; Patent No. 6297006
; GENERAL INFORMATION:
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Drmanac, Snezana
; APPLICANT: Hou, Aaron
; APPLICANT: Houser, Brian
; TITLE OF INVENTION: Methods and Compositions for
; TITLE OF INVENTION: Detection or Quantification of Nucleic Acid Species
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McCutchen, Doyle, Brown & Enersen LLP
; STREET: Three Embarcadero Center
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,951B
; FILING DATE: 04-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/784747
; FILING DATE: 16-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kumamoto, Andrew A.
; REGISTRATION NUMBER: 40,690
; REFERENCE/DOCKET NUMBER: 20411-701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-393-2000
; TELEFAX: 415-393-2286
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

```

Two


```

Sequence 2, Application US/08784747
Patent No. 6309824
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Detection or Quantification of Nucleic Acid Species
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen, Doyle, Brown & Enersen LLP
STREET: Three Embarcadero Center
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,747
FILING DATE: 16-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kumamoto, Andrew A
REGISTRATION NUMBER: 40,690
REFERENCE/DOCKET NUMBER: 20411-708
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-393-2000
TELEFAX: 415-393-2286
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-784-747-2

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.le+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTATTTTG 1876
DB 1 CCTTTTNTTTTGG 14

RESULT 166
US-08-784-747-3/C
Sequence 3, Application US/08784747
Patent No. 6309824
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Detection or Quantification of Nucleic Acid Species
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen, Doyle, Brown & Enersen LLP
STREET: Three Embarcadero Center
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/784,747
FILING DATE: 16-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kumamoto, Andrew A
REGISTRATION NUMBER: 40,690
REFERENCE/DOCKET NUMBER: 20411-708
TELEPHONE: 415-393-2000
TELEFAX: 415-393-2286
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
US-08-784-747-3

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876

DB 15 CCTTTTNTTTTG 2

RESULT 167

US-09-409-778-9
Sequence 9, Application US/09409778

Patent No. 6472173
GENERAL INFORMATION:
APPLICANT: Ford, John
TITLE OF INVENTION: A NOVEL CHEMOKINE RECEPTOR OBTAINED FROM
TITLE OF INVENTION: A CDNA LIBRARY OF FETAL LIVER-SPLEEN
FILE REFERENCE: 20411-742CON2 (now 28110/36057B)
CURRENT APPLICATION NUMBER: US/09/409,778
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/12829
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/236,166
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: US 09/106,800
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence assembly process
NAME/KEY: misc_feature
LOCATION: (8)...(8)
OTHER INFORMATION: n = A, T, C, G or 1-(2-deoxy-D-ribofuranosyl)-3-nitropyrrrole
US-09-409-778-9

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876

DB 1 CCTTTTNTTTTG 14

RESULT 168

US-09-409-778-10/c

Sequence 10, Application US/09409778
Patent No. 6472173
GENERAL INFORMATION:
APPLICANT: Ford, John
TITLE OF INVENTION: A NOVEL CHEMOKINE RECEPTOR OBTAINED FROM
TITLE OF INVENTION: A CDNA LIBRARY OF FETAL LIVER-SPLEEN
FILE REFERENCE: 20411-742CON2 (now 28110/36057B)
CURRENT APPLICATION NUMBER: US/09/409,778
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/12829
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/236,166
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: US 09/106,800
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence assembly process
NAME/KEY: misc_feature
LOCATION: (8)...(8)
OTHER INFORMATION: n = A, T, C, G or 1-(2-deoxy-D-ribofuranosyl)-3-nitropyrrrole
US-09-409-778-10

Query Match 1.2%; Score 13; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876

DB 15 CCTTTTNTTTTG 2

RESULT 169

US-09-479-005A-117
Sequence 117, Application US/09479005A
Patent No. 6656731
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MEB00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/444,209
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: US 09/159,274
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: US 60/059,473
PRIOR FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 1208
SOFTWARE: PatentIn version 3.0
SEQ ID NO 117
LENGTH: 16
TYPE: RNA
ORGANISM: Homo sapiens
US-09-479-005A-117

Query Match 1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 38.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 2268 TTTTTCCTATATAA 2280

DB 1 UUUUUUUAUAAA 13

RESULT 170

US-07-971-978-36

Sequence 36, Application US/07971978
Patent No. 5614617
GENERAL INFORMATION:
APPLICANT: Cook and Sanghvi
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate
TITLE OF INVENTION: Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5614617ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: July 27, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-0333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:

NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: 5-fluoro-2'-deoxyuridine
OTHER INFORMATION: substitution
US-07-971-978-36
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTATTGTTT 1880
Db 1 TTTTATTATTGTTT 16
RESULT 171
US-07-971-978-42
Sequence 42, Application US/07971978
Patent No. 5614617
GENERAL INFORMATION:
APPLICANT: Cook and Sanghvi
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate
TITLE OF INVENTION: Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5614617ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: July 27, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-0333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site

LOCATION: 10
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: 5-bromo-2'-deoxyuridine
OTHER INFORMATION: substitution
US-07-971-978-42
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
|||||
DB 1 TTTTATTTTGTGTTT 16

RESULT 172
US-07-971-978-60
Sequence 60, Application US/07971978
Patent No. 5614617
GENERAL INFORMATION:
APPLICANT: Cook and Sanghvi
TITLE OF INVENTION: Nuclease Resistant, Pyrimidine
TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate
TITLE OF INVENTION: Gene Expression
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5614617ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,978
FILING DATE: February 18, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/558,806
FILING DATE: July 27, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-0333

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13

OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: 5-iodo-2'-deoxyuridine
OTHER INFORMATION: substitution
US-07-971-978-60
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
DB 1 TTTTATTTTGTGTTT 16
RESULT 173
US-08-415-370-2
Sequence 2, Application US/08415370
Patent No. 580155
GENERAL INFORMATION:
APPLICANT: Kutyavin, Igor V.
APPLICANT: Lukhtanov, Eugeny A.
APPLICANT: Gamper, Howard B.
APPLICANT: Meyer, Jr., Rich B.
TITLE OF INVENTION: COVALENTLY LINKED OLIGONUCLEOTIDE MINOR
TITLE OF INVENTION: GROOVE BINDER CONJUGATES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: KLEIN & SZEKERES
CITY: Irvine
STATE: CA
COUNTRY: USA
ZIP: 92715
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,370
FILING DATE: 03-APR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Szekeres, Gabor L.
REGISTRATION NUMBER: 28,675
REFERENCE/DOCKET NUMBER: 491-09-PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-854-5502
TELEFAX: 714-854-4897
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-415-370-2
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1865 TTTTATTTTGTGTTT 1880
DB 1 TTTTATTTTGTGTTT 16

```
RESULT 174
US-08-687-551-15
; Sequence 15, Application US/08687551
; Patent No. 5856435
; GENERAL INFORMATION:
; APPLICANT: BAZILE, Didier
; APPLICANT: EMILE, Carole
; APPLICANT: HELENE, Claude
; APPLICANT: SPENLEHAUER, Gilles
; TITLE OF INVENTION: NUCLEIC ACID-CONTAINING COMPOSITION, ITS
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/687,551
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/01381
; FILING DATE: 08-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00098
; FILING DATE: 27-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph. D. Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST94007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
US-08-687-551-15
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 1 TTTTATTTTGTGTTT 16

RESULT 175
US-08-893-614-1
; Sequence 1, Application US/08893614
; Patent No. 5936077
; GENERAL INFORMATION:
; APPLICANT: PELEIDERER, Wolfgang
; APPLICANT: BEIER, Markus
; TITLE OF INVENTION: SOLID PHASE SYNTHESIS OF
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,614
; FILING DATE: 11-JUL-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19627898.8
; FILING DATE: 11-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 18748/343/HOCE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-893-614-1
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1836 ATCTAAGTTAATTAA 1851
DB 1 ATTTAATTAAATTAA 16

RESULT 176
US-09-141-764-2
; Sequence 2, Application US/09141764
; Patent No. 6084102
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Meyer, Jr., Rich B.
; TITLE OF INVENTION: COVALENTLY LINKED OLIGONUCLEOTIDE
; TITLE OF INVENTION: MINOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLEIN & SZEKERES
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: USA
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/141,764
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Szekeres, Gabor L.
REGISTRATION NUMBER: 28,675
REFERENCE/DOCKET NUMBER: 491-09-PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-854-5502
TELEFAX: 714-854-4897
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-141-764-2

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

RESULT 177
US-08-851-843A-131/c
Sequence 131, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-851-843A-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 178
US-08-854-050-131/c
Sequence 131, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 131:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-854-050-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
|||||
Db 16 TTTTATTTTGTGTTT 1

RESULT 179

US-09-430-323-131/c
; Sequence 131, Application US/09430323
; Patent No. 6309867

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-430-323-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
|||||
Db 16 TTTTATTTTGTGTTT 1

RESULT 180

US-09-507-345A-2
; Sequence 2, Application US/09507345A
; Patent No. 6426408

GENERAL INFORMATION:

APPLICANT: Kucyavin, Igor V.
Lukhtanov, Eugeny A.
Gamber, Howard B.
Meyer Jr., Rich B.

TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
Groove Binder Conjugates
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/507,345A
FILING DATE: 18-Feb-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
APPLICATION NUMBER: US 09/141,764
FILING DATE: 27-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003500US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-507-345A-2

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
|||||
Db 1 TTTTATTTTGTGTTT 16

RESULT 181

US-09-619-103-22/c
; Sequence 22, Application US/09619103
; Patent No. 6429300

GENERAL INFORMATION:


```
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/09/619,103
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-09-619-103-22

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTATTGTTT 1880
    ||||| ||||| |||||
Db 16 TTTTATTATTGTTT 1

RESULT 182
US-09-739-928-2
; Sequence 2, Application US/09739928
; Patent No. 6486308
; GENERAL INFORMATION:
; APPLICANT: Kutyavin, Igor V.
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Gamber, Howard B.
; APPLICANT: Meyer Jr., Rich B.
; TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor
; Groove Binder Conjugates
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,928
; FILING DATE: 11-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/415,370
; FILING DATE: 03-APR-1995
; APPLICATION NUMBER: US 09/141,764
; FILING DATE: 27-AUG-1998
; APPLICATION NUMBER: US 09/507,345
; FILING DATE: 18-FEB-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Kezer, William B.
; REGISTRATION NUMBER: 37,369
; REFERENCE/DOCKET NUMBER: 17682A-003510US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-928-2

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTATTGTTT 1880
    ||||| ||||| |||||
Db 1 TTTTATTATTGTTT 16

RESULT 183
US-09-371-772B-6072
; Sequence 6072, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6072
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Hmo sapiens
US-09-371-772B-6072

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
    ||||| ||||| |||||
Db 1 GUGUGUGUGUGUGGU 16

RESULT 184
US-09-371-772B-6074
; Sequence 6074, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 6074
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6074

Query Match          1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
DB 1 CUGGGUGUAGUGUGU 16

RESULT 185
US-09-479-005A-522
; Sequence 522, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 522
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-479-005A-522

Query Match          1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1832 AGTTATCTAAGTTAAT 1847
DB 1 AGUUAUGUAGUUAU 16

RESULT 186
US-08-373-124A-1058
; Sequence 1058, Application US/08373124A
; Patent No. 5645042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1058:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-1058

Query Match          1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826
DB 2 UUUUAUUAUUAUACA 17

RESULT 187
US-08-435-628-1058
; Sequence 1058, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
```

APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1058:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-1058

Query Match 1.2%; Score 12.8; DB 1; Length 17;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATA 1826
Db 2 UUAUAUAUAUAUA 17

RESULT 188
US-08-153-051B-57
Sequence 57, Application US/08153051B
Patent No. 5645986
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lycn & Lycn
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,051B
FILING DATE: No. 5645986ember 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-153-051B-57

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

RESULT 189
US-08-060-952C-56
Sequence 56, Application US/08060952C
Patent No. 5695932
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lycn & Lycn
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
U.S.A.
ZIP: 90071-2086
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,952C
FILING DATE: May 13, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/982,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-060-952C-56
Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14
RESULT 190
US-08-151-477A-57
Sequence 57, Application US/08151477A
Patent No. 5830644
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO TELEOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151.477A
FILING DATE: NO. 5830644ember 12, 1993
PRIOR APPLICATION NUMBER:
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-151-477A-57
Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

Db 1 TGGGTGTGTGTGTG 14
RESULT 191
US-08-819-867-78
Sequence 78, Application US/08819867
Patent No. 6007989
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine M. Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Jerry Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth H. Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TITLE OF INVENTION: TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/153,051
FILING DATE: NO. 6007989ember 12, 1993
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-867-78
Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14
RESULT 192
US-08-998-099-351

Sequence 351, Application US/08998099A
 Patent No. 6103890
 GENERAL INFORMATION:
 APPLICANT: JARVIS, THALE
 APPLICANT: MCSWIGGEN, JAMES A.
 APPLICANT: STINCHCOMB, DAN T.
 TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
 TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
 FILE REFERENCE: 231/175
 CURRENT APPLICATION NUMBER: US/08/998,099A
 EARLIER FILING DATE: 1997-12-24
 EARLIER APPLICATION NUMBER: 60/037,658
 EARLIER FILING DATE: 1997-01-23
 EARLIER APPLICATION NUMBER: 08/373,124
 EARLIER FILING DATE: 1995-01-13
 EARLIER APPLICATION NUMBER: 08/245,466
 EARLIER FILING DATE: 1994-05-18
 NUMBER OF SEQ ID NOS: 375
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 351
 LENGTH: 14
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-08-998-099-351

Query Match 1.2%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1567 TCACGACCTGCT 1580
 :|||:||||:
 Db 1 UCACCGACCGCT 14

RESULT 193
 US-08-464-011B-56
 Sequence 56, Application US/08464011B
 Patent No. 6368789
 GENERAL INFORMATION:
 APPLICANT: Michael D. West
 Jerry W. Shay
 Woodring E. Wright
 Elizabeth H. Blackburn
 Nam Woo Kim
 Homayoun Vaziri
 TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
 RELATED TO TELOMERE LENGTH AND/OR
 TELOMERASE ACTIVITY
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,011B
 FILING DATE: 05-Jun-1995
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/882,438
 FILING DATE: May 13, 1992
 APPLICATION NUMBER: 08/038,766
 FILING DATE: March 24, 1993
 APPLICATION NUMBER: 08/060,952
 FILING DATE: May 13, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 202/045
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 56:
 US-08-464-011B-56

Query Match 1.2%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 1.2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1793 TGTGTGTGTGTGTG 1806
 :|||||:
 Db 1 TGGGTGTGTGTG 14

RESULT 194
 US-09-378-535-78
 Sequence 78, Application US/09378535
 Patent No. 6551774
 GENERAL INFORMATION:
 APPLICANT: Michael D. West
 Calvin B. Harley
 Scott L. Weinrich
 Catherine M. Strahl
 Michael J. Mceachern
 Jerry Shay
 Woodring E. Wright
 Elizabeth H. Blackburn
 Nam Woo Kim
 Homayoun Vaziri
 TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
 CONDITIONS RELATED TO
 TELOMERE LENGTH AND/OR
 TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 80
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/378,535
 FILING DATE: 20-Aug-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/819,867
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Chambers, Daniel M.
 REGISTRATION NUMBER: 34,561
 REFERENCE/DOCKET NUMBER: 224/232
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-378-535-78

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
|||
Db 1 TGGGTGTGTGTGTG 14

RESULT 195

US-08-319-492B-474
; Sequence 474, Application US/08319492B
; Patent No. 5616488

GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994

PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895

Two

FILING DATE: January 19, 1993
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 474:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.3e+02;

Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1956 AAAGCATGAATGG 1969
|||||:||||
Db 1 AAAGCAAAAUGG 14

RESULT 196

US-08-319-492B-491
; Sequence 491, Application US/08319492B
; Patent No. 5616488

GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994

PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895

Two

FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 491:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-319-492B-491

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 35.7%; Pred. No. 1.3e+02;
Matches 5; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1284 TTATTTAAATCTGT 1297
:::||||:
Db 2 UUAUUAUUCUGU 15

RESULT 197

US-08-334-847-335/c
; Sequence 335, Application US/08334847
; Patent No. 5693532

```

; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Draper, Kenneth
; APPLICANT: Pavco, Pam
; APPLICANT: Woolf, Tod
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING RESPIRATORY
; TITLE OF INVENTION: SYNCTIAL VIRUS
; NUMBER OF SEQUENCES: 909
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,847
; FILING DATE: No. 5693532ember 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 335:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-334-847-335

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1784 TGTAAATATTGTGT 1797
Db 14 TGTGAATATTGTGT 1

RESULT 198
US-08-292-620A-331
; Sequence 331, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

```

```

; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 331:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-331

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.3e+02;
Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1801 TGTGTGTGTGTGTA 1814
Db 1 UGUGUGUAUGUGUA 14

RESULT 199
US-08-832-021-20
; Sequence 20, Application US/08832021
; Patent No. 6045998
; GENERAL INFORMATION:
; APPLICANT: Combates, N.
; APPLICANT: Pardini, J.
; APPLICANT: Parimoo, S.
; APPLICANT: Prouty, S.
; APPLICANT: Stenn, K.
; TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
; FILE REFERENCE: JBP-382
; CURRENT APPLICATION NUMBER: US/08/832,021
; CURRENT FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-08-832-021-20

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;

```

two

CLASSIFICATION:

; APPLICATION NUMBER: US/08/292,620
 ; FILING DATE: August 17, 1994
 ; APPLICATION NUMBER: 08/008,895
 ; FILING DATE: January 19, 1993
 ; APPLICATION NUMBER: 07/989,849
 ; FILING DATE: December 7, 1992

FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 208/149
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 331:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-0701-845-331

Query Match 1.2%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 1.3e+02;
 Match 6.0; Conservative 1.0; Indels

RESULT 202
US-08-444-818-203
; Sequence 203 Application US/08444818
; Patent No. 6150987
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANAV Diagnostics and Vaccines

Sequence 203, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANOV Diagnostic
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA

TITLE OF INVENTION: NANBV Diagnostics and Vaccin
 NUMBER OF SEQUENCES: 777
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94608-2916
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/444,818
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/403,590
 FILING DATE: 14-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Harbin, Alisa A.
 REGISTRATION NUMBER: 33,895
 REFERENCE/DOCKET NUMBER: 0110.002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508)359-3876
 TELEFAX: (508)359-3885
 INFORMATION FOR SEQ ID NO: 203:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer based on clone 11b."
US-08-444-818-203

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1378 CTGGTTTGAAGAAT 1391
DB 1 CTGGCTTGAAGAAT 14

RESULT 203
US-08-875-710-1
Sequence 1, Application US/08875710
Patent No. 6326139
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
TITLE OF INVENTION: METHOD OF SCREENING FOR GENETIC PREDISPOSITION TO
TITLE OF INVENTION: ANTICHOLINESTERASE THERAPY
FILE REFERENCE: 2391.00076
CURRENT APPLICATION NUMBER: US/08/875,710
CURRENT FILING DATE: 1997-10-06
EARLIER APPLICATION NUMBER: PCT/US96/00322
EARLIER FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
US-08-875-710-1

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2174 ACTTTCATGATGACT 2187
DB 2 ACTTTCATGATGACT 15

RESULT 204
US-09-475-947A-158
Sequence 158, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Mirra, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 158
LENGTH: 15
TYPE: DNA
ORGANISM: human
OTHER INFORMATION: n signifies a, t, c or g.
US-09-475-947A-158

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTATTGTTT 1879
TTTTT TTTT TTTT TTTT

Db 1 TTTTTTTTTTTT 15

RESULT 205
US-08-222-177A-433/c
Sequence 433, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:

INFORMATION FOR SEQ ID NO: 433:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-222-177A-433

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1805
DB 12 GTGTGTGTGTGT 1

RESULT 206
US-09-164-249B-2/c
Sequence 2, Application US/09164249B
Patent No. 6322571
GENERAL INFORMATION:
APPLICANT: Chetverin, Alexander B.
APPLICANT: Kramer, Fred Russel
TITLE OF INVENTION: NOVEL OLIGONUCLEOTIDE ARRAYS AND THEIR USE FOR SORTING,
TITLE OF INVENTION: ISOLATING, SEQUENCING, AND MANIPULATING NUCLEIC ACIDS
FILE REFERENCE: 07763-004003
CURRENT APPLICATION NUMBER: US/09/164,249B
CURRENT FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: US 08/473,010
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/247,530
PRIOR FILING DATE: 1994-05-23

QY 1793 TGTGTGTGTGTG 1804
Db 1 TGTGTGTGTGTG 12

RESULT 208
US-09-958-221A-1/c
; Sequence 1, Application US/09958221A
; Patent No. 6686160
; GENERAL INFORMATION:
; APPLICANT: Haeringen van, Willem A.
; TITLE OF INVENTION: UNIVERSAL VARIABLE FRAGMENTS
; FILE REFERENCE: 92750/64
; CURRENT APPLICATION NUMBER: US/09/958,221A
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: EP 00200757.3
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/NL01/00177
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-958-221A-1

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTG 1804
Db 12 TGTGTGTGTGTG 1

RESULT 209
US-08-291-932A-120/c
; Sequence 120, Application US/08291932A
; Patent No. 5658780
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2056
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below;

; PRIOR APPLICATION NUMBER: US 07/838,607
; PRIOR FILING DATE: 1992-02-19
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically derived DNA
US-09-164-249B-2

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1805
Db 12 GTGTGTGTGTGT 1

RESULT 207
US-09-281-481A-21
; Sequence 21, Application US/09281481A
; Patent No. 6383747
; GENERAL INFORMATION:
; APPLICANT: DANKINS, Roger L. and ABRAHAM, Lawrence J.
; TITLE OF INVENTION: GENETIC ANALYSIS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/281,481A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,971
; FILING DATE: 16-JUL-1997
; APPLICATION NUMBER: US 232,229
; FILING DATE: 29-APR-1994
; APPLICATION NUMBER: PK9279 (AU)
; FILING DATE: 01-NOV-1991
; APPLICATION NUMBER: PCT/AU92/00583
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGIGLIO, FRANK S
; REFERENCE/DOCKET NUMBER: 9279
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: +516 742 4343
; TELEFAX: +516 742 4366
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-281-481A-21

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-291-932A-120

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
|||||
DB 15 CACCTGGAAGCA 4

RESULT 210

US-08-291-932A-193/c
Sequence 193, Application US/08291932A
Patent No. 5658780

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:

Two

APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-291-932A-193

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
|||||
DB 15 CACCTGGAAGCA 4

RESULT 211

US-08-291-932A-309/c
Sequence 309, Application US/08291932A
Patent No. 5658780

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

Two

INFORMATION FOR SEQ ID NO: 309:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-291-932A-309

Query Match 1.1%; Score 12; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2153 CACCTGGAACGA 2164
 |||||
 Db 15 CACCTGGAACGA 4

RESULT 212
 US-08-143-219-16
 ; Sequence 16, Application US/08143219
 ; Patent No. 5670330
 ; GENERAL INFORMATION:
 ; APPLICANT: Sonenberg, Nahum
 ; APPLICANT: Katze, Michael G.
 ; APPLICANT: Roy, Sophie
 ; APPLICANT: Koromilas, Antonis E.
 ; APPLICANT: Barber, Glen N.
 ; TITLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 611 West Sixth Street
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90017
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: PC-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/143,219
 ; FILING DATE: October 25, 1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below:
 ; APPLICATION NUMBER: 08/141,244
 ; FILING DATE: October 22, 1993
 ; APPLICATION NUMBER: 07/953,681
 ; FILING DATE: September 29, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Douglas E. Olson
 ; REGISTRATION NUMBER: 22,798
 ; REFERENCE/DOCKET NUMBER: 204/139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEetical: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: COMPLEMENTARY TO THE RNA PROBE FOR
 ; INDIVIDUAL ISOLATE: PR-IV, FIGURE 5
 ; US-08-143-219-16

Query Match 1.1%; Score 12; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1784 TGTAATATTGT 1795
 |||||
 Db 3 TGTAATATTGT 14

RESULT 213
 US-08-334-847-32/c
 ; Sequence 32, Application US/08334847
 ; Patent No. 5693532
 ; GENERAL INFORMATION:
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: Woolf, Tod
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR
 ; TITLE OF INVENTION: INHIBITING RESPIRATORY
 ; TITLE OF INVENTION: SYNCYTIAL VIRUS
 ; NUMBER OF SEQUENCES: 909
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/334,847
 ; FILING DATE: No. 5693532ember 4, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 209/032
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-334-847-32

Query Match 1.1%; Score 12; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1347 TGCAACAAT 1358
 |||||
 Db 13 TGCAACAAT 2

RESULT 214
 US-08-334-847-33/c
 ; Sequence 33, Application US/08334847
 ; Patent No. 5693532
 ; GENERAL INFORMATION:
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: Woolf, Tod
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR
 ; TITLE OF INVENTION: INHIBITING RESPIRATORY
 ; TITLE OF INVENTION: SYNCYTIAL VIRUS
 ; NUMBER OF SEQUENCES: 909
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FILING DATE: No. 569352ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-334-847-33
Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1347 TGTCACAAAT 1358
Db 12 TGTCACAAAT 1
RESULT 215
US-09-340-798A-51/c
Sequence 51, Application US/09340798A
Patent No. 6534312
GENERAL INFORMATION:
APPLICANT: SHIVER, JOHN W.
LIU, MARGARET A.
PERRY, HELEN C.
DAVIES, MARY-ELLEN M.
FREED, DANIEL C.
TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,798A
FILING DATE: 28-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/877,418
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19729Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide"
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-340-798A-51
Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1521 ATGCCTGCTATT 1532
Db 13 ATGCCTGCTATT 2
RESULT 216
US-08-849-021-88
Sequence 88, Application US/08849021
Patent No. 5955276
GENERAL INFORMATION:
APPLICANT: MORGANTE, MICHELE
APPLICANT: VOGEL, JULIE M.
TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: DETECTION OF GENETIC
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND
ADDRESSEE: COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1064-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-992-7949
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single


```

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/060,952C
; FILING DATE: May 13, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-060-952C-50

Query Match 1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1804
Db 1 TGGTGTGTGTGTG 13

RESULT 220
US-08-431-080-2
; Sequence 2, Application US/08431080
; Patent No. 5898886
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,080
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SN 08/326,781
; FILING DATE: October 20, 1994
; CLASSIFICATION: 514

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD:155/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-431-080-2

Query Match 1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806
Db 1 GTGTGTGTGTGTG 13

RESULT 221
US-08-151-477A-51
; Sequence 51, Application US/08151477A
; Patent No. 5830644
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; APPLICANT: Nam Woo Kim
; APPLICANT: Calvin B. Harley
; APPLICANT: Scott L. Weinrich
; APPLICANT: Catherine Strahl
; APPLICANT: Michael J. McEachern
; APPLICANT: Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO TELOMERE
; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,477A
; FILING DATE: No. 5830644ember 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 51:

```

SEQUENCE CHARACTERISTICS:
 LENGTH: 13 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-151-477A-51

Query Match 1.1%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 1.4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1804
 DB 1 TGTGTGTGTGTG 13

RESULT 222

US-08-938-534-2
 Sequence 2, Application US/08938534
 Patent No. 5916752
 GENERAL INFORMATION:
 APPLICANT: Gottschling, Daniel E.
 APPLICANT: Singer, Miriam S.
 TITLE OF INVENTION: Telomerase Compositions and Methods
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TEXAS
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 77210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/938,534
 FILING DATE: 26-SEP-1997

CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/431,080
 FILING DATE:
 APPLICATION NUMBER: SN 08/326,781
 FILING DATE: October 20, 1994

ATTORNEY/AGENT INFORMATION:
 NAME: Parker, David L.
 REGISTRATION NUMBER: 32,165
 REFERENCE/DOCKET NUMBER: ARCD:155/PAR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (713) 789-2679
 TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-938-534-2

Query Match 1.1%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 1.4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806
 DB 1 GTGTGTGTGTGTG 13

RESULT 223

US-08-819-867-77

Sequence 77, Application US/08819867
 Patent No. 6007989
 GENERAL INFORMATION:
 APPLICANT: Michael D. West
 APPLICANT: Calvin B. Harley
 APPLICANT: Scott L. Weinrich
 APPLICANT: Catherine M. Strahl
 APPLICANT: Michael J. Moeachein
 APPLICANT: Jerry Shay
 APPLICANT: Woodring E. Wright
 APPLICANT: Elizabeth H. Blackburn
 APPLICANT: Nam Woo Kim
 APPLICANT: Homayoun Vaziri
 TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
 TITLE OF INVENTION: CONDITIONS RELATED TO
 TITLE OF INVENTION: TELOMERE LENGTH AND/OR
 TITLE OF INVENTION: TELOMERASE ACTIVITY
 NUMBER OF SEQUENCES: 80
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/819,867
 FILING DATE: March 14, 1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/153,051
 FILING DATE: No. 6007989ember 12, 1993
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Chambers, Daniel M.
 REGISTRATION NUMBER: 34,561
 REFERENCE/DOCKET NUMBER: 224/232
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 77:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-819-867-77

Query Match 1.1%; Score 11.4; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 1.4e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTG 1804
 DB 1 TGTGTGTGTGTG 13

RESULT 224

US-08-464-011B-50
 Sequence 50, Application US/08464011B
 Patent No. 638789
 GENERAL INFORMATION:
 APPLICANT: Michael D. West
 APPLICANT: Jerry W. Shay


```

;
; Woodring E. Wright
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; RELATED TO TELOMERASE LENGTH AND/OR
; TELOMERASE ACTIVITY
;
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; City: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; storage
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,011B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Watburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1800
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-08-464-011B-50
;
; Query Match 1.1%; Score 11.4; DB 1; Length 13;
; Best Local Similarity 92.3%; Pred. No. 1.4e+02;
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1792 TTGTGTGTGTGTG 1804
; | |||||
; Db 1 TTGTGTGTGTGTG 13
;
; RESULT 225
; US-09-345-294-2
; Sequence 2, Application US/09345294
; Patent No. 6387619
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; SINGER, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; City: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
;
; COMPUTER READABLE FORM:

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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,294
; FILING DATE: 30-Jun-1999
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/431,080
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD:155/PAR
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-345-294-2
;
; Query Match 1.1%; Score 11.4; DB 1; Length 13;
; Best Local Similarity 92.3%; Pred. No. 1.4e+02;
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1794 GTGTGTGTGTGTG 1806
; | |||||
; Db 1 GTGTGTGTGTGTG 13
;
; RESULT 226
; US-09-922-445-10
; Sequence 10, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.
; APPLICANT: Berglund, Lars G. T.
; APPLICANT: Reneland, Rikard H.
; APPLICANT: Adam, Gail I. R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
; FILE REFERENCE: G3126US
; CURRENT APPLICATION NUMBER: US/09/922,445
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 13
; TYPE: DNA
; ORGANISM: synthetic
;
; US-09-922-445-10
;
; Query Match 1.1%; Score 11.4; DB 1; Length 13;
; Best Local Similarity 92.3%; Pred. No. 1.4e+02;
; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1319 TTCCACCCCAATT 1331
; | |||||
; Db 1 TTCCACCCCAATT 13
;
; RESULT 227
; US-09-922-445-35/c
; Sequence 35, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.

```

APPLICANT: Berglund, Lars G. T.
APPLICANT: Rensland, Rikard H.
APPLICANT: Adam, Gail I. R.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
FILE REFERENCE: GGI2605
CURRENT APPLICATION NUMBER: US/09/922,445
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 13
TYPE: DNA
ORGANISM: synthetic
US-09-922-445-35

Query Match 1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. NO. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1319 TTCCACCCCAATT 1331
DB 13 TTCCACCCCAATT 1

RESULT 228
US-09-378-535-77
Sequence 77, Application US/09378535
Patent No. 6551774

GENERAL INFORMATION:

APPLICANT: Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/819,867

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-378-535-77

Query Match 1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. NO. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTG 1804
DB 1 TGGTGTGTGTG 13

RESULT 229

US-09-377-497-56
Sequence 56, Application US/09377497
Patent No. 6670119

GENERAL INFORMATION:

APPLICANT: YOSHIKAWA, YOSHIE
APPLICANT: MURAI, HIROYUKI
APPLICANT: ASADA, KIYOZO
APPLICANT: HINO, FUMITSUGU
APPLICANT: KATO, IKUNOSHIN
TITLE OF INVENTION: CANCER-ASSOCIATED GENES
FILE REFERENCE: 1422-388P
CURRENT APPLICATION NUMBER: US/09/377,497
CURRENT FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56

LENGTH: 13

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: any n or Xaa = unknown

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

US-09-377-497-56

Query Match 1.1%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. NO. 1.4e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1871 TTTTGTGTTTAA 1883
DB 1 TTTTGTGTTTAA 13

RESULT 230

US-08-264-534-28
Sequence 28, Application US/08264534
Patent No. 5648464

GENERAL INFORMATION:

APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains
TITLE OF INVENTION: In Topolythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/08/264,534
 ; APPLICATION NUMBER: US/08/264,534
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/695,189
 ; FILING DATE: 03-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 19,872
 ; REFERENCE/DOCKET NUMBER: 7326-004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEFAX: 212 8698864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: CDNA
 ; US-08-264-534-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 1.6e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1839 TAAGTTAACTTAA 1851
 Db 2 TAAGTTAACTTAA 14

RESULT 231
 US-08-264-534-28/c
 ; Sequence 28, Application US/08264534
 ; Patent No. 5648464
 ; GENERAL INFORMATION:
 ; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
 ; TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains
 ; TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/264,534
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/695,189
 ; FILING DATE: 03-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 19,872
 ; REFERENCE/DOCKET NUMBER: 7326-004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEFAX: 212 8698864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs

; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: CDNA
 ; US-08-264-534-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 1.6e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1839 TAAGTTAACTTAA 1851
 Db 13 TAAGTTAACTTAA 1

RESULT 232
 US-08-268-799-6
 ; Sequence 6, Application US/08268799
 ; Patent No. 5654195
 ; GENERAL INFORMATION:
 ; APPLICANT: Sodroski, Joseph
 ; APPLICANT: Haseltine, William A.
 ; APPLICANT: Letvin, No. 5654195man
 ; APPLICANT: Li, John
 ; TITLE OF INVENTION: Vectors Expressing Hybrid Viruses,
 ; TITLE OF INVENTION: Methods Of Use And No. 5654195el Assays
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dike, Bronstein, Roberts and Cushman
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/268,799
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/887,505
 ; FILING DATE: 22-MAY-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Eisenstein, Ronald I.
 ; REGISTRATION NUMBER: 30628
 ; REFERENCE/DOCKET NUMBER: 41858
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 523-3400
 ; TELEFAX: (617) 523-6440
 ; TELEX: 200291 stre ur
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; US-08-268-799-6

Query Match 1.1%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 1.6e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1958 AGCATGAATGGA 1970
 Db 1 AGCAAGAAATGGA 13

RESULT 233
 US-08-465-500-28

; Sequence 28, Application US/08465500
; Patent No. 5789195
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Muskavitch, Marc A.T.
; APPLICANT: Fehon, Richard G.
; APPLICANT: Rebay, Ilaria
; APPLICANT: Blumweller, Cristine M.
; APPLICANT: Shepard, Scott B.
; TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS
; TITLE OF INVENTION: IN TOPORHYTHMIC PROTEINS, AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,500
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leelle
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-465-500-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
Db 2 TAAGTTAACTTAA 14

RESULT 234
US-08-465-500-28/c
; Sequence 28, Application US/08465500
; Patent No. 5789195
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Muskavitch, Marc A.T.
; APPLICANT: Fehon, Richard G.
; APPLICANT: Rebay, Ilaria
; APPLICANT: Blumweller, Cristine M.
; APPLICANT: Shepard, Scott B.
; TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS
; TITLE OF INVENTION: IN TOPORHYTHMIC PROTEINS, AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,500
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leelle
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-465-500-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
Db 13 TAAGTTAACTTAA 1

RESULT 235
US-08-672-564-11
; Sequence 11, Application US/08672564
; Patent No. 5824503
; GENERAL INFORMATION:
; APPLICANT: KUROME, Yoko
; APPLICANT: IZU, Hiroyuki
; APPLICANT: IZUMI, Yoshiya
; APPLICANT: SANO, Mutsumi
; APPLICANT: KATO, Ikunoshin
; APPLICANT: ITO, Makoto
; TITLE OF INVENTION: GENE ENCODING ENDOGLYCOCERAMIDASE ACTIVATOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,564
; FILING DATE: 28 JUNE 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0263P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-08-672-564-11

Query Match
  1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
Db 2 TAAGTTAACTTAA 14

RESULT 236
US-08-672-564-11/c
; Sequence 11, Application US/08672564
; Patent No. 5824503
; GENERAL INFORMATION:
; APPLICANT: KURUME, Yoko
; APPLICANT: IZU, Hiroyuki
; APPLICANT: IZUMI, Yoshiya
; APPLICANT: SANO, Mutsumi
; APPLICANT: KATO, Ikunoshin
; APPLICANT: ITO, Makoto
; TITLE OF INVENTION: GENE ENCODING ENDOGLYCOCERAMIDASE ACTIVATOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,564
; Filing DATE: 28 JUNE 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0263P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid (synthetic DNA)
US-08-672-564-11

Query Match
  1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
Db 13 TAAGTTAACTTAA 1

RESULT 237
US-08-346-126-28
; Sequence 28, Application US/08346126

```

```

; Patent No. 5849869
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
; TITLE OF INVENTION: Human No. 5849869ch And Delta, Binding Domains
; TITLE OF INVENTION: In Topolythmic Proteins, And Methods Based Thereon
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,126
; Filing DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/791,923
; Filing DATE: 14-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 19,872
; REFERENCE/DOCKET NUMBER: 7326-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-346-126-28

Query Match
  1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1839 TAAGTTAACTTAA 1851
Db 2 TAAGTTAACTTAA 14

RESULT 238
US-08-346-126-28/c
; Sequence 28, Application US/08346126
; Patent No. 5849869
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
; TITLE OF INVENTION: Human No. 5849869ch And Delta, Binding Domains
; TITLE OF INVENTION: In Topolythmic Proteins, And Methods Based Thereon
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

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; APPLICATION NUMBER: US/08/346,126
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/791,923
; FILING DATE: 14-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-007
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
;
US-08-346-126-28

Query Match      1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1839 TAAGTTAACTTAA 1851
Db      13 TAAGTTAACTTAA 1

RESULT 239
US-08-346-128-28
; Sequence 28, Application US/08346128
; Patent No. 5856441
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
; TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,128
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879,038
; FILING DATE: 30-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-009
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
;
US-08-346-128-28

Query Match      1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1839 TAAGTTAACTTAA 1851
Db      13 TAAGTTAACTTAA 1

RESULT 239
US-08-346-128-28
; Sequence 28, Application US/08346128
; Patent No. 5856441
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
; TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,128
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879,038
; FILING DATE: 30-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-009
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
;
US-08-346-128-28
```

```
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
;
US-08-346-128-28

Query Match      1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1839 TAAGTTAACTTAA 1851
Db      2 TAAGTTAACTTAA 14

RESULT 240
US-08-346-128-28/c
; Sequence 28, Application US/08346128
; Patent No. 5856441
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon et al.
; TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,128
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879,038
; FILING DATE: 30-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-009
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
;
US-08-346-128-28

Query Match      1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1839 TAAGTTAACTTAA 1851
Db      13 TAAGTTAACTTAA 1

RESULT 241
US-08-682-847-8
; Sequence 8, Application US/08682847
; Patent No. 5858989
; GENERAL INFORMATION:
; APPLICANT: BABIUK, LORNE
```

APPLICANT: VAN DEN HURK, SYLVIA
APPLICANT: ZAMB, TIM
APPLICANT: FITZPATRICK, DAVID
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,847
FILING DATE: 12-JUL-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 29310-20005.10
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-682-847-8

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1839 TAAGTTAACTTAA 1851
DB 2 TAAGTTAACTTAA 14

RESULT 242
US-08-682-847-8/c
Sequence 8, Application US/08682847
Patent No. 585899
GENERAL INFORMATION:
APPLICANT: BABIUK, LORNE
APPLICANT: VAN DEN HURK, SYLVIA
APPLICANT: ZAMB, TIM
APPLICANT: FITZPATRICK, DAVID
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/682,847
FILING DATE: 12-JUL-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 29310-20005.10
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-682-847-8

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1839 TAAGTTAACTTAA 1851
DB 13 TAAGTTAACTTAA 1

RESULT 243
US-08-544-381B-216/C
Sequence 216, Application US/08544381B
Patent No. 6027880
GENERAL INFORMATION:
APPLICANT: Cronin, Maureen T.
APPLICANT: Miyada, Charles Garrett
APPLICANT: Hubbell, Earl A.
APPLICANT: Chee, Mark
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua C.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
TITLE OF INVENTION: Detecting Cystic Fibrosis
NUMBER OF SEQUENCES: 250
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,381B
FILING DATE: 10-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12305
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,064
FILING DATE: 02-AUG-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-00413005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-544-381B-216

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. NO. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1564 TGCTCACTGACCT 1576
Db 13 TGCTCACTGACCT 1

RESULT 244
US-08-832-021-5
Sequence 5, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
APPLICANT: Combates, N.
APPLICANT: Pardinas, J.
APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-5

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. NO. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1871 TTTTGGTTTAA 1883
Db 2 TTTTGGTTTAA 14

RESULT 245
US-08-832-021-16
Sequence 16, Application US/08832021
Patent No. 6045998
GENERAL INFORMATION:
APPLICANT: Combates, N.
APPLICANT: Pardinas, J.
APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION NUMBER: US/08/832,021

CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-832-021-16

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. NO. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTATTATTGT 1877
Db 2 TTTTATTATTGT 14

RESULT 246
US-08-724-466B-14
Sequence 14, Application US/08724466B
Patent No. 6063606
GENERAL INFORMATION:
APPLICANT: Petrovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-724-466B-14

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. NO. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1865 TTTTATTATTGT 1877
Db 2 TTTTATTATTGT 14

RESULT 247
US-08-724-466B-17
Sequence 17, Application US/08724466B

Patent No. 6063606
 GENERAL INFORMATION:
 APPLICANT: Petkovich, P. Martin, White, Jay A.
 APPLICANT: Beckett, Barbara R., Jones, Glenville
 TITLE OF INVENTION: Retinoid Metabolizing Protein
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Blake, Cassels & Graydon
 STREET: Box 25, Commerce Court West
 CITY: Toronto
 ZIP: M5L 1A9
 COUNTRY: Canada
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
 COMPUTER: COMPAQ, IBM PC compatible
 OPERATING SYSTEM: MS-DOS 5.1
 SOFTWARE: WORD PERFECT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/724,466B
 FILING DATE: October 1, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/667,546
 FILING DATE: June 21, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunt, John C.
 REGISTRATION NUMBER: 36,424
 REFERENCE/DOCKET NUMBER: 50767/00004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 863-4344
 TELEFAX: (416) 863-2653
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-724-466B-17

Query Match 1.1%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 1.6e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1871 TTTTGTGTTTAA 1883
 Db 2 TTTTGTGTTTAA 14

RESULT 248
 US-08-893-828-28
 Sequence 28, Application US/08893828
 Patent No. 6090922
 GENERAL INFORMATION:
 APPLICANT: Artavanis-Tsakonas, Spyridon
 APPLICANT: Muskavitch, Marc A.T.
 APPLICANT: Fehon, Richard G.
 APPLICANT: Rebay, Ilaria
 APPLICANT: Blaumueller, Cristine M.
 APPLICANT: Shepard, Scott B.
 TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/893,828
 FILING DATE: 11-JUL-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7326-050
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: CDNA
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/893,828
 FILING DATE: 11-JUL-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7326-050
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: CDNA
 US-08-893-828-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 1.6e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1839 TAAGTAAATTAA 1851
 Db 2 TAAGTAACTTAA 14

RESULT 249
 US-08-893-828-28/c
 Sequence 28, Application US/08893828
 Patent No. 6090922
 GENERAL INFORMATION:
 APPLICANT: Artavanis-Tsakonas, Spyridon
 APPLICANT: Muskavitch, Marc A.T.
 APPLICANT: Fehon, Richard G.
 APPLICANT: Rebay, Ilaria
 APPLICANT: Blaumueller, Cristine M.
 APPLICANT: Shepard, Scott B.
 TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PENNIE & EDMONDS
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/893,828
 FILING DATE: 11-JUL-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7326-050
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: CDNA

US-08-893-828-28

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1839 TAAGTTAATTAA 1851
Db 13 TAAGTTAATTAA 1

RESULT 250

US-09-019-095A-26

; Sequence 26, Application US/09019095A

; Patent No. 6287858

; GENERAL INFORMATION:

; APPLICANT: D'Andrea, Alan D.

; APPLICANT: Zhu, Yuan

; TITLE OF INVENTION: Deubiquitinating Enzymes That Regulate

; TITLE OF INVENTION: Cell Growth

; FILE REFERENCE: DFCI-435P2A2

; CURRENT APPLICATION NUMBER: US/09/019,095A

; CURRENT FILING DATE: 1998-02-05

; PRIOR APPLICATION NUMBER: PCT/US96/12884

; PRIOR FILING DATE: 1996-08-07

; PRIOR APPLICATION NUMBER: US 60/002,066

; PRIOR FILING DATE: 1995-08-09

; PRIOR APPLICATION NUMBER: US 60/019,787

; PRIOR FILING DATE: 1996-06-14

; NUMBER OF SEQ ID NOS: 51

; SEQ ID NO 26

; SOFTWARE: FastSeq for Windows Version 3.0

; LENGTH: 14

; TYPE: DNA

; ORGANISM: murine

US-09-019-095A-26

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGT 1877
Db 2 TTTTATTTTGT 14

RESULT 251

US-08-882-164D-14

; Sequence 14, Application US/08882164D

; Patent No. 6306624

; GENERAL INFORMATION:

; APPLICANT: Petkovich, P. Martin, White, Jay A.,

; APPLICANT: Beckett, Barbara R., Jones, Glenville

; TITLE OF INVENTION: Retinoid Metabolizing Protein

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Blake, Cassels & Graydon

; STREET: Box 25, Commerce Court West

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5L 1A9

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

; COMPUTER: COMPAQ, IBM PC compatible

; OPERATING SYSTEM: MS-DOS 5.1

; SOFTWARE: WORD PERFECT

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/882,164D

; FILING DATE: June 25, 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/667,546

; FILING DATE: June 21, 1996

APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Hunt, John C.

REGISTRATION NUMBER: 36,424

REFERENCE/DOCKET NUMBER: 50767/00010

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 863-4344

TELEFAX: (416) 863-2653

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-882-164D-14

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGT 1877
Db 2 TTTTATTTTGT 14

RESULT 252

US-08-882-164D-17

; Sequence 17, Application US/08882164D

; Patent No. 6306624

; GENERAL INFORMATION:

; APPLICANT: Petkovich, P. Martin, White, Jay A.,

; APPLICANT: Beckett, Barbara R., Jones, Glenville

; TITLE OF INVENTION: Retinoid Metabolizing Protein

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Blake, Cassels & Graydon

; STREET: Box 25, Commerce Court West

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5L 1A9

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage

; COMPUTER: COMPAQ, IBM PC compatible

; OPERATING SYSTEM: MS-DOS 5.1

; SOFTWARE: WORD PERFECT

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/882,164D

; FILING DATE: June 25, 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/667,546

; FILING DATE: June 21, 1996

; APPLICATION NUMBER: 08/724,466

; FILING DATE: October 1, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Hunt, John C.

; REGISTRATION NUMBER: 36,424

; REFERENCE/DOCKET NUMBER: 50767/00010

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 863-4344

; TELEFAX: (416) 863-2653

; INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-882-164D-17

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1871 TTTTGTGTTTAA 1883
| | | | | | | | | |
Db 2 TTTTGTGTTTAA 14

RESULT 253
US-09-475-947A-296
; Sequence 296, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 296
; LENGTH: 14
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-296

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806
| | | | | | | | | |
Db 1 GTGTGTGTGTGTG 13

RESULT 254
US-09-375-673B-13
; Sequence 13, Application US/09375673B
; Patent No. 6605431
; GENERAL INFORMATION:
; APPLICANT: GOURSE, RICHARD L.
; APPLICANT: ESTREM, SHAWN T.
; APPLICANT: ROSS, WILMA E.
; APPLICANT: GAAL, TAMAS
; TITLE OF INVENTION: PROMOTER ELEMENTS AND METHODS OF USE
; FILE REFERENCE: 11900130101
; CURRENT APPLICATION NUMBER: US/09/375,673B
; CURRENT FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Distal
; OTHER INFORMATION: accessory promoter element
US-09-375-673B-13

Query Match 1.1%; Score 11.4; DB 1; Length 14;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1773 AAAATTTATATTG 1785
| | | | | | | | | |
Db 2 AAAATTTATATTG 14

Search completed: April 2, 2004, 14:34:11
Job time : 3 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 14:38:01 ; Search time 3 seconds
(without alignments)
2.527 Million cell updates/sec

Title: us-10-006-191-19

Perfect score: 1049

Sequence: 1 tgaactgattcacatctca.....gtgtatatattttctataaa 1049

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 210 seqs, 3614 residues

Total number of hits satisfying chosen parameters: 420

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 239 summaries

Database : rnpb.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	2.4	25	1	US-10-101-040-9
C 2	23.4	2.2	25	1	US-10-101-040-10
C 3	23.4	2.2	27	1	US-09-754-853A-601
C 4	22.2	2.1	27	1	US-09-735-363A-5
C 5	22.2	2.1	27	1	US-09-263-959-770
C 6	21.8	2.1	27	1	US-09-735-363A-1
C 7	21.8	2.1	27	1	US-09-735-363A-66
C 8	21.4	2.0	24	1	US-10-168-327-2
C 9	21.4	2.0	24	1	US-09-735-363A-21
C 10	21.4	2.0	24	1	US-09-776-479-1068
C 11	21.4	2.0	24	1	US-10-112-653-1012
C 12	21.4	2.0	24	1	US-10-017-895-1068
C 13	21.4	2.0	24	1	US-09-735-363A-19
C 14	21.4	2.0	24	1	US-09-735-363A-19
C 15	21.4	2.0	24	1	US-09-776-479-907
C 16	21.4	2.0	24	1	US-10-112-653-876
C 17	21.4	2.0	24	1	US-10-017-895-907
C 18	20.0	1.9	20	1	US-09-845-742B-1
C 19	20.0	1.9	20	1	US-10-085-906-33
C 20	20.0	1.9	20	1	US-10-165-854-1
C 21	20.0	1.9	20	1	US-10-165-854-2
C 22	20.0	1.9	20	1	US-10-219-238-1
C 23	20.0	1.9	20	1	US-10-219-238-1
C 24	20.0	1.9	20	1	US-10-006-191-39
C 25	20.0	1.9	20	1	US-10-006-191-40
C 26	20.0	1.9	20	1	US-10-006-191-41
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C 28	20.0	1.9	20	1	US-10-006-191-43
C 29	20.0	1.9	20	1	US-10-006-191-44
C 30	20.0	1.9	20	1	US-10-006-191-45
C 31	20.0	1.9	20	1	US-10-006-191-46
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Sequence 48, Appl	US-10-006-191-48	20	1.9	20	C 34
Sequence 49, Appl	US-10-006-191-49	20	1.9	20	C 35
Sequence 59, Appl	US-10-006-191-59	20	1.9	20	C 36
Sequence 60, Appl	US-10-006-191-60	20	1.9	20	C 37
Sequence 61, Appl	US-10-006-191-61	20	1.9	20	C 38
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Sequence 93, Appl	US-10-006-191-93	20	1.9	20	C 44
Sequence 94, Appl	US-10-006-191-94	20	1.9	20	C 45
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Sequence 96, Appl	US-10-006-191-96	20	1.9	20	C 47
Sequence 97, Appl	US-10-006-191-97	20	1.9	20	C 48
Sequence 20, Appl	US-09-735-363A-20	21	1.9	20	C 49
Sequence 1, Appl	US-10-385-193-1	21	1.9	20	C 50
Sequence 2, Appl	US-10-385-193-2	21	1.9	20	C 51
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Sequence 7, Appl	US-09-557-423-7	19	1.8	19	C 54
Sequence 8, Appl	US-09-557-423-8	19	1.8	19	C 55
Sequence 3086, Ap	US-09-969-373-3086	19	1.8	19	C 56
Sequence 153, App	US-10-006-191-153	18	1.8	18	C 57
Sequence 17, Appl	US-09-735-363A-17	18	1.7	18	C 58
Sequence 18, Appl	US-09-735-363A-18	18	1.7	18	C 59
Sequence 28, Appl	US-09-896-650A-28	18	1.7	18	C 60
Sequence 1, Appl	US-10-011-204-1	18	1.7	18	C 61
Sequence 2, Appl	US-10-011-204-2	18	1.7	18	C 62
Sequence 26, Appl	US-10-357-488-26	18	1.7	18	C 63
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Sequence 68, Appl	US-10-340-192-68	17	1.6	17	C 69
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Sequence 135, App	US-10-006-191-135	20	1.6	20	C 72
Sequence 10, Appl	US-09-768-917-10	21	1.6	21	C 73
Sequence 412, App	US-10-085-906-412	21	1.6	21	C 74
Sequence 983, App	US-09-263-959-983	18	1.6	18	C 75
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Sequence 26, Appl	US-10-301-844-26	20	1.6	20	C 77
Sequence 26, Appl	US-10-301-844-26	20	1.6	20	C 78
Sequence 27, Appl	US-10-092-885-27	16	1.5	16	C 79
Sequence 971, App	US-09-263-959-971	18	1.5	18	C 80
Sequence 85, Appl	US-09-888-326-85	18	1.5	18	C 81
Sequence 16, Appl	US-09-735-363A-16	15	1.5	15	C 82
Sequence 222, App	US-10-085-906-222	15	1.4	15	C 83
Sequence 258, App	US-10-085-906-258	15	1.4	15	C 84
Sequence 540, App	US-09-263-959-540	15	1.4	15	C 85
Sequence 540, App	US-09-263-959-540	15	1.4	15	C 86
Sequence 231, App	US-10-085-906-231	16	1.4	16	C 87
Sequence 878, App	US-10-085-906-878	16	1.4	16	C 88
Sequence 57, Appl	US-08-463-404-57	16	1.4	16	C 89
Sequence 80, Appl	US-10-092-885-80	16	1.4	16	C 90
Sequence 13, Appl	US-10-232-927A-13	17	1.4	17	C 91
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Sequence 235, App	US-09-918-186A-235	20	1.4	20	C 95
Sequence 15, Appl	US-09-735-363A-15	14	1.3	14	C 96
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Sequence 659, App	US-09-263-959-659	14	1.3	14	C 98
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Sequence 811, App	US-09-263-959-811	14	1.3	14	C 100
Sequence 27, Appl	US-09-913-514-27	14	1.3	14	C 101
Sequence 27, Appl	US-09-913-514-27	14	1.3	14	C 102
Sequence 19, Appl	US-10-301-844-19	14	1.3	14	C 103

C 107	14	1.3	14	1	US-10-301-844-19	Sequence 19, Appl	180	12.4	1.2	14	1	US-08-463-404-56	Sequence 56, Appl
C 108	14	1.3	14	1	US-10-085-906-258	Sequence 258, App	181	12.4	1.2	14	1	US-09-263-959-530	Sequence 530, App
C 109	13.6	1.3	14	1	US-09-827-998-384	Sequence 384, App	C 182	12.4	1.2	14	1	US-09-263-959-530	Sequence 530, App
C 110	13.8	1.3	14	1	US-09-827-998-385	Sequence 385, App	C 183	12.4	1.2	14	1	US-09-263-959-532	Sequence 532, App
C 111	13.8	1.3	14	1	US-09-827-998-386	Sequence 386, App	C 184	12.4	1.2	14	1	US-09-263-959-532	Sequence 532, App
C 112	13.8	1.3	14	1	US-09-827-998-387	Sequence 387, App	C 185	12.4	1.2	14	1	US-09-263-959-562	Sequence 562, App
C 113	13.8	1.3	14	1	US-09-827-998-388	Sequence 388, App	C 186	12.4	1.2	14	1	US-09-263-959-562	Sequence 562, App
C 114	13.8	1.3	14	1	US-09-827-998-389	Sequence 389, App	C 187	12.4	1.2	14	1	US-09-263-959-562	Sequence 562, App
C 115	13.8	1.3	14	1	US-09-263-959-546	Sequence 546, App	C 188	12.4	1.2	14	1	US-09-263-959-592	Sequence 592, App
C 116	13.8	1.3	14	1	US-09-263-959-837	Sequence 837, App	C 189	12.4	1.2	14	1	US-09-263-959-726	Sequence 726, App
C 117	13.8	1.3	14	1	US-09-843-676-132	Sequence 132, App	C 190	12.4	1.2	14	1	US-09-263-959-726	Sequence 726, App
C 118	13.8	1.3	14	1	US-09-766-253-132	Sequence 132, App	C 191	12.4	1.2	14	1	US-09-263-959-730	Sequence 730, App
C 119	13.8	1.3	14	1	US-09-438-486-132	Sequence 132, App	C 192	12.4	1.2	14	1	US-09-263-959-730	Sequence 730, App
C 120	13.8	1.3	14	1	US-09-848-754A-2098	Sequence 2098, App	C 193	12.4	1.2	14	1	US-09-263-959-730	Sequence 730, App
C 121	13.8	1.3	14	1	US-10-028-357-23	Sequence 23, Appl	C 194	12.4	1.2	14	1	US-09-263-959-752	Sequence 752, App
C 122	13.8	1.3	14	1	US-10-053-758-132	Sequence 132, App	C 195	12.4	1.2	14	1	US-09-263-959-752	Sequence 752, App
C 123	13.8	1.3	14	1	US-10-054-295-132	Sequence 132, App	C 196	12.4	1.2	14	1	US-09-263-959-764	Sequence 764, App
C 124	13.8	1.3	14	1	US-10-117-267-5	Sequence 5, Appl	C 197	12.4	1.2	14	1	US-09-263-959-822	Sequence 822, App
C 125	13.8	1.3	14	1	US-10-060-756A-087	Sequence 4087, App	C 198	12.4	1.2	14	1	US-09-263-959-822	Sequence 822, App
C 126	13.8	1.3	14	1	US-10-054-611-132	Sequence 132, App	C 199	12.4	1.2	14	1	US-10-232-927A-78	Sequence 78, Appl
C 127	13.8	1.3	14	1	US-10-566-306-1628	Sequence 1628, App	C 200	12.4	1.2	14	1	US-09-263-959-543	Sequence 543, App
C 128	13.8	1.3	14	1	US-09-263-959-971	Sequence 971, App	C 201	12.4	1.2	15	1	US-09-263-959-545	Sequence 545, App
C 129	13.6	1.3	14	1	US-08-463-404-51	Sequence 51, Appl	C 202	12.4	1.2	15	1	US-09-263-959-877	Sequence 877, App
C 130	13.4	1.3	14	1	US-09-263-959-543	Sequence 543, App	C 203	12.4	1.2	15	1	US-09-877-478-6011	Sequence 6011, App
C 131	13.4	1.3	14	1	US-09-263-959-545	Sequence 545, App	C 204	12.4	1.2	15	1	US-09-877-478-6085	Sequence 6085, App
C 132	13.4	1.3	14	1	US-09-263-959-877	Sequence 877, App	C 205	12.4	1.2	15	1	US-10-342-902-6011	Sequence 6011, App
C 133	13.4	1.3	14	1	US-10-287-919-582	Sequence 582, App	C 206	12.4	1.2	15	1	US-10-342-902-6085	Sequence 6085, App
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C 135	13.4	1.3	14	1	US-10-287-919-2620	Sequence 2620, App	C 208	12.4	1.2	15	1	US-10-287-919-2317	Sequence 2317, App
C 136	13.4	1.3	14	1	US-10-232-927A-79	Sequence 79, Appl	C 209	12.4	1.2	15	1	US-10-287-919-2441	Sequence 2441, App
C 137	13.4	1.3	14	1	US-10-271-602B-208	Sequence 208, App	C 210	12.4	1.2	15	1	US-10-091-281-81	Sequence 81, Appl
C 138	13.4	1.3	14	1	US-09-263-959-541	Sequence 541, App	C 211	12.4	1.2	15	1	US-10-271-602B-184	Sequence 184, App
C 139	13.4	1.3	14	1	US-09-263-959-541	Sequence 541, App	C 212	12.4	1.2	15	1	US-10-271-602B-192	Sequence 192, App
C 140	13.4	1.3	14	1	US-09-263-959-541	Sequence 541, App	C 213	12.4	1.2	15	1	US-10-271-602B-200	Sequence 200, App
C 141	13.4	1.3	14	1	US-09-263-959-544	Sequence 544, App	C 214	12.4	1.2	15	1	US-10-271-602B-207	Sequence 207, App
C 142	13.4	1.3	14	1	US-09-263-959-544	Sequence 544, App	C 215	12	1.1	12	1	US-09-735-363A-13	Sequence 13, Appl
C 143	13	1.2	13	1	US-09-263-959-548	Sequence 508, App	C 216	12	1.1	12	1	US-09-735-363A-13	Sequence 13, Appl
C 144	13	1.2	13	1	US-09-263-959-548	Sequence 508, App	C 217	12	1.1	12	1	US-09-263-959-649	Sequence 649, App
C 145	13	1.2	13	1	US-09-263-959-548	Sequence 548, App	C 218	12	1.1	12	1	US-09-263-959-649	Sequence 649, App
C 146	13	1.2	13	1	US-09-263-959-704	Sequence 704, App	C 219	12	1.1	12	1	US-09-263-959-768	Sequence 768, App
C 147	13	1.2	13	1	US-09-263-959-723	Sequence 723, App	C 220	12	1.1	12	1	US-09-263-959-768	Sequence 768, App
C 148	13	1.2	13	1	US-08-892-503-1	Sequence 1, Appl	C 221	12	1.1	12	1	US-09-263-959-832	Sequence 832, App
C 149	13	1.2	13	1	US-08-892-503-2	Sequence 2, Appl	C 222	12	1.1	12	1	US-09-263-959-832	Sequence 832, App
C 150	13	1.2	13	1	US-09-918-995-38044	Sequence 38044, A	C 223	12	1.1	12	1	US-09-263-959-838	Sequence 838, App
C 151	13	1.2	13	1	US-09-918-995-38045	Sequence 38045, A	C 224	12	1.1	12	1	US-09-263-959-972	Sequence 972, App
C 152	13	1.2	13	1	US-09-896-095-2845	Sequence 245, App	C 225	12	1.1	12	1	US-09-263-959-975	Sequence 975, App
C 153	13	1.2	13	1	US-09-896-095-2845	Sequence 121, App	C 226	12	1.1	12	1	US-09-263-959-981	Sequence 981, App
C 154	13	1.2	13	1	US-10-056-414-121	Sequence 121, App	C 227	12	1.1	12	1	US-09-263-959-981	Sequence 981, App
C 155	13	1.2	13	1	US-10-056-414-194	Sequence 194, App	C 228	12	1.1	12	1	US-08-841-157A-11	Sequence 11, Appl
C 156	13	1.2	13	1	US-10-056-414-310	Sequence 310, App	C 229	12	1.1	12	1	US-08-841-157A-11	Sequence 11, Appl
C 157	13	1.2	13	1	US-10-187-251A-1	Sequence 1, Appl	C 230	12	1.1	12	1	US-10-077-275A-11	Sequence 11, Appl
C 158	13	1.2	13	1	US-10-187-251A-1	Sequence 1, Appl	C 231	12	1.1	12	1	US-10-331-780-2	Sequence 2, Appl
C 159	12.8	1.2	16	1	US-09-739-928-2	Sequence 2, Appl	C 232	12	1.1	15	1	US-09-877-478-6010	Sequence 6010, App
C 160	12.8	1.2	16	1	US-09-152-059-70	Sequence 70, Appl	C 233	12	1.1	15	1	US-09-848-754A-9167	Sequence 9167, App
C 161	12.8	1.2	16	1	US-09-263-959-950	Sequence 950, App	C 234	12	1.1	15	1	US-10-342-902-6010	Sequence 6010, App
C 162	12.8	1.2	16	1	US-09-805-296D-9	Sequence 9, Appl	C 235	12	1.1	15	1	US-10-056-414-120	Sequence 120, App
C 163	12.8	1.2	16	1	US-09-843-676-131	Sequence 131, App	C 236	12	1.1	15	1	US-10-056-414-193	Sequence 193, App
C 164	12.8	1.2	16	1	US-09-766-253-131	Sequence 131, App	C 237	12	1.1	15	1	US-10-056-414-309	Sequence 309, App
C 165	12.8	1.2	16	1	US-09-438-486-131	Sequence 131, App	C 238	12	1.1	15	1	US-10-287-919-2049	Sequence 2049, App
C 166	12.8	1.2	16	1	US-09-438-486-131	Sequence 131, App	C 239	12	1.1	15	1	US-10-041-414-52	Sequence 52, Appl
C 167	12.8	1.2	16	1	US-09-438-486-131	Sequence 131, App	C 240	12	1.1	15	1	US-10-365-131-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-10-101-040-9/c
; Sequence 9, Application US/10101040
; Publication No. US2020142353A1
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret

```
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: FIBRO100-1
; CURRENT APPLICATION NUMBER: US/10/101,040
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense CTGF oligonucleotide
US-10-101-040-9

Query Match      2.4%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1718 ATTAGACTGGACAGCTTGTGGCAAG 1742
Db 25 ATTAGACTGGACAGCTTGTGGCAAG 1

RESULT 2
US-10-101-040-10/c
; Sequence 10, Application US/10101040
; Publication No. US20020142353A1
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF
; FILE REFERENCE: FIBRO100-1
; CURRENT APPLICATION NUMBER: US/10/101,040
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Antisense CTGF oligonucleotide
US-10-101-040-10

Query Match      2.2%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 5.1;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1742 GTGAATTCCTGTAACAGCCAGA 1766
Db 25 GTGAATTCCTGTAACAGCCAGA 1

RESULT 3
```

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US-09-754-853A-601/c
; Sequence 601, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Farnell, Laurence D.
; APPLICANT: Parsons, Jeremy D.
; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Soybean Cyst Nematode Resistance
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/174,880
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 601
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 240017_region_G3_11301_29_Forward_Primer
US-09-754-853A-601

Query Match      2.2%; Score 23.4; DB 1; Length 27;
Best Local Similarity 96.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1795 TGTGTGTGTGTGTGTGTGTATAT 1819
Db 27 TGTGTGTGTGTGTGTGTATAAT 3

RESULT 4
US-09-735-363A-5
; Sequence 5, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-5

Query Match      2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTATATAT 1819
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 5
US-09-263-959-770
; Sequence 770, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
```

APPLICANT: Rowen, Lee
 APPLICANT: Koop, Ben F.
 TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 NUMBER OF SEQUENCES: 1279
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: McWaters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 770:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-263-959-770

```
Query Match      2.1%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 24: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1793 TGTGTGTGTGTGTGTGTATAT 1819
 |||||
 Db 1 TGTGTGTGTGTGTGTGTGTGT 27

```

RESULT 6
US-09-735-363A-1
; Sequence 1, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Philip, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-1

```

```
Query Match      2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      1793 TGTGTGTGTGTGTGTGTGTATAT 1817
          |||||
Db       2   TGTGTGTGTGTGTGTGTGT 26
          |||||

RESULT 7
US-09-735-363A-66
; Sequence 66, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-66

```

Query Match 2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTAT 1817
|||
db 2 TGTGTGTGTGTGTGTGT 26

```

RESULT 8
US-10-168-327-2
; Sequence 2, Application US/10168327
; Publication No. US20030176381A1
; GENERAL INFORMATION:
; APPLICANT: Phillips, Nigel C.
; APPLICANT: Fallon, Mario C.
; TITLE OF INVENTION: Hyaluronic Acid in the Treatment of Cancer
; FILE REFERENCE: 02811-0211 (42368-274915)
; CURRENT APPLICATION NUMBER: US/10/168,327
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/CA00/01562
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-10-168-327-2

```

```

Query Match          2.1%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 8.8;
Matches 23: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1793 TGTGTGTGTGTGTGTAT 1817
|||
Db 2 TGTGTGTGTGTGTGTGT 26

RESULT 9
US-09-735-363A-21

```
; Sequence 21, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-21

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 10
US-09-735-363A-22
; Sequence 22, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-22

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
Db 2 TGTGTGTGTGTGTGTGTGT 24

RESULT 11
US-09-776-479-1068
; Sequence 1068, Application US/09776479
; Patent No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
```

```
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1068
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-1068

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 12
US-10-112-653-1012
; Sequence 1012, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1012
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-1012

Query Match      2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTAT 1815
Db 1 TGTGTGTGTGTGTGTGTGT 23

RESULT 13
US-10-017-995-1068
; Sequence 1068, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
```


SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1068
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-1068

Query Match 2.0%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGT 1815
Db 1 TGTGTGTGTGTGTGTGTGTGT 23

RESULT 14
US-09-735-363A-19
; Sequence 19, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Philip, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 19
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-19

Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 15
US-09-776-479-907
; Sequence 907, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 907
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-907

Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 16
US-10-112-653-876
; Sequence 876, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060 (AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,842
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 876
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-876

Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGT 1813
Db 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 17
US-10-017-995-907
; Sequence 907, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 907
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-907

Query Match 2.0%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTGTGTGTGT 1813

; PRIOR APPLICATION NUMBER: 60/296,685
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1:
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Nucleic Acid Ligand
US-10-165-854-1

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812
DB 20 TGTGTGTGTGTGTGTGTG 1

RESULT 22
US-10-165-854-2
; Sequence 2, Application US/10165854
; Publication No. US20030059807A1
; GENERAL INFORMATION:
; APPLICANT: Roach, Jeffrey Shawn
; TITLE OF INVENTION: MICROCALORIMETRIC DETECTION OF ANALYTES AND BINDING EVENTS
; FILE REFERENCE: PRO6
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US/10/165,854
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Nucleic Acid Ligand
US-10-165-854-2

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812
DB 1 TGTGTGTGTGTGTGTGTG 20

RESULT 23
US-10-219-238-1
; Sequence 1, Application US/10219238
; Publication No. US20030114405A1
; GENERAL INFORMATION:
; APPLICANT: Linnik, Matthew D.
; APPLICANT: Hepburn, Bonnie
; TITLE OF INVENTION: METHODS OF TREATING SYSTEMIC LUPUS
; TITLE OF INVENTION: ERYTHEMATOSUS IN INDIVIDUALS HAVING
; TITLE OF INVENTION: SIGNIFICANTLY IMPAIRED RENAL FUNCTION
; FILE REFERENCE: 252312007800
; CURRENT APPLICATION NUMBER: US/10/219,238
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/314,281
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/311,858
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-219-238-1

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTG 1813
DB 1 GTGTGTGTGTGTGTGTGTG 20

RESULT 24
US-10-219-238-2/c
; Sequence 2, Application US/10219238
; Publication No. US20030114405A1
; GENERAL INFORMATION:
; APPLICANT: Linnik, Matthew D.
; APPLICANT: Hepburn, Bonnie
; TITLE OF INVENTION: METHODS OF TREATING SYSTEMIC LUPUS
; TITLE OF INVENTION: ERYTHEMATOSUS IN INDIVIDUALS HAVING
; TITLE OF INVENTION: SIGNIFICANTLY IMPAIRED RENAL FUNCTION
; FILE REFERENCE: 252312007800
; CURRENT APPLICATION NUMBER: US/10/219,238
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/314,281
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/311,858
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-219-238-2

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812
DB 20 TGTGTGTGTGTGTGTGTG 1

RESULT 25
US-10-006-191-39/c
; Sequence 39, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-39

Query Match 1.9%; Score 20; DB 1; Length 20;

```
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1719 TTAGACTGGACAGCTTGTTGG 1738
Db 20 TTAGACTGGACAGCTTGTTGG 1

RESULT 26
US-10-006-191-40/c
; Sequence 40, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-40
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1724 CTGGACAGCTTGTCGCAAGT 1743
Db 20 CTGGACAGCTTGTCGCAAGT 1

RESULT 27
US-10-006-191-41/c
; Sequence 41, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-41
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1727 TGTACAGTTATCTAAGTTAA 1846
Db 20 TGTACAGTTATCTAAGTTAA 1

RESULT 28
US-10-006-191-42/c
; Sequence 42, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-42
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1732 AGTTATCTAAGTTAATTAA 1851
Db 20 AGTTATCTAAGTTAATTAA 1

RESULT 29
US-10-006-191-43/c
; Sequence 43, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-43
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2058 GAACAATGGCCTTTATTAA 2117
Db 20 GAACAATGGCCTTTATTAA 1

RESULT 30
US-10-006-191-44/c
; Sequence 44, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-44
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2198 CAGTTTATTGTGAGTG 2217
DB 20 CAGTTTATTGTGAGTG 1
RESULT 31
US-10-006-191-45/c
; Sequence 45, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-45
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2203 TATTGTTGAGAGTGAGC 2222
DB 20 TATTGTTGAGAGTGAGC 1
RESULT 32
US-10-006-191-46/c
; Sequence 46, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-46
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2208 GTTGAGAGTGACCAAG 2227
DB 20 GTTGAGAGTGACCAAG 1
RESULT 33
US-10-006-191-47/c
; Sequence 47, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION

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; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-47
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2213 GAGTGTGACCAAAAGTTACA 2232
DB 20 GAGTGTGACCAAAAGTTACA 1
RESULT 34
US-10-006-191-48/c
; Sequence 48, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-48
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2218 TGACCAAAAGTTACATGTTT 2237
DB 20 TGACCAAAAGTTACATGTTT 1
RESULT 35
US-10-006-191-49/c
; Sequence 49, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-49
Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2242 CTTTCTAGTTGAATAAAG 2261
|||||
Db 20 CTTTCTAGTTGAATAAAG 1

RESULT 36

US-10-006-191-59/c
; Sequence 59, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-59

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1723 ACTGGACAGCTTGTGGCAAG 1742
|||||
Db 20 ACTGGACAGCTTGTGGCAAG 1

RESULT 37

US-10-006-191-60/c
; Sequence 60, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-60

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1752 CTGTAAACAGCCAGATTTT 1771
|||||
Db 20 CTGTAAACAGCCAGATTTT 1

RESULT 38

US-10-006-191-61/c
; Sequence 61, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274

; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-61

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1834 TTATCTAAGTTAATTTAAAG 1853
|||||
Db 20 TTATCTAAGTTAATTTAAAG 1

RESULT 39

US-10-006-191-62/c
; Sequence 62, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-62

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2206 TTGTTGAGAGTGTGACCAA 2225
|||||
Db 20 TTGTTGAGAGTGTGACCAA 1

RESULT 40

US-10-006-191-63/c
; Sequence 63, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-63

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2212 AGAGTGTGACCAAAAGTTAC 2231
 |||||
 Db 20 AGAGTGTGACCAAAAGTTAC 1

RESULT 41

US-10-006-191-64/c
 ; Sequence 64, Application US/10006191
 ; Publication No. US20030144223A1
 ; GENERAL INFORMATION:
 ; APPLICANT: William Gaarde
 ; APPLICANT: Andrew T. Watt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
 ; FILE REFERENCE: RTS-0274
 ; CURRENT APPLICATION NUMBER: US/10/006,191
 ; CURRENT FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 64
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-006-191-64

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2219 GACCAAAAGTTACATGTTG 2238
 |||||
 Db 20 GACCAAAAGTTACATGTTG 1

RESULT 42

US-10-006-191-65/c
 ; Sequence 65, Application US/10006191
 ; Publication No. US20030144223A1
 ; GENERAL INFORMATION:
 ; APPLICANT: William Gaarde
 ; APPLICANT: Andrew T. Watt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
 ; FILE REFERENCE: RTS-0274
 ; CURRENT APPLICATION NUMBER: US/10/006,191
 ; CURRENT FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 65
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-006-191-65

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2243 TTTCTAGTTGAAATAAAGT 2262
 |||||
 Db 20 TTTCTAGTTGAAATAAAGT 1

RESULT 43

US-10-006-191-92/c
 ; Sequence 92, Application US/10006191
 ; Publication No. US20030144223A1
 ; GENERAL INFORMATION:
 ; APPLICANT: William Gaarde
 ; APPLICANT: Andrew T. Watt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
 ; FILE REFERENCE: RTS-0274
 ; CURRENT APPLICATION NUMBER: US/10/006,191

; CURRENT FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 92
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-006-191-92

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1242 TCACATCTCATTTTCCGTA 1261
 |||||
 Db 20 TCACATCTCATTTTCCGTA 1

RESULT 44

US-10-006-191-93/c
 ; Sequence 93, Application US/10006191
 ; Publication No. US20030144223A1
 ; GENERAL INFORMATION:
 ; APPLICANT: William Gaarde
 ; APPLICANT: Andrew T. Watt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
 ; FILE REFERENCE: RTS-0274
 ; CURRENT APPLICATION NUMBER: US/10/006,191
 ; CURRENT FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 93
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-006-191-93

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1274 GTAGCACAAGTTATTAAAT 1293
 |||||
 Db 20 GTAGCACAAGTTATTAAAT 1

RESULT 45

US-10-006-191-94/c
 ; Sequence 94, Application US/10006191
 ; Publication No. US20030144223A1
 ; GENERAL INFORMATION:
 ; APPLICANT: William Gaarde
 ; APPLICANT: Andrew T. Watt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
 ; FILE REFERENCE: RTS-0274
 ; CURRENT APPLICATION NUMBER: US/10/006,191
 ; CURRENT FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 153
 ; SEQ ID NO 94
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-006-191-94

Query Match 1.9%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1371 CCAGACACTGGTTTCAAGAA 1390

```
Db 20 CCAGACACTGGTTTGAGAA 1
|||||
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-97

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1553 AAATTTAGCGTCTCACTG 1572
|||||
Db 20 AAATTTAGCGTCTCACTG 1

RESULT 47
US-10-006-191-96/c
; Sequence 96, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 95
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-95

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1553 AAATTTAGCGTCTCACTG 1572
|||||
Db 20 AAATTTAGCGTCTCACTG 1

RESULT 48
US-10-006-191-97/c
; Sequence 97, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RTS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; PRIOR FILING DATE: 2001-12-10
```

```
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-97

Query Match 1.9%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1713 TGTCGATTAGCTGGACAGC 1732
|||||
Db 20 TGTCGATTAGCTGGACAGC 1

RESULT 49
US-09-735-363A-20
; Sequence 20, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-20

Query Match 1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
|||||
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 50
US-10-385-193-1/c
; Sequence 1, Application US/10385193
; Publication No. US20030229218A1
; GENERAL INFORMATION:
; APPLICANT: Nanda D. Sinha
; TITLE OF INVENTION: Synthesis for Oligonucleotide Synthesis
; FILE REFERENCE: 2733.1001-001
; CURRENT APPLICATION NUMBER: US/10/385,193
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/230,685
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-385-193-1
```



```
Query Match      1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 51
US-10-385-193-2
; Sequence 2, Application US/10385193
; Publication No. US20030229218A1
; GENERAL INFORMATION:
; APPLICANT: Nanda D. Sinha
; TITLE OF INVENTION: Synthons for Oligonucleotide Synthesis
; FILE REFERENCE: 2733.1001-001
; CURRENT APPLICATION NUMBER: US/10/385,193
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/230,685
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-385-193-2

Query Match      1.9%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
DB 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 52
US-09-263-959-774/c
; Sequence 774, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
```

```
TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 774:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-774

Query Match      1.9%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTAT 1815
DB 23 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 53
US-10-357-488-5
; Sequence 5, Application US/10357488
; Publication No. US20030194730A1
; GENERAL INFORMATION:
; APPLICANT: Centre For DNA Fingerprinting and Diagnostics
; TITLE OF INVENTION: No. US20030194730A1 FISSR-PCR primers and markers and a method c
; TITLE OF INVENTION: Primers and markers for identifying genetic constitution and bree
; TITLE OF INVENTION: varieties.
; FILE REFERENCE: 782-Indian
; CURRENT APPLICATION NUMBER: US/10/357,488
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 260/MAS/2002
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A novel FISSR-PCR primer for genotyping eukaryotes
US-10-357-488-5

Query Match      1.8%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGTGT 1813
DB 3 TATGTGTGTGTGTGTGTGTGT 23

RESULT 54
US-09-557-423-7/c
; Sequence 7, Application US/09557423
; Patent No. US20020094555A1
; GENERAL INFORMATION:
; APPLICANT: Belotserkovskii, Boris
; APPLICANT: Reddy, Gurucharan
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Locked Nucleic Acid Hybrids and Methods of Use
; FILE REFERENCE: A-68112-1/RPT/RMS/BTC
; CURRENT APPLICATION NUMBER: US/09/557,423
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: USSN 60/130,345
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 2-DNA
```

US-09-557-423-7

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811
DB 19 TGTGTGTGTGTGTGTGTGT 1

RESULT 55

US-09-557-423-8
; Sequence 8, Application US/09557423
; Patent No. US20020094555A1
; GENERAL INFORMATION:
; APPLICANT: Belotserkovskii, Boris
; APPLICANT: Reddy, Gurucharan
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Locked Nucleic Acid Hybrids and Methods of Use
; FILE REFERENCE: A-68112-1/FT/RMS/BTC
; CURRENT APPLICATION NUMBER: US/09/557,423
; CURRENT FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: USSN 60/130,345
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Z-DNA

US-09-557-423-8

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811
DB 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 56

US-09-369-373-3086/c
; Sequence 3086, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 39-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3086
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Glycine max

US-09-369-373-3086

Query Match 1.8%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1811

Db 19 TGTGTGTGTGTGTGTGTGT 1

RESULT 57

US-10-006-191-153/c
; Sequence 153, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: RFS-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 153
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-153

Query Match 1.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2247 TAGTTGAAATAAAGTGTAT 2266
DB 20 TAGTTGAAATAAAGTATAT 1

RESULT 58

US-09-735-363A-17
; Sequence 17, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-17

Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTGT 1810
DB 1 TGTGTGTGTGTGTGTGTGT 18

RESULT 59

US-09-735-363A-18
; Sequence 18, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario

APPLICANT: Phillip, Nigel
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02811-0181
CURRENT APPLICATION NUMBER: US/09/735,363A
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/170,325
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 60/228,925
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patent in version 3.0
SEQ ID NO 18
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-18
Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1794 TGCTGTGTGTGTGTGTG 1811
Db 1 TGCTGTGTGTGTGTGTG 18
RESULT 60
US-09-896-650A-28
Sequence 28, Application US/09896650A
Patent No. US20020146704A1
GENERAL INFORMATION:
APPLICANT: Head, Steven
APPLICANT: Boyce-Jacino, Michael
APPLICANT: Karn, Jonathan
APPLICANT: Golet, Philip
TITLE OF INVENTION: De No. US20020146704A1 or "Universal" Sequencing Array
FILE REFERENCE: 13019-2
CURRENT APPLICATION NUMBER: US/09/896,650A
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent in version 3.1
SEQ ID NO 28
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Reagent Sequence
US-09-896-650A-28
Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1793 TGCTGTGTGTGTGTGTG 1810
Db 1 TGCTGTGTGTGTGTGTG 18
RESULT 61
US-10-011-204-1/c
Sequence 1, Application US/10011204
Publication No. US20020182617A1
GENERAL INFORMATION:
APPLICANT: EKINS, Roger P
TITLE OF INVENTION: Binding assay using binding agents with tail groups
FILE REFERENCE: 0380-P01180US0
CURRENT APPLICATION NUMBER: US/10/011,204
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US/08/700,530
PRIOR FILING DATE: 1996-10-23
PRIOR APPLICATION NUMBER: PCT/GB95/00521

PRIOR FILING DATE: 1995-03-10
PRIOR APPLICATION NUMBER: GB 9404709.9
PRIOR FILING DATE: 1994-03-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 1
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide
US-10-011-204-1
Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1793 TGCTGTGTGTGTGTGTG 1810
Db 18 TGCTGTGTGTGTGTGTG 1
RESULT 62
US-10-011-204-2
Sequence 2, Application US/10011204
Publication No. US20020182617A1
GENERAL INFORMATION:
APPLICANT: EKINS, Roger P
TITLE OF INVENTION: Binding assay using binding agents with tail groups
FILE REFERENCE: 0380-P01180US0
CURRENT APPLICATION NUMBER: US/10/011,204
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US/08/700,530
PRIOR FILING DATE: 1996-10-23
PRIOR APPLICATION NUMBER: PCT/GB95/00521
PRIOR FILING DATE: 1995-03-10
PRIOR APPLICATION NUMBER: GB 9404709.9
PRIOR FILING DATE: 1994-03-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 2
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide
US-10-011-204-2
Query Match 1.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1794 TGCTGTGTGTGTGTGTG 1811
Db 1 TGCTGTGTGTGTGTGTG 18
RESULT 63
US-10-357-488-26
Sequence 26, Application US/10357488
Publication No. US20030194730A1
GENERAL INFORMATION:
APPLICANT: Centre For DNA Fingerprinting and Diagnostics
TITLE OF INVENTION: No. US20030194730A1el FISRR-PCR primers and markers and a method c
TITLE OF INVENTION: primers and markers for identifying genetic constitution and bre
TITLE OF INVENTION: varieties.
FILE REFERENCE: 782-indian
CURRENT APPLICATION NUMBER: US/10/357,488
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 260/MAS/2002
PRIOR FILING DATE: 2002-04-08

; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent version 3.1
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A novel FISSR-PCR primer for genotyping eukaryotes
US-10-357-488-26

Query Match 1.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1798 GTGTGTGTGTGTGTAT 1815
|||||
Db 1 GTGTGTGTGTGTGTAT 18

RESULT 64
US-09-918-186A-235/c
; Sequence 235, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0585
; CURRENT APPLICATION NUMBER: US/09/918,186A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,594
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 235
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-186A-235

Query Match 1.7%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1811 TGTATATATATATATGT 1829
|||||
Db 19 TGTATATATATATATGT 1

RESULT 65
US-09-263-959-557
; Sequence 557, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 557:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-557

Query Match 1.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGT 1809
|||||
Db 1 TGTGTGTGTGTGTGT 17

RESULT 66
US-09-263-959-705
; Sequence 705, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 705:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-705

```
Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809
DB 1 TGTGTGTGTGTGTGTGT 17

RESULT 67
US-09-263-959-970
; Sequence 970, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 970:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-970

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGT 1809
DB 1 TGTGTGTGTGTGTGTGT 17

RESULT 68
US-10-339-782-333
; Sequence 333, Application US/10339782
; Publication No. US20030166026A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Goodman, Laurie J
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells
; FILE REFERENCE: 37-000110US
; CURRENT APPLICATION NUMBER: US/10/339,782
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 495
```

```
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 333
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-339-782-333

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2141 GATCAGTTTTTTCACCT 2157
DB 1 GATCAGTTTTTTCACCT 17

RESULT 69
US-10-340-192-68
; Sequence 68, Application US/10340192
; Publication No. US20030170700A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: SECRETED AND CELL SURFACE POLYPEPTIDES AFFECTED BY CHOLESTEROL ANI
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 37-000610US
; CURRENT APPLICATION NUMBER: US/10/340,192
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 68
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-340-192-68

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2141 GATCAGTTTTTTCACCT 2157
DB 1 GATCAGTTTTTTCACCT 17

RESULT 70
US-09-969-373-2420
; Sequence 2420, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauger, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2420
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2420

Query Match
Best Local Similarity 90.0%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1793 TGTGTGTGTGTGTGTGTG 1812
Db 1 TCTGTGTGTGTGTGTGTG 20

RESULT 71
US-09-969-373-2422
; Sequence 2422, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Haug, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2422
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2422

Query Match 1.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1812
Db 1 TCTGTGTGTGTGTGTGTG 20

RESULT 72
US-10-006-191-135/c
; Sequence 135, Application US/10006191
; Publication No. US20030144223A1
; GENERAL INFORMATION:
; APPLICANT: William Gaarde
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION
; FILE REFERENCE: R1S-0274
; CURRENT APPLICATION NUMBER: US/10/006,191
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-006-191-135

Query Match 1.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1675 ATTCTGATTCGAATGACACT 1694
Db 20 ATTCTGATTCGAATGACACT 1

RESULT 73
US-09-768-917-10/c
; Sequence 10, Application US/09768917
; Patent No. US20020034494A1
; GENERAL INFORMATION:
; APPLICANT: Vicari, Alain P.
; APPLICANT: Cauc, Christophe
; APPLICANT: Laface, Drake
; TITLE OF INVENTION: Chemokines as Adjuvants of Immune Response
; FILE REFERENCE: SF0896K US
; CURRENT APPLICATION NUMBER: US/09/768,917
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: EP 0 974 357
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-768-917-10

Query Match 1.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
Db 21 GTGTGTGTGTGTGTGTGTGT 2

RESULT 74
US-10-085-906-412
; Sequence 412, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-412

Query Match 1.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGTGT 1813
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 75
US-09-263-959-983/c
; Sequence 983, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/263.959
FILING DATE: 05-MAR-1999
CLASSIFICATION: US/09-263-959-983
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 983:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-983

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTGTG 1810
DB 18 TGTGTGTGTGTGTGTGTG 1

RESULT 76
US-10-085-906-135
Sequence 135, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
FILE REFERENCE: GNN-5343CP2
CURRENT APPLICATION NUMBER: US/10/085.906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 09/534,061
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 135
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-135

Query Match 1.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1811

DB 1 GTGTGTGTGTGTGTGTGT 18
RESULT 77
US-10-301-844-26
Sequence 26, Application US/10301844
Publication No. US20030100747A1
GENERAL INFORMATION:
APPLICANT: Ruddy, David A.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-NOV-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-301-844-26

Query Match 1.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATATATGTA 1830
DB 2 TATATATATATATATATA 19

RESULT 78
US-10-301-844-26/c
Sequence 26, Application US/10301844
Publication No. US20030100747A1
GENERAL INFORMATION:
APPLICANT: Ruddy, David A.
TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/301,844
FILING DATE: 20-NOV-1997
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/852,495C
FILING DATE: 07-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-301-844-26

Query Match 1.6%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATGTA 1830
DB 19 TATATATATATATATA 2

RESULT 79
US-10-092-885-27
Sequence 27, Application US/10092885
Publication No. US20030150618A1
GENERAL INFORMATION:
APPLICANT: SAWAL, BABRU
APPLICANT: LI, YUAN
APPLICANT: HERMIDA, LEANDRO C.
APPLICANT: HOPPA, NANCY L.
APPLICANT: JOHE, KARL K.
TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG
FILE REFERENCE: 0109015/026
CURRENT APPLICATION NUMBER: US/10/092,885
CURRENT FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 16
TYPE: DNA
ORGANISM: Homo sapiens
US-10-092-885-27

Query Match 1.5%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGTGT 1809
DB 1 GTGTGTGTGTGTGTGTGT 16

RESULT 80
US-09-263-959-971
Sequence 971, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 971:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-971

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1816 ATATATATATATGTACA 1832
DB 1 ATATATATATATGTATA 17

RESULT 81
US-09-888-326-85
Sequence 85, Application US/09888326
Publication No. US20030026801A1
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Hartmann, Gunther
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
FILE REFERENCE: C1039/7052 (AWS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 85
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc_feature

LOCATION: (0)...(0)
OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-85

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830
|||||
Db 1 ATATATATATATATA 17

RESULT 82

US-09-888-326-85/c
; Sequence 85, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-85

Query Match 1.5%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 57;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830
|||||
Db 18 ATATATATATATATA 2

RESULT 83

US-09-735-363A-16
; Sequence 16, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-16

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTG 1808
|||||
Db 1 GTGTGTGTGTGTGTG 15

RESULT 84

US-10-085-906-222
; Sequence 222, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 222
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-222

Query Match 1.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1807
|||||
Db 1 TGTGTGTGTGTGTG 15

RESULT 85

US-10-085-906-258/c
; Sequence 258, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-258

Query Match 1.4%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
 DB 15 TATATATATATAT 1

RESULT 86
 US-09-263-959-540
 ; Sequence 540, Application US/09263959
 ; Patent No. US20020150891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hood, Leroy E.
 ; APPLICANT: Rowen, Lee
 ; APPLICANT: Koop, Ben F.
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 ; NUMBER OF SEQUENCES: 1279
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/09/263,959
 ; FILING DATE: 05-MAR-1999
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMasters, David D.
 ; REGISTRATION NUMBER: 33,963
 ; REFERENCE/DOCKET NUMBER: 920010.426C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 622-6031
 ; INFORMATION FOR SEQ ID NO: 540:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-263-959-540

Query Match 1.4%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
 DB 2 TATATATATATAT 16

RESULT 87
 US-09-263-959-540/c
 ; Sequence 540, Application US/09263959
 ; Patent No. US20020150891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hood, Leroy E.
 ; APPLICANT: Rowen, Lee
 ; APPLICANT: Koop, Ben F.
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 ; NUMBER OF SEQUENCES: 1279
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle

STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 622-6031
 INFORMATION FOR SEQ ID NO: 540:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-263-959-540

Query Match 1.4%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
 DB 15 TATATATATATAT 1

RESULT 88
 US-10-085-906-231
 ; Sequence 231, Application US/10085906
 ; Publication No. US20030054371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ying, Vincent
 ; APPLICANT: Wu, Paul
 ; APPLICANT: Gray, Gary S.
 ; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
 ; FILE REFERENCE: GNN-5343CP2
 ; CURRENT APPLICATION NUMBER: US/10/085,906
 ; CURRENT FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 60/126,215
 ; PRIOR FILING DATE: 1999-03-25
 ; PRIOR APPLICATION NUMBER: US 09/534,061
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: PCT/US00/07938
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 545
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 231
 ; LENGTH: 16
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-085-906-231

Query Match 1.4%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1827
 DB 2 TATATATATATAT 16

RESULT 89

US-10-085-906-231/c
; Sequence 231, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 231
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-231
Query Match 1.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1813 TATATATATATATAT 1827
DB 15 TATATATATATATAT 1
RESULT 90
US-10-238-700-878
; Sequence 878, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (WEH01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 878
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-878
Query Match 1.4%; Score 15; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1391 TGTAAAGACTTGACA 1405
DB 2 UGUUAAGACUUGACA 16
RESULT 91
US-08-463-404-57
; Sequence 57, Application US/08463404
; Publication No. US20020127634A1
; GENERAL INFORMATION:
; APPLICANT: Michael D. West

APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,404
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-404-57
Query Match 1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1793 TGTGTGTGTGTGTGTG 1808
DB 1 TGGGTGTGTGTGTGTG 16
RESULT 92
US-10-092-885-28
; Sequence 28, Application US/10092885
; Publication No. US20030190618A1
; GENERAL INFORMATION:
; APPLICANT: SAMAL, BABRU
; APPLICANT: LI, YUAN
; APPLICANT: HERMIDA, LEANDRO C.
; APPLICANT: HOPPA, NANCY L.
; APPLICANT: JOHE, KARL K.
; TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG
; TITLE OF INVENTION: LIBRARIES OF CDNAS
; FILE REFERENCE: 0109015/026
; CURRENT APPLICATION NUMBER: US/10/092,885
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 60

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-895-28

Query Match      1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGTGT 1809
Db 1 GTTTGTGTGTGTGTGT 16

RESULT 93
US-10-232-927A-80
; Sequence 80, Application US/10232927A
; Publication No. US20030190638A1
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Calvin B. Harley
; Scott L. Weinrich
; Catherine M. Strahl
; Michael J. Meeachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homayoun Vaziri
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO
; TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,927A
; FILING DATE: 29-AUG-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,535
; FILING DATE: 20-AUG-1999
; APPLICATION NUMBER: 08/819,867
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chambers, Daniel M.
; REGISTRATION NUMBER: 34,561
; REFERENCE/DOCKET NUMBER: 224/232
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-10-232-927A-80
Query Match      1.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 75;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTGTG 1808
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 94
US-09-321-005A-13/C
; Sequence 13, Application US/09321005A
; Patent No. US20020162622A1
; GENERAL INFORMATION:
; APPLICANT: Gut, Ivo
; TITLE OF INVENTION: Mutation Analysis Using Mass Spectrometry
; FILE REFERENCE: B0004/7065
; CURRENT APPLICATION NUMBER: US/09/321,005A
; CURRENT FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Hypothetical Sequence for Exemplary Purposes
US-09-321-005A-13

Query Match      1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1891 ATATTTCATGTAGC 1906
Db 16 ATATTTCATGTAGC 1

RESULT 95
US-10-060-756A-4088
; Sequence 4088, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4088
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-060-756A-4088
Query Match      1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 GCATTGTTTCTACTT 2177
Db 2 GCATTGTTTCTAGTT 17

RESULT 96
US-10-060-756A-4089
; Sequence 4089, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 4089
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-4089

Query Match      1.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 76;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 GCATTGTTTCTACTT 2177
Db 1 GCATTGTTTCTAGTT 16

RESULT 97
US-10-297-068-1015
; Sequence 1015, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 13140P1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1015
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-297-068-1015

Query Match      1.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1470 GGGTACCAGCAGAAAG 1485
Db 2 GGGTACCAGCAGAAAG 17

RESULT 98
US-09-918-186A-235
; Sequence 235, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0595
; CURRENT APPLICATION NUMBER: US/09/918,186A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 235
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-186A-235

Query Match      1.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTACA 1832
Db 1 ACATATATATATATAACA 19

RESULT 99
US-09-735-363A-15
; Sequence 15, Application US/09735363A
; Patent No. US20010041691A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 14
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; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Oligonucleotide
 US-09-735-363A-15

Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
 Db 1 TGTGTGTGTGTGTG 14

RESULT 100

US-09-263-959-479/c
 ; Sequence 479, Application US/09263959
 ; Patent No. US20020150891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hood, Leroy E.
 ; APPLICANT: Rowen, Lee
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 ; NUMBER OF SEQUENCES: 1279
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 479:

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-263-959-479
 Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGT 1807
 Db 14 GTGTGTGTGTGTGT 1

RESULT 101

US-09-263-959-658
 ; Sequence 658, Application US/09263959
 ; Patent No. US20020150891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hood, Leroy E.
 ; APPLICANT: Rowen, Lee
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 479:

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-263-959-479
 Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTGT 1807
 Db 14 GTGTGTGTGTGTGT 1

; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 ; NUMBER OF SEQUENCES: 1279
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 658:

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-263-959-658
 Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
 Db 1 TGTGTGTGTGTGTG 14

RESULT 102
 US-09-263-959-811
 ; Sequence 811, Application US/09263959
 ; Patent No. US20020150891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hood, Leroy E.
 ; APPLICANT: Rowen, Lee
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 811:

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-263-959-811
 Query Match 1.3%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGTG 1806
 Db 1 TGTGTGTGTGTGTG 14

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 811:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-811

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1814 ATATATATATATAT 1827
Db 1 ATATATATATATAT 14

RESULT 103
US-09-263-959-811/c
Sequence 811, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 811:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-811

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1814 ATATATATATATAT 1827
Db 14 ATATATATATATAT 1

RESULT 104
US-09-913-514-27
Sequence 27, Application US/09913514
Publication No. US20030082210A1

GENERAL INFORMATION:
APPLICANT: GOMI, Yasuyuki
APPLICANT: SUNAMACHI, Hiroki
APPLICANT: TAKAHASHI, Michiaki
APPLICANT: YAMANISHI, Koichi
TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine
FILE REFERENCE: 0216-0454P
CURRENT APPLICATION NUMBER: US/09/913,514
CURRENT FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: PCT/JP01/00678
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: JP 2000-62734
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 14
TYPE: DNA
ORGANISM: Varicella virus
US-09-913-514-27

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1813 TATATATATATATA 1826
Db 1 TATATATATATATA 14

RESULT 105
US-09-913-514-27/c
Sequence 27, Application US/09913514
Publication No. US20030082210A1
GENERAL INFORMATION:
APPLICANT: GOMI, Yasuyuki
APPLICANT: SUNAMACHI, Hiroki
APPLICANT: TAKAHASHI, Michiaki
APPLICANT: YAMANISHI, Koichi
TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine
FILE REFERENCE: 0216-0454P
CURRENT APPLICATION NUMBER: US/09/913,514
CURRENT FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: PCT/JP01/00678
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: JP 2000-62734
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 14
TYPE: DNA
ORGANISM: Varicella virus
US-09-913-514-27

Query Match 1.3%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1813 TATATATATATATA 1826
Db 14 TATATATATATATA 1

RESULT 106
US-10-301-844-19
Sequence 19, Application US/10301844
Publication No. US20030100747A1
GENERAL INFORMATION:
APPLICANT: Ruddy, David A.
Wolff, Roger K.
TITLE OF INVENTION: HEMOCHROMATOSIS GENE

```

;
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/301,844
; FILING DATE: 20-NO. US20030100747A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,495C
; FILING DATE: 07-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0057-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-301-844-19

; Query Match 1.3%; Score 14; DB 1; Length 14;
; Best Local Similarity 100.0%; Pred. No. 82;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826
DB 1 TATATATATATATA 14

RESULT 107
US-10-301-844-19/c
; Sequence 19, Application US/10301844
; Publication No. US20030100747A1
; GENERAL INFORMATION:
; APPLICANT: Ruddy, David A.
; TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
; HEMOCHROMATOSIS GENE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/301,844
; FILING DATE: 20-NO. US20030100747A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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```

;
; APPLICATION NUMBER: US/08/852,495C
; FILING DATE: 07-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0057-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-301-844-19

; Query Match 1.3%; Score 14; DB 1; Length 14;
; Best Local Similarity 100.0%; Pred. No. 82;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826
DB 14 TATATATATATATA 1

RESULT 108
US-10-085-906-258
; Sequence 258, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 258
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-085-906-258

; Query Match 1.3%; Score 14; DB 1; Length 15;
; Best Local Similarity 100.0%; Pred. No. 83;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 1 ATATATATATATAT 14

RESULT 109
US-09-827-998-384
; Sequence 384, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Ch, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8

```


Fri Apr 2 14:41:47 2004

```
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 384
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-384
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Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1794 GTGTGTGTGTGTGTGTG 1810
Db 1 GTGTGTGTGTGTGTG 17
```

RESULT 110

```
US-09-827-998-385
; Sequence 385, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 385
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-385
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```
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1793 TGTGTGTGTGTGTGTGT 1809
Db 1 TGTGTGTGTGTGTGTGT 17
```

RESULT 111

```
US-09-827-998-386
; Sequence 386, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 386
```

```
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-386
```

```
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1794 GTGTGTGTGTGTGTGTG 1810
Db 1 GTGTGTGTGTGTGTG 17
```

RESULT 112

```
US-09-827-998-387
; Sequence 387, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 387
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-387
```

```
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1793 TGTGTGTGTGTGTGTGT 1809
Db 1 TGTGTGTGTGTGTGTGT 17
```

RESULT 113

```
US-09-827-998-388
; Sequence 388, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 388
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-388
```

```
Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1798 GTGTGTGTGTGTGTAT 1814
|||||
Db 1 GTGTGTGTGTGTGTAT 17

RESULT 114

US-09-827-998-389
; Sequence 389, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 389
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-389

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTAT 1815
|||||
Db 1 TGTGTGTGTGTGTAT 17

RESULT 115

US-09-263-959-546
; Sequence 546, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 546:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-546

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTAT 1815
|||||
Db 1 TGTGTGTGTGTGTAT 17

RESULT 117
US-09-843-676-132
; Sequence 132, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-546

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1814 ATATATATATATATGTA 1830
|||||
Db 1 ATGTATGTATATATGTA 17

RESULT 116

US-09-263-959-837/c
; Sequence 837, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 837:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-837

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1799 TGTGTGTGTGTGTAT 1815
|||||
Db 1 TGTATGTGTGTATGTA 17

RESULT 117

US-09-843-676-132
; Sequence 132, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.

```

; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
;
; US-09-843-676-132
;
; Query Match 1.3%; Score 13.8; DB 1; Length 17;
; Best Local Similarity 88.2%; Pred. No. 91;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1865 TTTTATTTTGTGTTTT 1881
; Db 1 TTTTATTTTGTGTTTT 17
;
; RESULT 118
; US-09-766-253-132
; Sequence 132, Application US/09766253
; Publication No. US2002018747A1el
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US2002018747A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco

```

```

; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
;
; US-09-766-253-132
;
; Query Match 1.3%; Score 13.8; DB 1; Length 17;
; Best Local Similarity 88.2%; Pred. No. 91;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1865 TTTTATTTTGTGTTTT 1881
; Db 1 TTTTATTTTGTGTTTT 17
;
; RESULT 119
; US-09-438-486-132
; Sequence 132, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-438-486-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1881
Db 1 TTTTATTTTGTGTTT 17

RESULT 120
US-09-848-754A-2098/c
Sequence 2098, Application US/09848754A
Publication No. US20030073207A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
FILE REFERENCE: MEH800-958-I (400/018)
CURRENT APPLICATION NUMBER: US/09/848,754A
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 9645
SOFTWARE: Patent in version 3.0
SEQ ID NO 2098
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-848-754A-2098

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1789 ATATTGTGTGTGTGT 1805
Db 17 ATTTGTATGTGTGTGT 1

RESULT 121
US-10-208-357-23/c
Sequence 23, Application US/10208357
Publication No. US20020182687A1
GENERAL INFORMATION:
APPLICANT: Kurz, Markus

APPLICANT: Lohse, Peter
APPLICANT: Wagner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/10/208,357
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/09/619,103
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,834
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-23

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1881
Db 17 TTTTATTTTGTGTTT 1

RESULT 122
US-10-053-758-132
Sequence 132, Application US/10053758
Publication No. US20030032075A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-053-758-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTTT 1881
|||||
Db 1 TTTTATTTTGTGTTTT 17

RESULT 123

US-10-054-295-132

; Sequence 132, Application US/10054295

; Publication No. US20030044953A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: NO. US20030044953A1el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/054,295

; FILING DATE: 18-Jan-2002

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/854,050

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 23-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 132:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-054-295-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTTT 1881
|||||
Db 1 TTTTATTTTGTGTTTT 17

RESULT 124

US-10-117-267-5

; Sequence 5, Application US/10117267

; Publication No. US20030045698A1

; GENERAL INFORMATION:

; APPLICANT: Manoharan, Muthiah

; TITLE OF INVENTION: Compounds, Processes And Intermediates For Synthesis Of Mixed Back

; TITLE OF INVENTION: Oligomeric Compounds

; FILE REFERENCE: ISIS-5039

; CURRENT APPLICATION NUMBER: US/10/117,267

; CURRENT FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: 09/726,096

; PRIOR FILING DATE: 2000-11-29

; PRIOR APPLICATION NUMBER: 09/250,075

; PRIOR FILING DATE: 1999-02-12

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 5

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

; NAME/KEY: misc feature

; LOCATION: (1)..(19)

; OTHER INFORMATION: 2'-methoxyethoxy (MOE); phosphorothioate

; OTHER INFORMATION: internucleoside linkage

US-10-117-267-5

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTTT 1881
|||||
Db 1 TTTTATTTTGTGTTTT 17

RESULT 125

US-10-060-756A-4087

; Sequence 4087, Application US/10060756A

; Publication No. US20030046717A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Jian

; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

; FILE REFERENCE: PB0177

; CURRENT APPLICATION NUMBER: US/10/060,756A

; CURRENT FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/327,898
;; PRIOR FILING DATE: 2001-10-09
;; NUMBER OF SEQ ID NOS: 4804
;; SOFTWARE: Acemica Sequence Listing Engine
;; SEQ ID NO 4087
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-060-756A-4087

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2160 AAGCATTGTTCTACT 2176
Db 1 ATGCATTGTTCTACT 17

RESULT 126

US-10-054-611-132
; Sequence 132, Application US/10054611
; Publication No. US20030059787A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

INVENTOR: Lingner, Joachim

INVENTOR: Nakamura, Toru

INVENTOR: Chapman, Karen B.

INVENTOR: Morin, Gregg B.

INVENTOR: Harley, Calvin

INVENTOR: Andrews, William H.

TITLE OF INVENTION: No. US20030059787A1 Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,611

FILING DATE: 18-Jan-2002

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: UNKNOWN

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 132:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-054-611-132

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTCTTTT 1881
Db 1 TTTTATTTTCTTTT 17

RESULT 127

US-10-156-306-1628/c

; Sequence 1628, Application US/10156306

; Publication No. US20030119017A1

; GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

INVENTOR: McSwiggen, James

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

TO INVENTION: Levels of IKK-gamma and PKR

FILE REFERENCE: MEH01-664-A (400/050)

CURRENT APPLICATION NUMBER: US/10/156,306

CURRENT FILING DATE: 2002-05-28

NUMBER OF SEQ ID NOS: 8013

SOFTWARE: Patent In version 3.0

SEQ ID NO 1628

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-10-156-306-1628

Query Match 1.3%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1476 CAGCAGAAAGTTAGTA 1492
Db 17 CTGCAGAAAGATTAGTA 1

RESULT 128

US-09-263-959-971/c

; Sequence 971, Application US/09263959

; Patent No. US20020150891A1

; GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

INVENTOR: Rowen, Lee

INVENTOR: Koop, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

FILING DATE: 05-MAR-1999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 920010.426C2

Fri Apr 2 14:41:47 2004

mcgarry191-19.rnpb

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 971:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-971

Query Match 1.3%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 92;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1811 TGTATATATATATAT 1827
DB 17 TATACATATATATAT 1

RESULT 129
US-10-187-251A-2/c
; Sequence 2, Application US/10187251A
; Publication No. US2003010897A1
; GENERAL INFORMATION:
; APPLICANT: Dmanac, Radoje
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OR QUANTIFICATION OF NUCLE
; FILE REFERENCE: 30311/0018A
; CURRENT APPLICATION NUMBER: US/10/187,251A
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 08/947,779
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: US 08/912,885
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: US 08/892,503
; PRIOR FILING DATE: 1997-07-14
; PRIOR APPLICATION NUMBER: US 08/812,951
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: US 08/784,787
; PRIOR FILING DATE: 1997-01-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-10-187-251A-2

Query Match 1.3%; Score 13.6; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 94;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1863 CCTTTTATTTTG 1876
DB 15 CCTTTTITTTTG 2

RESULT 130
US-08-463-404-51
; Sequence 51, Application US/08463404
; Publication No. US20020127634A1
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,404
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/060,952
; FILING DATE: May 13, 1993
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Waiburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-404-51

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806
DB 1 TGGTGTGTGTGTGTG 15

RESULT 131
US-03-263-959-543/c
; Sequence 543, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hoog, Leroy E.
; APPLICANT: Rower, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mcmasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 543:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-263-959-543

Query Match 1.3%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 99;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
 Db 15 TATATATATATAT 1

RESULT 132
 US-09-263-959-545/c
 Sequence 545, Application US/09263959
 Patent No. US20020150891A1
 GENERAL INFORMATION:
 APPLICANT: Hood, Leroy E.
 APPLICANT: Rowen, Lee
 APPLICANT: Koop, Ben F.
 TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 NUMBER OF SEQUENCES: 1279
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mcmasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 545:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-263-959-545

Query Match 1.3%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 99;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827

Db 15 TATATATATATAT 1

RESULT 133
 US-09-263-959-877/c
 Sequence 877, Application US/09263959
 Patent No. US20020150891A1
 GENERAL INFORMATION:
 APPLICANT: Hood, Leroy E.
 APPLICANT: Rowen, Lee
 APPLICANT: Koop, Ben F.
 TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 NUMBER OF SEQUENCES: 1279
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/263,959
 FILING DATE: 05-MAR-1999

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Mcmasters, David D.
 REGISTRATION NUMBER: 33,963
 REFERENCE/DOCKET NUMBER: 920010.426C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 877:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-263-959-877

Query Match 1.3%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 99;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
 Db 15 TATATATATATATAT 1

RESULT 134
 US-10-287-919-582/c
 Sequence 582, Application US/10287919
 Publication No. US20030085830A1
 GENERAL INFORMATION:
 APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 TITLE OF INVENTION: Methanococcus jannaschii complete genome.
 FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 CURRENT APPLICATION NUMBER: US/10/287,919
 CURRENT FILING DATE: 2002-11-05
 NUMBER OF SEQ ID NOS: 2706
 SOFTWARE: Proprietary
 SEQ ID NO 582
 LENGTH: 15
 TYPE: DNA
 ORGANISM: Methanococcus jannaschii complete genome.
 FEATURE:
 LOCATION: (167867)...(167881)
 OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 690

US-10-287-919-582

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGGTTT 1880
|||||
DB 15 TTTTATTTTGGTTT 1

RESULT 135

US-10-287-919-583/c
; Sequence 583, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 583
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (167867)...(167881)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
; ConnectonObjectNumber = 589

US-10-287-919-583

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGGTTT 1880
|||||
DB 15 TTTTATTTTGGTTT 1

RESULT 136

US-10-287-919-2620/c
; Sequence 2620, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 2620
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1596075)...(1596090)
; OTHER INFORMATION: Chromosome = 1 Strand = positive
; ConnectonObjectNumber = 3341

US-10-287-919-2620

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1879 TTTAATGCTTTGATA 1893
|||||
DB 15 TTTAATGCTTTAATA 1

RESULT 137

US-10-232-927A-79

; Sequence 79, Application US/10232927A
; Publication No. US20030190638A1

; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; Calvin B. Harley
; Scott L. Weinrich
; Catherine M. Strahl
; Michael J. Mceachern
; Jerry Shay
; Woodring E. Wright
; Elizabeth H. Blackburn
; Nam Woo Kim
; Homayoun Vaziri

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
; CONDITIONS RELATED TO
; TELOMERE LENGTH AND/OR
; TELOMERASE ACTIVITY

; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700

; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,927A

; FILING DATE: 29-Aug-2002
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/378,535

; FILING DATE: 20-Aug-1999

; APPLICATION NUMBER: 08/819,867

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Chambers, Daniel M.

; REGISTRATION NUMBER: 34,561

; REFERENCE/DOCKET NUMBER: 224/232

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; INFORMATION FOR SEQ ID NO: 79:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 79:

US-10-232-927A-79

Query Match 1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1792 TTGTGTGTGTGTGTG 1806
|||||
DB 1 TGGTGTGTGTGTGTG 15

RESULT 138

US-10-271-602B-208
; Sequence 208, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
; APPLICANT: Alice Xiang Li

```

; APPLICANT: Ghazala Hashmi
; APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; TITLE OF INVENTION: BY CONCURRENT INTERROGATION AND ENZYME-MEDIATED DETECTION
; FILE REFERENCE: ewap-us
; CURRENT APPLICATION NUMBER: US/10/271.602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; PRIOR FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-208

Query Match      1.3%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1580 TGTAGCCCGCAGTGAC 1594
Db 1 TGTACCCCGCAGTGAC 15

RESULT 139
US-09-263-959-541
; Sequence 541, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 541:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-541

Query Match      1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
Db 16 TATATATATATATAT 2

RESULT 141
US-09-263-959-544
; Sequence 544, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-541

Query Match      1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
Db 1 TATATATATATATAT 15

RESULT 140
US-09-263-959-541/c
; Sequence 541, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 541:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-541

Query Match      1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
Db 16 TATATATATATATAT 2

RESULT 141
US-09-263-959-544
; Sequence 544, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seed and Berry LLP
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: US
;; ZIP: 98104-7092
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/263,959
;; FILING DATE: 05-MAR-1999
;;
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mcmasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 920010.426C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;;
;; INFORMATION FOR SEQ ID NO: 544:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-09-263-959-544

Query Match 1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
Db 1 TATATATGTTATAT 15

RESULT 142
US-09-263-959-544/c
; Sequence 544, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

;; INFORMATION FOR SEQ ID NO: 544:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-09-263-959-544

Query Match 1.3%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATAT 1827
Db 16 TATATATACATATAT 2

RESULT 143
US-09-263-959-508
; Sequence 508, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 508:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;;
;; US-09-263-959-508

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTGT 1805
Db 1 TGTGTGTGTGTGT 13

RESULT 144
US-09-263-959-548
; Sequence 548, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.

APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 548:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-548

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATATA 1826
DB 1 ATATATATATATA 13

RESULT 145
US-09-263-959-548/C
Sequence 548, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 548:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-548

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1813 TATATATATATAT 1825
DB 13 TATATATATATAT 1

RESULT 146
US-09-263-959-704
Sequence 704, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 704:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-704

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGTG 1806
DB 1 GTGTGTGTGTGTG 13

RESULT 147
US-09-263-959-723

```
; Sequence 723, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 723:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-723

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1813 TATATATATATAT 1825
Db 1 TATATATATATAT 13

RESULT 148
US-09-263-959-723/c
; Sequence 723, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
```

```
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 723:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-723

Query Match 1.2%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1814 ATATATATATATA 1826
Db 13 ATATATATATATA 1

RESULT 149
US-08-892-503-1
; Sequence 1, Application US/08892503
; Publication No. US20020042048A1
; GENERAL INFORMATION:
; APPLICANT: Dmanac, Radoje
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
; FILE REFERENCE: 9598-0013-999
; CURRENT APPLICATION NUMBER: US/08/892,503
; CURRENT FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(15)
; OTHER INFORMATION: n = A,T,C or G
; US-08-892-503-1

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1863 CCTTTTATTTTG 1876
Db 1 CCTTTTNTTTTG 14

RESULT 150
US-08-892-503-2/c
; Sequence 2, Application US/08892503
; Publication No. US20020042048A1
; GENERAL INFORMATION:
; APPLICANT: Dmanac, Radoje
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
; FILE REFERENCE: 9598-0013-999
; CURRENT APPLICATION NUMBER: US/08/892,503
; CURRENT FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)...(15)
; OTHER INFORMATION: n = A,T,C or G
US-08-892-503-2

Query Match          1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1863 CCCTTTTATTTTGG 1876
Db 15 CCCTTTTATTTTGG 2

RESULT 151
US-09-918-995-38044
; Sequence 38044, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38044
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence
; OTHER INFORMATION: assembly process
; NAME/KEY: misc feature
; LOCATION: (8)...(8)
; OTHER INFORMATION: n=a, t, c, g or
; OTHER INFORMATION: 1-(2-deoxy-D-ribofuranosyl)-3-nitropyrrrole
US-09-918-995-38044

Query Match          1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1863 CCCTTTTATTTTGG 1876
Db 1 CCCTTTTATTTTGG 14

RESULT 152
US-09-918-995-38045/c
; Sequence 38045, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38045
; LENGTH: 15
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary oligonucleotide primer used in sequence
; OTHER INFORMATION: assembly process
; NAME/KEY: misc feature
; LOCATION: (8)...(8)
; OTHER INFORMATION: n=a, t, c, g or
; OTHER INFORMATION: 1-(2-deoxy-D-ribofuranosyl)-3-nitropyrrrole
US-09-918-995-38045

Query Match          1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1863 CCCTTTTATTTTGG 1876
Db 15 CCCTTTTATTTTGG 2

RESULT 153
US-09-896-095-245/c
; Sequence 245, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 245
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic 805:814 junction
US-09-896-095-245

Query Match          1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1846 ATTAAAGTTGTT 1858
Db 13 ATTAAAGTTGTT 1

RESULT 154
US-10-056-414-121/c
; Sequence 121, Application US/10056414
; Publication No. US2003003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
```

RELATED TO LEVELS OF
NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
US-10-056-414-121

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2152 TCACCTGGAAGCA 2164
DB 15 TCACCTGGAAGCA 3

RESULT 155
US-10-056-414-194/c
Sequence 194, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California

COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-056-414-194

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2152 TCACCTGGAAGCA 2164
DB 15 TCACCTGGAAGCA 3

RESULT 156
US-10-056-414-310/c
Sequence 310, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
RELATED TO LEVELS OF
NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 310:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 310:
US-10-056-414-310

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2152 TCACCTGGAGCA 2164
Db 15 TCACCTGGAGCA 3

RESULT 157

US-10-187-251A-1
Sequence 1, Application US/10187251A
Publication No. US20030108897A1
GENERAL INFORMATION:
APPLICANT: Drmanac, Radoje
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OR QUANTIFICATION OF NUCLEIC ACID SPECIES
FILE REFERENCE: 30311/0015A
CURRENT APPLICATION NUMBER: US/10/187,251A
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US 08/947,779
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: US 08/912,885
PRIOR FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: US 08/892,503
PRIOR FILING DATE: 1997-07-14
PRIOR APPLICATION NUMBER: US 08/812,951
PRIOR FILING DATE: 1997-03-04
PRIOR APPLICATION NUMBER: US 08/784,787
PRIOR FILING DATE: 1997-01-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent in version 3.1
SEQ ID NO 1
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic primer
NAME/KEY: misc feature
LOCATION: (8)
OTHER INFORMATION: n = A or T or G or C or M
US-10-187-251A-1

Query Match 1.2%; Score 13; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.1e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1863 CCTTTTATTG 1876
Db 1 CCTTTTATTG 14

RESULT 158

US-10-191-997-67
Sequence 67, Application US/10191997
Publication No. US20030207834A1
GENERAL INFORMATION:
APPLICANT: Oligos Etc., Inc.
APPLICANT: DALE, Roderic M. K.
APPLICANT: ARROW, Amy
APPLICANT: THOMPSON, Terry
TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their Use
FILE REFERENCE: 54800-5019
CURRENT APPLICATION NUMBER: US/10/191,997
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,820
PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patent in version 3.1
SEQ ID NO 67
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: CD40L oligonucleotide
US-10-191-997-67

Query Match 1.2%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1688 TGACACTGTTTCAG 1700
Db 4 TGACACTGTTTCAG 16

RESULT 159

US-09-739-928-2
Sequence 2, Application US/09739928
Patent No. US20020052482A1
GENERAL INFORMATION:
APPLICANT: Kutyavin, Igor V.
Lukhtanov, Eugeny A.
Gamber, Howard B.
Meyer Jr., Rich B.
TITLE OF INVENTION: Covalently Linked Oligonucleotide Minor Groove Binder Conjugates
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/739,928
FILING DATE: 11-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/415,370
FILING DATE: 03-APR-1995
APPLICATION NUMBER: US 09/141,764

FILING DATE: 27-AUG-1998
APPLICATION NUMBER: US 09/507,345
FILING DATE: 18-FEB-2000
ATTORNEY/AGENT INFORMATION:
NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKET NUMBER: 17682A-003510US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-739-928-2

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 1 TTTTATTTTGTGTTT 16

RESULT 160
US-09-152-059-70
Sequence 70, Application US/09152059
Patent No. US20020068708A1
GENERAL INFORMATION:
APPLICANT: WENGEL, JESPER
APPLICANT: NIELSEN, POUL
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
FILE REFERENCE: 49165 (71994)
CURRENT APPLICATION NUMBER: US/09/152,059
CURRENT FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/058,541
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 60/088,293
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/071,682
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 60/076,591
PRIOR FILING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: 60/083,507
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/088,309
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/094,355
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 70
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
US-09-152-059-70

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 1 TTTTATTTTGTGTTT 16

RESULT 161
US-09-263-959-950
Sequence 950, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 950:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-950

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1866 TTTTATTTTGTGTTT 1881
DB 1 TTTTATTTTGTGTTT 16

RESULT 162
US-09-805-296D-9
Sequence 9, Application US/09805296D
Patent No. US20020155989A1
GENERAL INFORMATION:
APPLICANT: Active Motif
APPLICANT: Efimov, Vladimir
APPLICANT: Fernandez, Joseph
APPLICANT: Archdeacon, Dorothy
APPLICANT: Archdeacon, John
APPLICANT: Chakmakchcheau, Oksana
APPLICANT: Buryakova, Alla
APPLICANT: Choob, Mikhail
APPLICANT: Hondorp, Kyle
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
FILE REFERENCE: AM102.P.1US
CURRENT APPLICATION NUMBER: US/09/805,296D
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: US 60/189,190
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: US 60/250,334
PRIOR FILING DATE: 2000-11-30

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
US-09-805-296D-9

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

RESULT 163
US-09-843-676-131/c
; Sequence 131, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-843-676-131
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 164
US-09-766-253-131/c
; Sequence 131, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-766-253-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 165

```

US-09-438-486-131/c
; Sequence 131, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 08-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-438-486-131
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 16 TTTTATTTTGTGTTT 1

RESULT 166
US-10-208-357-22/c
; Sequence 22, Application US/10208357
; Publication No. US20020182687A1

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; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; APPLICANT: Lohse, Peter
; APPLICANT: Wagner, Richard
; TITLE OF INVENTION: Peptide Acceptor Ligation Methods
; FILE REFERENCE: 50036/031002
; CURRENT APPLICATION NUMBER: US/10/208,357
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/619,103
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/145,834
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: designed sequence for nucleic acid purification
US-10-208-357-22
Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
DB 16 TTTTATTTTGTGTTT 1

RESULT 167
US-10-053-758-131/c
; Sequence 131, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:

```

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-053-758-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
Db 16 TTTTATTTTTTTT 1

RESULT 168
US-10-054-295-131/c
Sequence 131, Application US/10054295
Publication No. US20030044953A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-054-295-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-054-295-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTGTTT 1880
Db 16 TTTTATTTTTTTT 1

RESULT 169
US-10-054-611-131/c
Sequence 131, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-054-611-131

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1880
Db 16 TTTTATTTTGTGTTT 1

RESULT 170

US-10-072-975-9
; Sequence 9, Application US/10072975
; Publication No. US20030059789A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakmakthreau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1.1US
; CURRENT APPLICATION NUMBER: US/10/072,975
; CURRENT FILING DATE: 2002-02-09
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/805,296
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/0811
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc_feature
; OTHER INFORMATION: Synthetic Construct
US-10-072-975-9

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

RESULT 171

US-10-287-919-1350
; Sequence 1350, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1350
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (644443) ... (644458)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-287-919-1350

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1869 TATTTTGTGTTTAAAT 1884
Db 1 TATTTTGTGTTTAAAT 16

RESULT 172

US-10-287-919-2293
; Sequence 2293, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 2293
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1424659) ... (1424675)
; OTHER INFORMATION: Chromosome = 1 Strand = negative
US-10-287-919-2293

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1869 TATTTTGTGTTTAAAT 1884
Db 1 TATTTTGTGTTTAAAT 16

RESULT 173

US-10-227-001-21
; Sequence 21, Application US/10227001
; Publication No. US20030113765A1
; GENERAL INFORMATION:
; APPLICANT: Demcoy, Robert O.
; APPLICANT: Afonina, Irina Aleksandrovna
; APPLICANT: Vermeulen, Nicolaas M.J.
; APPLICANT: Epoch Biosciences, Inc.
; TITLE OF INVENTION: Hybridization-Triggered Fluorescent
; FILE REFERENCE: 17682A-004210US
; CURRENT APPLICATION NUMBER: US/10/227,001
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 09/428,236
; PRIOR FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: R2 (ODN) of fluorophore-MGB-ODN
; OTHER INFORMATION: conjugate
US-10-227-001-21

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1880
Db 1 TTTTATTTTGTGTTT 16

```
Db 1 TTTTATTTTGTGTTT 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Construct
US-10-051-436-9

Query Match 1.2% Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
||||| ||||| |||||
Db 1 TTTTATTTTGTGTTT 16

RESULT 174
US-10-008-029-70
; Sequence 9, Application US/10008029
; Publication No. US2003013480A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/008,029
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-008-029-70

Query Match 1.2% Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
||||| ||||| |||||
Db 1 TTTTATTTTGTGTTT 16

RESULT 175
US-10-051-436-9
; Sequence 9, Application US/10051436
; Publication No. US20030138045A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakmakicheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1US
; CURRENT APPLICATION NUMBER: US/10/051,436
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18

RESULT 176
US-10-208-650-70
; Sequence 70, Application US/10208650
; Publication No. US20030144231A1
; GENERAL INFORMATION:
; APPLICANT: WENGEL, JESPER
; APPLICANT: NIELSEN, POUL
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES
; FILE REFERENCE: 49165-C2(71994)
; CURRENT APPLICATION NUMBER: US/10/208,650
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/10/008,029
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/152,059
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/058,541
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/068,293
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/071,682
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 60/076,591
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: 60/083,507
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/088,309
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/094,355
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-208-650-70

Query Match 1.2% Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1865 TTTTATTTTGTGTTT 1880
||||| ||||| |||||
Db 1 TTTTATTTTGTGTTT 16

RESULT 177
US-10-203-780-9
; Sequence 9, Application US/10203780
; Publication No. US20030165914A1
; GENERAL INFORMATION:
```

APPLICANT: CUZIN, MARC
APPLICANT: BELTIE, PHILIPPE
APPLICANT: FONTECAVE, MARC
APPLICANT: DECOUT, JEAN-LUC
APPLICANT: DUEYMES, CECILE
TITLE OF INVENTION: ANALYSIS OF BIOLOGICAL TARGETS USING A BIOCHIP COMPRISING A FLUOR
TITLE OF INVENTION: MARKER
FILE REFERENCE: 226286USOXPCT
CURRENT APPLICATION NUMBER: US/16/203,780
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: PCT/FR01/00516
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: FR 00 02236
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 16
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: (1) (1)_base
OTHER INFORMATION: t is modified with a covalent linkage to flavin
US-10-203-780-9

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1880
|||||
Db 1 TTTTATTTTGTGTTT 16

RESULT 178
US-10-309-775A-71
Sequence 71, Application US/10309775A
Publication No. US20040006032A1
GENERAL INFORMATION:
APPLICANT: LOPEZ, Ricardo A.
TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND USES THEREOF
FILE REFERENCE: 2901/0M327
CURRENT APPLICATION NUMBER: US/10/309,775A
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: CA 2,388,049
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin version 3.1
SEQ ID NO 71
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
US-10-309-775A-71

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1866 TTTTATTTTGTGTTT 1881
|||||
Db 1 TTTTATTTTGTGTTT 16

RESULT 179
US-10-360-275-9
Sequence 9, Application US/10360275
Publication No. US2004001464A1
GENERAL INFORMATION:
APPLICANT: Active Motif
APPLICANT: Efimov, Vladimir
APPLICANT: Fernandez, Joseph
APPLICANT: Archdeacon, Dorothy
APPLICANT: Archdeacon, John
APPLICANT: Choob, Mikhail
TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: AM102.P.1.1.US
CURRENT APPLICATION NUMBER: US/10/360,275
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 10/072,975
PRIOR FILING DATE: 2002-02-09
PRIOR APPLICATION NUMBER: US 09/805,296
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: US 60/189,190
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthetic Construct
US-10-360-275-9

Query Match 1.2%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1865 TTTTATTTTGTGTTT 1880
|||||
Db 1 TTTTATTTTGTGTTT 16

RESULT 180
US-08-463-404-56
Sequence 56, Application US/08463404
Publication No. US20020127634A1
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,404
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993

APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-404-56

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1793 TGGGTGTGTGTGTG 1806
Db 1 TGGGTGTGTGTGTG 14

RESULT 181
US-09-263-959-530
Sequence 530, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 530:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-530

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATATATATAT 14

RESULT 182
US-09-263-959-530/c
Sequence 530, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 530:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-530

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATATATATAT 14

RESULT 183
US-09-263-959-532
Sequence 532, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATATATATAT 14

RESULT 182
US-09-263-959-530/c
Sequence 530, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 530:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-530

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATATATATAT 14

RESULT 183
US-09-263-959-532
Sequence 532, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 532:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-532

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 14 ATATATATATATAT 1

RESULT 185
US-09-263-959-562
Sequence 562, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 562:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-562

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 14 ATATATCTATATAT 14

RESULT 186
US-09-263-959-562/c
Sequence 562, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 532:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 532:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-532

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 1 ATATATCTATATAT 14

RESULT 184
US-09-263-959-532/c
Sequence 532, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 532:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-532

CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 562:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-562

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 14 ATATATAGATATAT 1

RESULT 187
US-09-263-959-592
Sequence 592, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 592:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-592

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 14 ATATATATGTATAT 14

RESULT 188
US-09-263-959-592/c
Sequence 592, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 592:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-592

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 14 ATATACATATATAT 1

RESULT 189
US-09-263-959-726
Sequence 726, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

; NUMBER OF SEQUENCES: 1279
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/263,959
 ; FILING DATE: 05-MAR-1999
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMasters, David D.
 ; REGISTRATION NUMBER: 33,963
 ; REFERENCE/DOCKET NUMBER: 920010.426C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 726:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-263-959-726

Query Match 1.2%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 1.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1814 ATATATATATATAT 1827
 Db 1 ATATATGATATATAT 14

RESULT 190
 US-09-263-959-726/c
 ; Sequence 726, Application US/09263959
 ; Patent No. US20020150891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hood, Leroy E.
 ; APPLICANT: Rowen, Lee
 ; APPLICANT: Koop, Ben F.
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 ; NUMBER OF SEQUENCES: 1279
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/263,959
 ; FILING DATE: 05-MAR-1999
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMasters, David D.
 ; REGISTRATION NUMBER: 33,963
 ; REFERENCE/DOCKET NUMBER: 920010.426C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 726:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-263-959-726

Query Match 1.2%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 1.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1814 ATATATATATATAT 1827
 Db 14 ATATATACATATAT 1

RESULT 191
 US-09-263-959-730
 ; Sequence 730, Application US/09263959
 ; Patent No. US20020150891A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hood, Leroy E.
 ; APPLICANT: Rowen, Lee
 ; APPLICANT: Koop, Ben F.
 ; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
 ; NUMBER OF SEQUENCES: 1279
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Seed and Berry LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/263,959
 ; FILING DATE: 05-MAR-1999
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McMasters, David D.
 ; REGISTRATION NUMBER: 33,963
 ; REFERENCE/DOCKET NUMBER: 920010.426C2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 730:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-263-959-730

Query Match 1.2%; Score 12.4; DB 1; Length 14;
 Best Local Similarity 92.9%; Pred. No. 1.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1813 TATATATATATATAT 1826
 Db 1 TATATATAATATAT 14

RESULT 192
 US-09-263-959-730/c
 ; Sequence 730, Application US/09263959
 ; Patent No. US20020150891A1
 ; GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESS: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 730:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-730

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 1 ATATATATATATAT 14

RESULT 194
US-09-263-959-752/c
Sequence 752, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 752:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-752

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 1 ATATATATATATAT 14

RESULT 195
US-09-263-959-752/c
Sequence 752, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.

APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESS: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 730:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-730

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1813 TATATATATATATA 1826
DB 14 TATATATATATATA 1

RESULT 193
US-09-263-959-752
Sequence 752, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.

US-09-263-959-764
; Sequence 764, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 764:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-764

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 1 ATATATATATATAT 14

RESULT 196
US-09-263-959-764/c
; Sequence 764, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959

US-09-263-959-822
; Sequence 822, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 822:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-822

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 14 ATATATATATATAT 1

RESULT 197
US-09-263-959-822
; Sequence 822, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 822:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-822

Query Match 1.2%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
DB 14 ATATATATATATAT 1

Db 1 ATATATGTATAT 14

RESULT 198

US-09-263-959-822/c

; Sequence 822, Application US/09263959

; Patent No. US20020150891A1

; GENERAL INFORMATION:

; APPLICANT: Hood, Leroy E.

; APPLICANT: Rowen, Lee

; APPLICANT: Koop, Ben F.

; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

; NUMBER OF SEQUENCES: 1279

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/263,959

; FILING DATE: 05-MAR-1999

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: McWaters, David D.

; REGISTRATION NUMBER: 33,963

; REFERENCE/DOCKET NUMBER: 920010.426C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 822:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-263-959-822

Query Match 1.2%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1814 ATATATATATAT 1827

Db 14 ATATATACATATAT 1

RESULT 199

US-10-232-927A-78

; Sequence 78, Application US/10232927A

; Publication No. US20030190638A1

; GENERAL INFORMATION:

; APPLICANT: Michael D. West

; Calvin B. Harley

; Scott L. Weinrich

; Catherine M. Strahl

; Michael J. Mceachern

; Jerry Shay

; Woodring E. Wright

; Elizabeth H. Blackburn

; Nam Woo Kim

; Homayoun Vaziri

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF

; CONDITIONS RELATED TO

; TELOMERE LENGTH AND/OR

; TELOMERASE ACTIVITY

; NUMBER OF SEQUENCES: 80

US-10-232-927A-78

Query Match 1.2%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1793 TGTGTGTGTGTGTG 1806

Db 1 TGGGTGTGTGTGTG 14

RESULT 200

US-09-263-959-543

; Sequence 543, Application US/09263959

; Patent No. US20020150891A1

; GENERAL INFORMATION:

; APPLICANT: Hood, Leroy E.

; APPLICANT: Rowen, Lee

; APPLICANT: Koop, Ben F.

; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

; NUMBER OF SEQUENCES: 1279

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/263,959

; FILING DATE: 05-MAR-1999

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Chambers, Daniel M.

; REGISTRATION NUMBER: 34,561

; REFERENCE/DOCKET NUMBER: 224/232

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 78:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-10-232-927A-78

Query Match 1.2%; Score 12.4; DB 1; Length 14;

Best Local Similarity 92.9%; Pred. No. 1.3e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 543:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-543

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATGATATAT 14

RESULT 201
US-09-263-959-545
; Sequence 545, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 545:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-263-959-545

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATGATATAT 14

RESULT 203
US-09-877-478-6011/c
; Sequence 6011, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; US-09-877-478-6011/c

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1814 ATATATATATATAT 1827
Db 1 ATATATGATATAT 14

RESULT 203
US-09-877-478-6011/c
; Sequence 6011, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; US-09-877-478-6011/c
```

PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: Patent in version 3.0
SEQ ID NO 6011
LENGTH: 15
TYPE: RNA
ORGANISM: Hepatitis B virus
US-09-877-478-6011

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2095 AATGAACAATGGC 2108
DB 15 ACTGAACAATGGC 2

RESULT 204
US-09-877-478-6085/c
Sequence 6085, Application US/09877478
Publication No. US2003068301A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH00-845-H (400/829)
CURRENT APPLICATION NUMBER: US/09/877,478
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: Patent in version 3.0
SEQ ID NO 6085
LENGTH: 15
TYPE: RNA
ORGANISM: Hepatitis B virus
US-09-877-478-6085

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2095 AATGAACAATGGC 2108
DB 14 ACTGAACAATGGC 1

RESULT 205
US-10-342-902-6011/c
Sequence 6011, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MBH00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: Patent in version 3.2
SEQ ID NO 6011
LENGTH: 15
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-342-902-6011

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2095 AATGAACAATGGC 2108
DB 15 ACTGAACAATGGC 2

RESULT 206
US-10-342-902-6085/c
Sequence 6085, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MBH00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430

;; PRIOR FILING DATE: 1999-11-08
;; NUMBER OF SEQ ID NOS: 6592
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 6085
;; LENGTH: 15
;; TYPE: RNA
;; ORGANISM: Hepatitis B virus
US-10-342-902-6085

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2095 AATGAACAATGGC 2108
DB 14 ACTGACAAATGGC 1

RESULT 207

US-10-287-919-1563/c
; Sequence 1563, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 1563
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.

;; LOCATION: (868160)...(868174)
;; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 1981
US-10-287-919-1563

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1867 TTTATTTTGTGTTT 1880
DB 14 TTTATTTTGTGTTAT 1

RESULT 208

US-10-287-919-2317
; Sequence 2317, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 2317
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.

;; LOCATION: (1438072)...(1438086)
;; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2967
US-10-287-919-2317

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1966 ATGATACTTATAT 1979
DB 1 ATGAAACTTATAT 14

RESULT 209

US-10-287-919-2441/c
; Sequence 2441, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zeeger Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 2441
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.

;; LOCATION: (1512879)...(1512893)
;; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 3130
US-10-287-919-2441

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1867 TTTATTTTGTGTTT 1880
DB 14 TTTATTTTGTGTTAT 1

RESULT 210

US-10-091-281-81/c
; Sequence 81, Application US/10091281
; Publication No. US20030490617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: ST. ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens

;; FEATURE:
;; OTHER INFORMATION: Putative OCTB/TST1.01 motif
US-10-091-281-81

Query Match 1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1535 AAGTGAATTGAGA 1548
DB 14 AAGTGAATTGAAA 1

RESULT 211

US-10-271-602B-184
; Sequence 184, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
; APPLICANT: Alice Xiang Li
; APPLICANT: Ghazala Hashmi

```
; APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; FILE REFERENCE: eWAP-US
; CURRENT APPLICATION NUMBER: US/10/271,602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-184

Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1581 GTAGCCCCAGTGAC 1594
DB 2 GTAGCCCCAGTGAC 15

RESULT 212
US-10-271-602B-192
; Sequence 192, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
; APPLICANT: Alice Xiang Li
; APPLICANT: Ghazala Hashmi
; APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; FILE REFERENCE: eWAP-US
; CURRENT APPLICATION NUMBER: US/10/271,602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-192

Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1581 GTAGCCCCAGTGAC 1594
DB 2 GTAGCCCCAGTGAC 15
```

```
DB 2 GTAGCCCCAGTGAC 15

RESULT 213
US-10-271-602B-200
; Sequence 200, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
; APPLICANT: Alice Xiang Li
; APPLICANT: Ghazala Hashmi
; APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; FILE REFERENCE: eWAP-US
; CURRENT APPLICATION NUMBER: US/10/271,602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe sequence derived from human genomic sequence
US-10-271-602B-200

Query Match      1.2%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1581 GTAGCCCCAGTGAC 1594
DB 2 GTAGCCCCAGTGAC 15

RESULT 214
US-10-271-602B-207
; Sequence 207, Application US/10271602B
; Publication No. US20040002073A1
; GENERAL INFORMATION:
; APPLICANT: Alice Xiang Li
; APPLICANT: Ghazala Hashmi
; APPLICANT: Michael Seul
; TITLE OF INVENTION: MULTIPLEXED ANALYSIS OF POLYMORPHIC LOCI
; FILE REFERENCE: eWAP-US
; CURRENT APPLICATION NUMBER: US/10/271,602B
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,427
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,620
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/329,428
; PRIOR FILING DATE: 2001-10-14
; PRIOR APPLICATION NUMBER: 60/329,619
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/364,416
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 15
```

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Probe sequence derived from human genomic sequence

US-10-271-602B-207

Query Match 1.1%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1580 TGTAGCCCACTGA 1593

Db 1 TGTACCCCACTGA 14

RESULT 215

US-09-735-363A-13

Sequence 13, Application US/09735363A

Patent No. US20010041681A1

GENERAL INFORMATION:

APPLICANT: Fillon, Mario

APPLICANT: Phillip, Nigel

TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides

FILE REFERENCE: 02811-0181

CURRENT APPLICATION NUMBER: US/09/735,363A

CURRENT FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: 60/170,325

PRIOR FILING DATE: 1999-12-13

PRIOR APPLICATION NUMBER: 60/228,925

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PatentIn version 3.0

SEQ ID NO 13

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

US-09-735-363A-13

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Length 12;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTG 1804

Db 1 TGTGTGTGTGTG 12

RESULT 216

US-09-735-363A-14

Sequence 14, Application US/09735363A

Patent No. US20010041681A1

GENERAL INFORMATION:

APPLICANT: Fillon, Mario

APPLICANT: Phillip, Nigel

TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides

FILE REFERENCE: 02811-0181

CURRENT APPLICATION NUMBER: US/09/735,363A

CURRENT FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: 60/170,325

PRIOR FILING DATE: 1999-12-13

PRIOR APPLICATION NUMBER: 60/228,925

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 87

SOFTWARE: PatentIn version 3.0

SEQ ID NO 14

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

US-09-735-363A-14

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1805

Db 1 GTGTGTGTGTGT 12

RESULT 217

US-09-263-959-649

Sequence 649, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Koop, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,959

FILING DATE: 05-MAR-1999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 920010.426C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 649:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-263-959-649

Query Match 1.1%; Score 12; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825

Db 1 ATATATATATAT 12

RESULT 218

US-09-263-959-649/c

Sequence 649, Application US/09263959

Patent No. US20020150891A1

GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.

APPLICANT: Koop, Ben F.

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

City: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 649:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-649

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825
DB 12 ATATATATATAT 1

RESULT 219
US-09-263-959-768
Sequence 768, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 768:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-768

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825
DB 12 ATATATATATAT 1

RESULT 220
US-09-263-959-768/c
Sequence 768, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 768:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-768

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825
DB 12 ATATATATATAT 1

RESULT 221
US-09-263-959-832/c
Sequence 832, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI

NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 832:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-832
Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1793 TGTGTGTGTGTG 1804
Db 12 TGTGTGTGTGTG 1
RESULT 222
US-09-263-959-838/c
Sequence 838, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 832:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-838

TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 838:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-838
Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1793 TGTGTGTGTGTG 1804
Db 12 TGTGTGTGTGTG 1
RESULT 223
US-09-263-959-972/c
Sequence 972, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 972:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-972
Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1793 TGTGTGTGTGTG 1804
Db 12 TGTGTGTGTGTG 1
RESULT 224
US-09-263-959-975/c
Sequence 975, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 975:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-975

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTG 1804
|||||
Db 12 TGTGTGTGTGTG 1

RESULT 225
US-09-263-959-981/c
Sequence 981, Application US/09/263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 981:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-981

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1793 TGTGTGTGTGTG 1804
|||||
Db 12 TGTGTGTGTGTG 1

RESULT 226
US-09-841-157A-11
Sequence 11, Application US/09841157A
Publication No. US20020192648A1
GENERAL INFORMATION:
APPLICANT: NISHIGAKI, KOICHI
APPLICANT: TAKASAWA, TSUTOMU
APPLICANT: HAWANO, KEIICHI
TITLE OF INVENTION: METHODS OF IDENTIFYING AN ORGANISM BASED ON ITS GENOTYPE
FILE REFERENCE: 12637/P66602USO
CURRENT APPLICATION NUMBER: US/09/841,157A
CURRENT FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-841-157A-11

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825
|||||
Db 1 ATATATATATAT 12

RESULT 227
US-09-841-157A-11/c
Sequence 11, Application US/09841157A
Publication No. US20020192648A1
GENERAL INFORMATION:
APPLICANT: NISHIGAKI, KOICHI
APPLICANT: TAKASAWA, TSUTOMU
APPLICANT: HAWANO, KEIICHI
TITLE OF INVENTION: METHODS OF IDENTIFYING AN ORGANISM BASED ON ITS GENOTYPE
FILE REFERENCE: 12637/P66602USO
CURRENT APPLICATION NUMBER: US/09/841,157A
CURRENT FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-841-157A-11

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1814 ATATATATATAT 1825

Db 12 ATATATATATAT 1

RESULT 228

US-10-077-275A-1
; Sequence 1, Application US/10077275A
; Publication No. US20030032028A1
; GENERAL INFORMATION:
; APPLICANT: Dace, Gayle
; APPLICANT: Kimmerly, William
; APPLICANT: Goff, Stephen
; APPLICANT: Oeller, Paul
; TITLE OF INVENTION: In vitro capture of nucleic acids via modified oligonucleotides
; TITLE OF INVENTION: magnetic beads.
; FILE REFERENCE: TM0076-CIP
; CURRENT APPLICATION NUMBER: US/10/077,275A
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 09/879,279
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LNA Homopolymer
US-10-077-275A-1

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1805

Db 1 GTGTGTGTGTGT 12

RESULT 229

US-10-331-780-2/c
; Sequence 2, Application US/10331780
; Publication No. US20030162210A1
; GENERAL INFORMATION:
; APPLICANT: Chetverin, Alexander B.
; APPLICANT: Kramer, Fred Russel
; TITLE OF INVENTION: NOVEL OLIGONUCLEOTIDE ARRAYS AND THEIR USE FOR SORTING,
; TITLE OF INVENTION: ISOLATING, SEQUENCING, AND MANIPULATING NUCLEIC ACIDS
; FILE REFERENCE: 07763-004002
; CURRENT APPLICATION NUMBER: US/10/331,780
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/08/473,010
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/247,530
; PRIOR FILING DATE: 1994-05-25
; PRIOR APPLICATION NUMBER: US 07/833,607
; PRIOR FILING DATE: 1992-02-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically derived DNA
US-10-331-780-2

Query Match 1.1%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1794 GTGTGTGTGTGT 1805

Db 12 GTGTGTGTGTGT 1

RESULT 230

US-09-877-478-6010/c
; Sequence 6010, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6010
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-6010

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2097 TGAACAAATGGC 2108

Db 14 TGAACAAATGGC 3

RESULT 231

US-09-848-754A-9167/c
; Sequence 9167, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9167
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-9167

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2059 TGATTCTAGGT 2070
Db 15 TGATTCTAGGT 4

RESULT 232
US-10-342-902-6010/c
Sequence 6010, Application US/10342902
Publication No. US20040054156A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MBH00-845-1)
CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6010
LENGTH: 15
TYPE: RNA
ORGANISM: Hepatitis B virus
US-10-342-902-6010

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2097 TGAACAAATGCC 2108
Db 14 TGAACAAATGCC 3

RESULT 233
US-10-056-414-120/c
Sequence 120, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,414
FILING DATE: 23-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 120:
US-10-056-414-120

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAGCA 2164
Db 15 CACCTGGAGCA 4

RESULT 234
US-10-056-414-193/c
Sequence 193, Application US/10056414
Publication No. US20030003469A1
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage


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;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,414
; FILING DATE: 23-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,932A
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 193:
US-10-056-414-193

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 235
US-10-056-414-309/c
; Sequence 309, Application US/10056414
; Publication No. US20030003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; Draper, Kenneth G.
; MCSwiggan, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; RELATED TO LEVELS OF
; NF-KB
; NUMBER OF SEQUENCES: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,414
; FILING DATE: 23-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/291,932A
```

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;
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 309:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 309:
US-10-056-414-309

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2153 CACCTGGAAGCA 2164
Db 15 CACCTGGAAGCA 4

RESULT 236
US-10-287-919-590/c
; Sequence 590, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
; SEQ ID NO 590
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (174470)...(174484)
; OTHER INFORMATION: Chromosome = 1 Strand = positive
US-10-287-919-590

Query Match 1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1892 TATTTCAATGTT 1903
Db 14 TATTTCAATGTT 3

RESULT 237
US-10-287-919-2049/c
; Sequence 2049, Application US/10287919
; Publication No. US20030085830A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,919
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 2706
; SOFTWARE: Proprietary
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; SEQ ID NO 2049
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii complete genome.
; FEATURE:
; LOCATION: (1247186)...(1247200)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectionObjectNumber = 2622
US-10-287-919-2049

Query Match      1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1892 TATTCAATGTT 1903
      |||||
Db      14 TATTCAATGTT 3

RESULT 238
US-10-041-414-52/c
; Sequence 52, Application US/10041414
; Publication No. US20030087225A1
; GENERAL INFORMATION:
; APPLICANT: SHIVER, JOHN W.
; DAVIES, MARY ELLEN
; FREED, DANIEL C.
; LIU, MARGARET A.
; PERRY, HELEN C.
; TITLE OF INVENTION: SYNTHETIC HIV ENV GENES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/041,414
; FILING DATE: 08-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,368
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3905
; TELEFAX: 732-594-4720
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-041-414-52

Query Match      1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1521 ATGCCTGCTATT 1532
      |||||
Db      13 ATGCCTGCTATT 2

US-10-369-121-51/c
; Sequence 51, Application US/10369121
; Publication No. US20030229214A1
; GENERAL INFORMATION:
; APPLICANT: SHIVER, JOHN W.
; LIU, MARGARET A.
; PERRY, HELEN C.
; DAVIES, MARY-ELLEN M.
; FREED, DANIEL C.
; TITLE OF INVENTION: VACCINES COMPRISING SYNTHETIC GENES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/369,121
; FILING DATE: 17-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,798A
; FILING DATE: 28-Jun-1999
; APPLICATION NUMBER: US/08/877,418
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J. MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19729Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-369-121-51

Query Match      1.1%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1521 ATGCCTGCTATT 1532
      |||||
Db      13 ATGCCTGCTATT 2

Search completed: April 2, 2004, 14:38:06
Job time : 4 secs
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